

CC from N. meningitidis strain EG329 is 1 of 10 Nhma polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.

XX Sequence 591 AA:

Query Match 98.7%; Score 2720; DB 22; Length 591;
Best Local Similarity 99.1%; Pred. No. 4.3e-157;
Matches 535; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NNEOEELYLHPVORTVAALIVNSDKREGAGEKEKEVENSMDAVYNEKEGYLAREITLK 60
DB 52 NNEOEEDLYLDPVORTVAALIVNSDKREGAGEKEKEVENSMDAVYNEKEGYLAREITLK 111
QY 61 AGDLKIKONGTNETYSLKDLDTLSVTEKLSFSHANGKVNITSTPKGLNFAKEAGT 120
DB 112 AGDLKIKONGTNETYSLKDLDTLSVTEKLSFSHANGKVNITSTPKGLNFAKEAGT 171
QY 121 NGDTVHLNGIGSTLDTLNTGATNTVNDVYDDEKKRAASVKDVLNAGWNIKGYKPG 180
DB 172 NGDTVHLNGIGSTLDTLNTGATNTVNDVYDDEKKRAASVKDVLNAGWNIKGYKPG 231
QY 181 TTASDNVDFVRYDYVEFLSADRTKTTVNVESKDNKGKTEYKIGAKTSVKEKDKGLVTG 240
DB 232 TTASDNVDFVRYDYVEFLSADRTKTTVNVESKDNKGKTEYKIGAKTSVKEKDKGLVTG 291
QY 241 KDKGENSSSTDEGEGLTAKEDVAVKAGMRKTTTANGOTGADFEYVTSCTNTFA 300
DB 292 KDKGENSSSTDEGEGLTAKEDVAVKAGMRKTTTANGOTGADFEYVTSCTNTFA 351
QY 301 SGKGTATVSKDDOGNTTVMYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKYISGNVSP 360
DB 352 SGKGTATVSKDDOGNTTVMYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKYISGNVSP 411
QY 361 SKRKMETVYVNNAGNIEITRNKNDIATSKTPPOSSVSLGAGADAPTLSPGDALNVG 420
DB 412 SKRKMETVYVNNAGNIEITRNKNDIATSKTPPOSSVSLGAGADAPTLSPGDALNVG 471
QY 421 SKRKNPVRTTNAPGVKEDGVNVAOLKGAQNLNRINNVGNARAGIAOAIATAGLV 480
DB 472 SKRKNPVRTTNAPGVKEDGVNVAOLKGAQNLNRINNVGNARAGIAOAIATAGLV 531
QY 481 QAVLPKSMMAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYQW 540
DB 532 QAVLPKSMMAIGGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYQW 591

RESULT 6

AAV57045
ID AAV57045 standard; Protein; 591 AA.

XX AAV57045;

XX 21-FEB-2000 (first entry)

DE BASB029 amino acid sequence from N. meningitidis strain H44/76.

XX BASB029; Nisseria meningitidis; surface fibril protein; HSP; diagnosis;

KW Infection; treatment; prevent; antibacterial drug.

XX Neisseria meningitidis.

XX Key Location/Qualifiers

FT MISC-difference 90 /note- "Encoded by AAT"

FT MISC-difference 92 /note- "Encoded by GAT"

FT MISC-difference 98 /note- "Encoded by AAC"

FT MISC-difference 108 /note- "Encoded by AATC"

FT MISC-difference 123 /note- "Encoded by ACA"

FT MISC-difference 269 /note- "Encoded by AAA"
FT MISC-difference 389 /note- "Encoded by CGT"
XX

PN W09958683-A2.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-EP03255.

XX 13-MAY-1998; 98GB-0010276.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Ruelle J;

XX WPI; 2000-053103/04.

DR N-PSDB; AA239865.

PT New polypeptide from neisseria meningitidis useful for diagnosis,
treatment or prevention of bacterial infections in mammal

XX Claim 4; Fig 2; 74pp; English.

CC This is the Nisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSP) protein. The invention
CC relates to BASB029 polynucleotide sequences (AA239864-239865) and
CC polypeptide sequences (AAV57044-V57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.

XX Sequence 591 AA;

Query Match 98.1%; Score 2705; DB 21; Length 591;
Best Local Similarity 98.3%; Pred. No. 3.5e-156;

Matches 531; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNEOEELYLHPVORTVAALIVNSDKREGAGEKEKEVENSMDAVYNEKEGYLAREITLK 60
DB 52 NNEOEEDLYLDPVORTVAALIVNSDKREGAGEKEKEVENSMDAVYNEKEGYLAREITLK 111
QY 61 AGDLKIKONGTNETYSLKDLDTLSVTEKLSFSHANGKVNITSTPKGLNFAKEAGT 120
DB 112 AGDLKIKONGTNETYSLKDLDTLSVTEKLSFSHANGKVNITSTPKGLNFAKEAGT 171
QY 121 NGDTVHLNGIGSTLDTLNTGATNTVNDVYDDEKKRAASVKDVLNAGWNIKGYKPG 180
DB 172 NGDTVHLNGIGSTLDTLNTGATNTVNDVYDDEKKRAASVKDVLNAGWNIKGYKPG 231
QY 181 TTASDNVDFVRYDYVEFLSADRTKTTVNVESKDNKGKTEYKIGAKTSVKEKDKGLVTG 240
DB 232 TTASDNVDFVRYDYVEFLSADRTKTTVNVESKDNKGKTEYKIGAKTSVKEKDKGLVTG 291
QY 241 KDKGENSSSTDEGEGLTAKEDVAVKAGMRKTTTANGOTGADFEYVTSCTNTFA 300
DB 292 KDKGENSSSTDEGEGLTAKEDVAVKAGMRKTTTANGOTGADFEYVTSCTNTFA 351
QY 301 SGKGTATVSKDDOGNTTVMYDVNVGDALNVNOLNSGWNLDKRAVAGSSGKYISGNVSP 360

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Db      352  SGKGTATATVSKDDGNITVMDVNVGDLNVNOLNSGMNLDKSKAVAGSSGKVIISGNVSP 411
OY      361  SKGKMDFTVNIAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGDALNVG 420
Db      412  SKGKMDFTVNIAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGDALNVG 471
OY      421  SRKDNKPVRTITNVAAPGVKEGDVTNVVQOLKGVAAQNLNRRIDNVGNARAGIAQAIATAGLV 480
Db      472  SKRDNKPVRTITNVAAPGVKEGDVTNVVQOLKGVAAQNLNRRIDNVGNARAGIAQAIATAGLV 531
OY      481  QAVLPKSKMAIIGGTYRGEAGYAIQYSSISDGMWIIKGTASGNSRGHFGASASVGYQW 540
Db      532  QAVLPKSKMAIIGGTYRGEAGYAIQYSSISDGMWIIKGTASGNSRGHFGASASVGYQW 591

RESULT 7
AAV23737
ID      AAV23737 standard; Protein; 592 AA.
AC      AAV23737;
XX      08-SEP-1999 (first entry)
DE      A surface protein of Neisseria meningitidis.
XX      Surface protein; surface glycoprotein; infection; vaccine;
KM      Immunoreactive peptide.
XX      Neisseria meningitidis.
OS      Neisseria meningitidis.
PN      WO9931132-A1.
XX      24-JUN-1999.
PD      14-DEC-1998; 98WO-AU01031.
XX      12-DEC-1997; 97GB-0026398.
PR      (ISIS-) ISIS INNOVATION LTD.
PA      (UYOU) UNITV QUEENSLAND.
XX      Jennings MP, Moxon ER, Peak IRA;
PI      WPI; 1999-418754/35.
XX      DR      N-PSDB; AAX85788.
XX      PT      Neisseria meningitidis surface proteins useful for treating N.
PT      meningitidis infections
XX      Claim 1; Page 86-87; 132pp; English.
PS      The present sequence represents a surface protein of Neisseria
XX      meningitidis which is approximately 62 kDa. The N. meningitidis
CC      surface glycoproteins, nucleic acids, the primers and optionally
CC      a thermostable polymerase, or antibodies are useful in a kit for
CC      the detection or diagnosis of N. meningitidis infection in humans.
CC      The N. meningitidis surface glycoproteins can also be used to
CC      prevent or treat N. meningitidis infection in humans, especially
CC      in the form of vaccines. The proteins and antibodies can also
CC      be used to identify immunoreactive peptides.
XX      CC
SQ      Sequence 592 AA;
Query Match 97.8%; Score 2695.5; DB 20; Length 592;
Best Local Similarity 98.2%; Pred. No. 13e-155;
Matches 531; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
OY      1 NNEE-OEEYLYLHPQRTVAVLIVNSDEKAGEKEKVENSDMAVYFNKGVLTAREITL 59
DB      52 NNERRRKDLVDYDQRTVAVLIVNSDEKAGEKEKVENSDMAVYFNKGVLTAREITL 111
OY      60 KAGDNLKIKONGTFTYSLKDLDTLTSVGTETKLSFSAHGKNVITSDTKGLNFAKETAG 119

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Db      112  KAGDNLKIKONGTFTYSLKDLDTLTSVGTETKLSFSAHGKNVITSDTKGLNFAKETAG 171
OY      120  TNGDTTVLNGIGSTLPTTLNTGATTVNTNDNTJDDKKRAASVKVDLNGWNIKGVKP 179
Db      172  TNGDTTVLNGIGSTLPTTLNTGATTVNTNDNTJDDKKRAASVKVDLNGWNIKGVKP 231
OY      180  GTTASDNVDVFRYTDVTEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVIREKDKLVT 239
Db      232  GTTASDNVDVFRYTDVTEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVIREKDKLVT 291
OY      240  GKDKGENSSYDDEGEGLYTAKEVIDAVNKKAGMRKTTTANQOTQADKFEVTSGTNVTF 299
Db      292  GKDKGENSSYDDEGEGLYTAKEVIDAVNKKAGMRKTTTANQOTQADKFEVTSGTNVTF 351
OY      300  ASGKGTATVSKDDGNITVMDVNVGDLNVNOLNSGMNLDKSKAVAGSSGKVIISGNVSP 359
Db      352  ASGKGTATVSKDDGNITVMDVNVGDLNVNOLNSGMNLDKSKAVAGSSGKVIISGNVSP 411
OY      360  PSKGMDETVNIAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGDALNV 419
Db      412  PSKGMDETVNIAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDGDALNV 471
OY      420  GSKKDNKPVRTITNVAAPGVKEGDVTNVVQOLKGVAAQNLNRRIDNVGNARAGIAQAIATAGL 479
Db      472  GSKKDNKPVRTITNVAAPGVKEGDVTNVVQOLKGVAAQNLNRRIDNVGNARAGIAQAIATAGL 531
OY      480  VQAVLPKSKMAIIGGTYRGEAGYAIQYSSISDGMWIIKGTASGNSRGHFGASASVGYQ 539
Db      532  VQAVLPKSKMAIIGGTYRGEAGYAIQYSSISDGMWIIKGTASGNSRGHFGASASVGYQ 591
OY      540  W 540
Db      592  W 592

RESULT 8
AAV23740
ID      AAV23740 standard; Protein; 594 AA.
AC      AAV23740;
XX      08-SEP-1999 (first entry)
DE      A surface protein of Neisseria meningitidis.
XX      Surface protein; surface glycoprotein; infection; vaccine;
KM      Immunoreactive peptide.
XX      Neisseria meningitidis.
OS      Neisseria meningitidis.
PN      WO9931132-A1.
XX      24-JUN-1999.
PD      14-DEC-1998; 98WO-AU01031.
XX      12-DEC-1997; 97GB-0026398.
PR      (ISIS-) ISIS INNOVATION LTD.
PA      (UYOU) UNITV QUEENSLAND.
XX      Jennings MP, Moxon ER, Peak IRA;
PI      WPI; 1999-418754/35.
XX      DR      N-PSDB; AAX85792.
XX      PT      Neisseria meningitidis surface proteins useful for treating N.
PT      meningitidis infections
XX      Claim 1; Page 100-101; 132pp; English.
XX      The present sequence represents a surface protein of Neisseria
CC

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CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.

XX Sequence 594 AA:

Query Match 91.1%; Score 2512; DB 20; Length 594;
 Best Local Similarity 92.4%; Pred. No. 1.8e-144;
 Matches 501; Conservative 13; Mismatches 20; Indels 8; Gaps 3;

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QY 6 EEVLYHPVQRTVAVLIVNSDKGAGEKEKEVENSMDAVYENKGVLTAREITLKAGDNL 65
DB 54 DDDLYLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNMGVYFDKKGVLTAETITLKAGDNL 112
QY KIKQ-----NGTNFTYSLKKDLTDLTSVTEKLSFSAHGKNVITSDFKGLNFAKETAG 119
DB 113 KIKQNTNEMNTASSFTYSLKKDLTDLTSVTEKLSFSAHGKNVITSDFKGLNFAKETAG 172
QY 120 TNGDTTVHLNGISLTLDLTLNTGATTNTVNDVTDDEKKRAASVCDVLAAGNNIKGVP 179
DB 173 TNGDTTVHLNGISLTLDLTLNTGATTNTVNDVTDDEKKRAASVCDVLAAGNNIKGVP 232
QY 180 GTTASDNVDFVRYTDFVEFLSADTKTTTVVESKDNKGKTEVIGAKTSYIKERDGLVT 239
DB 233 GTTASDNVDFVRYTDFVEFLSADTKTTTVVESKDNKGKTEVIGAKTSYIKERDGLVT 292
QY 240 GKDKEGNSSTDEGEGLVTAKEVIDAVNKGMRKTTTANGQGTQADKFEFTVSGTNVTF 299
DB 293 GKDKEGNSSTDEGEGLVTAKEVIDAVNKGMRKTTTANGQGTQADKFEFTVSGTNVTF 352
QY 300 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVIISGNVS 359
DB 353 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVIISGNVS 412
QY 360 PSKGGKDEVTNINAGNNIETTRNGKNIDTATSMTPQSSVSLGAGADAPLSTADG-ALN 418
DB 413 PSKGGKDEVTNINAGNNIETTRNGKNIDTATSMTPQSSVSLGAGADAPLSTADG-ALN 472
QY 419 VGSKKRNKPYRTNVAAPGVEGSDVTNVAOLKGAONLNINIDVNDGNARAGIAQATATAG 478
DB 473 VGSKKRNKPYRTNVAAPGVEGSDVTNVAOLKGAONLNINIDVNDGNARAGIAQATATAG 532
QY 479 LVQAYLPGKSMAGIGGTYRGEAGYVAGYSSISDGGNMIKTGASGNSRCHFGASASVGY 538
DB 533 LVQAYLPGKSMAGIGGTYRGEAGYVAGYSSISDGGNMIKTGASGNSRCHFGASASVGY 592
QY 539 QW 540
DB 593 QW 594

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RESULT 9

AAV57044 standard; Protein; 594 AA.

AAV57044;

21-FEB-2000 (first entry)

BASB029 amino acid sequence from N. meningitidis strain ATCC13090.

BASB029; *Neisseria meningitidis*; surface fibril protein; HSF; diagnosis;
 infection; treatment; prevent; antibacterial drug.

Neisseria meningitidis.

Key Location/Qualifiers
 Misc-difference 104

/note="Encoded by AATC"

W09958683-A2.

18-NOV-1999.

07-MAY-1999; 99MO-EP03255.

13-MAY-1998; 98GB-0010276.

(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

Ruelle J;

WPI: 2000-053103/04.

DR N-P-SDB: AAZ39864.

New polypeptide from *Neisseria meningitidis* useful for diagnosis,
 treatment or prevention of bacterial infections in mammal

Claim 4; Fig 2; 74pp; English.

This is the *Neisseria meningitidis* BASB029 amino acid sequence from
 CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the
 CC Hemophilus influenzae surface fibril (HSF) protein. The invention
 CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
 CC polypeptide sequences (AAV57044-y57045) and their immunogenic fragments.
 CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*
 CC meningitidis infection in a mammal. Compositions containing BASB029
 CC polynucleotides and polypeptides are useful for generating an immune
 CC response in an animal. A therapeutic composition comprising an antibody
 CC directed against BASB029 is useful in treating humans with *Neisseria*
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of
 CC the stage of infection, type of infection, susceptibility to an
 CC infection which results from increased or decreased expression of the
 CC polynucleotide, and for therapeutic or prophylactic purposes,
 CC particularly genetic immunisation. Antibodies against BASB029
 CC polynucleotides and polypeptides are also useful for treating infections
 CC particularly bacterial infections. The protein is useful in the
 CC screening and development of antibacterial drugs. Pused recombinant
 CC protein is useful for the stimulation of the immune system of an organism
 CC receiving the protein.

XX Sequence 594 AA:

Query Match 91.1%; Score 2512; DB 21; Length 594;
 Best Local Similarity 92.4%; Pred. No. 1.8e-144;
 Matches 501; Conservative 13; Mismatches 20; Indels 8; Gaps 3;

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QY 6 EEVLYHPVQRTVAVLIVNSDKGAGEKEKEVENSMDAVYENKGVLTAREITLKAGDNL 65
DB 54 DDDLYLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNMGVYFDKKGVLTAETITLKAGDNL 112
QY KIKQ-----NGTNFTYSLKKDLTDLTSVTEKLSFSAHGKNVITSDFKGLNFAKETAG 119
DB 113 KIKQNTNEMNTASSFTYSLKKDLTDLTSVTEKLSFSAHGKNVITSDFKGLNFAKETAG 172
QY 120 TNGDTTVHLNGISLTLDLTLNTGATTNTVNDVTDDEKKRAASVCDVLAAGNNIKGVP 179
DB 173 TNGDTTVHLNGISLTLDLTLNTGATTNTVNDVTDDEKKRAASVCDVLAAGNNIKGVP 232
QY 180 GTTASDNVDFVRYTDFVEFLSADTKTTTVVESKDNKGKTEVIGAKTSYIKERDGLVT 239
DB 233 GTTASDNVDFVRYTDFVEFLSADTKTTTVVESKDNKGKTEVIGAKTSYIKERDGLVT 292
QY 240 GKDKEGNSSTDEGEGLVTAKEVIDAVNKGMRKTTTANGQGTQADKFEFTVSGTNVTF 299
DB 293 GKDKEGNSSTDEGEGLVTAKEVIDAVNKGMRKTTTANGQGTQADKFEFTVSGTNVTF 352
QY 300 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVIISGNVS 359
DB 353 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVIISGNVS 412

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OY 360 PSKGMDETVNINAGNNIEITRNKNIDIAISMTPOESSVSLGAGADAPTLISVGD-ALN 418
XX |||
DB 413 PSKGMDETVNINAGNNIEITRNKNIDIAISMTPOESSVSLGAGADAPTLISVDEGALN 472
OY 419 VGSKKDNKPVRLITNAPGVKEGADVTVNAQLGVAGNLLNRRIDNVDGNARAGIAQAIATAG 478
DB 473 VGSKDNKPVRLITNAPGVKEGADVTVNAQLGVAGNLLNRRIDNVDGNARAGIAQAIATAG 532
OY 479 LVQAYLPGKSMMAIGGTYRGEGAGYAIGYSSISDGNMIKGTASGNSRGHFGASASVGY 538
DB 533 LVQAYLPGKSMMAIGGTYRGEGAGYAIGYSSISDGNMIKGTASGNSRGHFGASASVGY 592
OY 539 QW 540
DB 593 QW 594

RESULT 10
AAU06174
ID AAU06174 standard; Protein; 594 AA.
XX
AC AAU06174;
XX
DE 24-OCT-2001 (first entry)
XX
DE N. meningitidis EG327 surface antigen Nhma polypeptide sequence.
XX
KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain EG327.
XX
FH Key
FT Location/Qualifiers
FT /label= C1
FT /note= "Conserved region 1"
FT /label= V1
FT /note= "Variable region 1"
FT /label= C2
FT /note= "Conserved region 2"
FT /label= V2
FT /note= "Variable region 2"
FT /label= C3
FT /note= "Conserved region 3"
FT /label= V3
FT /note= "Variable region 3"
FT /label= C4
FT /note= "Conserved region 4"
FT /label= V4
FT /note= "Variable region 4"
FT /label= C5
FT /note= "Conserved region 5"
XX
PM W020015182-AL.
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYOU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI; 2001-488774/53.
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DR N-PSDB; AAS09164.
XX
PT New Nhma surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 9; Fig 1; 91pp: English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhma
CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhma
CC from N. meningitidis strain EG327 is 1 of 10 Nhma polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 594 AA:
XX
Query Match 91.1%; Score 2512; DB 22; Length 594;
Best Local Similarity 92.4%; Pred. No. 1.8e-144;
Matches 501; Conservative 13; Mismatches 20; Indels 8; Gaps 3;
OY 6 EEYLTHPVORTVAVLIYNSDKEGAGEKEKEENSMAVYENKGVTLAREITLAKAGNTL 65
DB 54 DDDLYLEPVQRAVAVLSRSDQEGTEKE-VTESSNMVQVYDKKGVLLAGITTLKAGNTL 112
OY 66 KIKQ-----NGTNETYSLKKDLDLTSVGTETLSFSAHGKRVNTSDTKLNFAKETAG 119
DB 113 KIKONTNNTNNTASSFTYSLKKDLDLTSVGTETLSFSAHNSKVNITSPDKLNFARKRAE 172
OY 120 TNGDTVHLNGIGSTLDTLNLNGATTVNTNDVNTDDEKKRAASVQVYLAAGNMIKGVK 179
DB 173 TNGDTVHLNGIGSTLDTLNLNGATTVNTNDVNTDDEKKRAASVQVYLAAGNMIKGVK 232
OY 180 GTTASDNDVFRYDTVFEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLYT 239
DB 233 GTTASDNDVFRYDTVFEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLYT 292
OY 240 GKDKGENSSYDDEGGLYTAKEVIDAVNKAQRMTTANGOTGQADKFEFVTSNTVF 299
DB 293 GKDKGENSSYDDEGGLYTAKEVIDAVNKAQRMTTANGOTGQADKFEFVTSNTVF 352
OY 300 ASGKGTATVSKDDGNTTVMYDVNVGDALNVNQLNSGMWLDKRAVAGSSGKVIISGNVS 359
DB 353 ASGKGTATVSKDDGNTTVMYDVNVGDALNVNQLNSGMWLDKRAVAGSSGKVIISGNVS 412
OY 360 PSKGMDETVNINAGNNIEITRNKNIDIAISMTPOESSVSLGAGADAPTLISVGD-ALN 418
DB 413 PSKGMDETVNINAGNNIEITRNKNIDIAISMTPOESSVSLGAGADAPTLISVDEGALN 472
OY 419 VGSKKDNKPVRLITNAPGVKEGADVTVNAQLGVAGNLLNRRIDNVDGNARAGIAQAIATAG 478
DB 473 VGSKDNKPVRLITNAPGVKEGADVTVNAQLGVAGNLLNRRIDNVDGNARAGIAQAIATAG 532
OY 479 LVQAYLPGKSMMAIGGTYRGEGAGYAIGYSSISDGNMIKGTASGNSRGHFGASASVGY 538
DB 533 LVQAYLPGKSMMAIGGTYRGEGAGYAIGYSSISDGNMIKGTASGNSRGHFGASASVGY 592
OY 539 QW 540
DB 593 QW 594

RESULT 11
AAU23739
ID AAU23739 standard; Protein; 594 AA.
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XX AAY23739;
 AC 08-SEP-1999 (first entry)
 DT A surface protein of Neisseria meningitidis.
 DE A surface protein of Neisseria meningitidis.
 XX Surface protein: surface glycoprotein; infection; vaccine;
 KM Immunoreactive peptide.
 OS Neisseria meningitidis.
 XX WO9931132-A1.
 PN 24-JUN-1999.
 XX PD 14-DEC-1998; 98WO-AU01031.
 PF 12-DEC-1997; 97GB-0026398.
 PR (ISIS-) ISIS INNOVATION LTD.
 PA (UYOU) UNIV QUEENSLAND.
 XX Jennings MP, Moxon ER, Peak IRA;
 PI WPI: 1999-418754/35.
 DR N-PSDB; AAX65791.
 XX Neisseria meningitidis surface proteins useful for treating N.
 PT meningitidis infections
 PS Claim 1; Page 95-97; 132pp; English.
 XX The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 XX
 XX Sequence 594 AA;
 SO
 Query Match 90.4%; Score 2493; DB 20; Length 594;
 Best Local Similarity 91.6%; Pred. No. 2.6e-143;
 Matches 500; Conservative 9; Mismatches 29; Indels 8; Gaps 3;

QY 356 GNVSPSKGKDEYVINAANNIEITRNGKNIDATSMTPQFSSVSLGADAPTLSDYGD 415
 DB 409 GNVSPSKGKDEYVINAANNIEITRNGKNIDATSMAPQFSSVSLGADAPTLSDYDE 468
 QY 416 -ALNVGSKKONKPVRTINVAEGVEGDTNVAQLKVAQININRIDVNGNARAGIAQAI 474
 DB 469 GALNVGSKDTRKPVRTINVAAGVEGDTNVAQLKVAQININRIDVNGNARAGIAQAI 528
 QY 475 ATAGLVQAYLPKSKMAIGGTYRGEAGYALGSSISDGGWITIKGTASGNSRGHFGASA 534
 DB 529 ATAGLVQAYLPKSKMAIGGTYRGEAGYALGSSISDGGWITIKGTASGNSRGHFGASA 588
 QY 535 SVGYQW 540
 DB 589 SVGYQW 594
 RESULT 12
 AAU06179
 ID AAU06179 standard; Protein: 594 AA.
 XX AAU06179;
 AC 24-OCT-2001 (first entry)
 DT N. meningitidis BZ198 surface antigen Nhha polypeptide sequence.
 XX N. meningitidis BZ198 surface antigen Nhha polypeptide sequence.
 DE Surface antigen Nhha; meningococcal disease; meningitis vaccine.
 KM Neisseria meningitidis strain BZ198.
 OS
 XX location/Qualifiers
 FH 1..50
 FT /label=C1
 FT /note="Conserved region 1"
 FT 51..104
 FT /label=V1
 FT /note="Variable region 1"
 FT 105..116
 FT /label=C2
 FT /note="Conserved region 2"
 FT 117..126
 FT /label=V2
 FT /note="Variable region 2"
 FT 127..190
 FT /label=C3
 FT /note="Conserved region 3"
 FT 191..212
 FT /label=V3
 FT /note="Variable region 3"
 FT 213..231
 FT /label=C4
 FT /note="Conserved region 4"
 FT 232..238
 FT /label=V4
 FT /note="Variable region 4"
 FT 239..354
 FT /label=C5
 FT /note="Conserved region 5"
 MO200155182-A1.
 PD 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-AU00069.
 PF 25-JAN-2000; 2000US-0177917.
 PR (UYOU) UNIV QUEENSLAND.
 PA Jennings MP;
 XX Peak IRA, Jennings MP;
 PI WPI: 2001-48874/53.
 DR

DR N-PSDB; AAS09169.
XX
PT New NhbA surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX
PS Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen NhbA
CC (AAU06182-AAU06186). The modified or mutant NhbA polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen NhbA
CC from N. meningitidis strain B2198 is 1 of 10 NhbA polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
XX

SO Sequence 594 AA:

Query Match 90.4%; Score 2493; DB 22; Length 594;
Best Local Similarity 91.6%; Pred. No. 2,6e-143;
Matches 500; Conservative 9; Mismatches 29; Indels 8; Gaps 3;

QY 2 NEEDEBYLYLHPVORTAVAVLIVNSDKEGAGEKEKEVENSMAVFNKGVLTARETTKA 61
DB 50 NATDDDDLYLEPVQRTAVAVLSFRSDKEGEGEGED-SNMAVYFDEKRVLAAGAITTLKA 108
QY 62 GDNLIKIQ-----NGTNETYSILKKDLTDLTSVGEKISFSAHGKVNITSDTKGLNFAK 115
DB 109 GDNLIKQNTMENTNMENTDSSFTYSLKKDLTDLTSVEFEKLSFGANGKKNVITSDTKGLNFAK 168
QY 116 ETAGNGDTTVHLNGIGSTLTDLTLLNTGATTVNTDNDVTDDEKRRASVYKDVNLNAGWNIK 175
DB 169 ETAGNGDTTVHLNGIGSTLTDLTLLNTGATTVNTDNDVTDDEKRRASVYKDVNLNAGWNIK 228
QY 176 GYKPGTTASDNDVFRYDVEFLSADRTTVVNESKONGKTEKIGAKTSVYKEKDG 235
DB 229 GYKPGTTASDNDVFRYDVEFLSADRTTVVNESKONGKTEKIGAKTSVYKEKDG 288
QY 236 KLVYTKDNGENGSSTDEGEGLVTAKEVIDAVNKAAGRMKTTTANGQTGAADFETYSGT 295
DB 289 KLVYTKDNGENGSSTDEGEGLVTAKEVIDAVNKAAGRMKTTTANGQTGAADFETYSGT 348
QY 296 NTFEASGKGTATVSKDDOGNTTVMYDVAVGDLVNLQNSGWNLSKAVAGSSGKVIYS 355
DB 349 NTFEASGKGTATVSKDDOGNTTVMYDVAVGDLVNLQNSGWNLSKAVAGSSGKVIYS 408
QY 356 GAVSSKGMDETVININAGNNIETIRNGKNIDIASMPFOSSVSLGACADAPTLTSSVOD 415
DB 409 GAVSSKGMDETVININAGNNIETIRNGKNIDIASMPFOSSVSLGACADAPTLTSSVOD 468
QY 416 -ALANYSKRDKNRPVRTITNAPGVKEGDVTNVAQLGVAQNLNRRIDNDVGNARAGIAQAI 474
DB 469 GALNYSKRDKNRPVRTITNAPGVKEGDVTNVAQLGVAQNLNRRIDNDVGNARAGIAQAI 528
QY 475 ATAGLVQAVLPKSKMAIIGGTYRBEAGYAIIGYSSISDGGNNITIGTASGNSRGHFGASA 534
DB 529 ATAGLVQAVLPKSKMAIIGGTYRBEAGYAIIGYSSISDGGNNITIGTASGNSRGHFGASA 588
QY 535 SVGYQW 540
DB 589 SVGYQW 594

RESULT 13
AAV23738
ID AAV23738 standard; Protein; 598 AA.

XX
AC AAV23738;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
XX Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQV) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI; 1999-418754/35.
DR N-PSDB; AAX85790.
XX

PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
PS Claim 1; Page 91-93; 132pp; English.
XX

CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX

SO Sequence 598 AA:

Query Match 89.9%; Score 2478; DB 20; Length 598;
Best Local Similarity 90.2%; Pred. No. 2,1e-142;
Matches 496; Conservative 11; Mismatches 31; Indels 12; Gaps 3;

QY 2 NEEDEBYLYLHPVORTAVAVLIVNSDKEGAGEKEKEVENSMAVFNKGVLTARETTKA 61
DB 50 NATDDDDLYLEPVQRTAVAVLSFRSDKEGEGEGED-SNMAVYFDEKRVLAAGAITTLKA 108
QY 62 GDNLIKIQ-----NGTNETYSILKKDLTDLTSVGEKISFSAHGKVNITSDTKGL 111
DB 109 GDNLIKQNTMENTNMENTDSSFTYSLKKDLTDLTSVEFEKLSFGANGKKNVITSDTKGL 168
QY 112 NFAKETAGNGDTTVHLNGIGSTLTDLTLLNTGATTVNTDNDVTDDEKRRASVYKDVNLNAG 171
DB 169 NFAKETAGNGDTTVHLNGIGSTLTDLTLLNTGATTVNTDNDVTDDEKRRASVYKDVNLNAG 228
QY 172 NNIKGVKPGTTASDNDVFRYDVEFLSADRTTVVNESKONGKTEKIGAKTSVYK 231
DB 229 NNIKGVKPGTTASDNDVFRYDVEFLSADRTTVVNESKONGKTEKIGAKTSVYK 288
QY 232 EKDGLVYTKDNGENGSSTDEGEGLVTAKEVIDAVNKAAGRMKTTTANGQTGAADFETIV 291
DB 289 EKDGLVYTKDNGENGSSTDEGEGLVTAKEVIDAVNKAAGRMKTTTANGQTGAADFETIV 348
QY 292 TSGTNTVTFASGKGTATVSKDDOGNTTVMYDVAVGDLVNLQNSGWNLSKAVAGSSG 351
DB 349 TSGTNTVTFASGKGTATVSKDDOGNTTVMYDVAVGDLVNLQNSGWNLSKAVAGSSG 408

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QY 352 KVISGVSPSKGMDFTVINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTL 411
    |||
DB 409 KVISGVSPSKGMDFTVINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTL 468
QY 412 VDGD-ALNVGSKDKNKPVRTTNVAPGVKEGDVTNVQOLKGAONLNNRIDNVGNAAGI 470
    || : |||
DB 469 VDDEGALNVGSKDKNKPVRTTNVAPGVKEGDVTNVQOLKGAONLNNRIDNVGNAAGI 528
QY 471 AQAIAATAGLAQAVLPKSKMAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHF 530
    |||
DB 529 AQAIAATAGLAQAVLPKSKMAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHF 588
QY 531 GASASVGYOW 540
    |||
DB 589 GASASVGYOW 598

```

RESULT 14
AAI23742
ID AAY23742 standard; Protein; 598 AA.

XX AC AAY23742;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KM Surface protein; surface glycoprotein; infection; vaccine;

XX OS Neisseria meningitidis.

PN MO9931132-AI.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PI (UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

DR WPI: 1999-418754/35.

DR N-PSDB; AAX85794.

PS Claim 1; Page 108-110; 132pp; English.

XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

SO Sequence 598 AA;

Query Match 89.9%; Score 2478; DB 20; Length 598;

Best Local Similarity 90.4%; Pred. No. 2,1e-142;

Matches 497; Conservative 10; Mismatches 31; Indels 12; Gaps 3;

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QY 62 GDNLIKIKQ-----NCTNFTYSLKDLDTLTSVTEKLSFSAHGNKVNITSPTKGL 111
    |||
DB 109 GDNLIKIKQNTNENMTNENTNDSFTYSLKDLDTLTSVTEKLSFSAHGNKVNITSPTKGL 168
QY 112 NFAKETAGTGDPTVHLNGISITLDTLTLTGATNTNNDVDDKERRAASVQDVNAG 171
    |||
DB 169 NFAKETAGTGDPTVHLNGISITLDTLTLTGATNTNNDVDDKERRAASVQDVNAG 228
QY 172 WNIKGVKPGTASDNDVFRTYDVEFLSADTKTTTVNVESKNGKTEVKIGAKTSVIR 231
    |||
DB 229 WNIKGVKPGTASDNDVFRTYDVEFLSADTKTTTVNVESKNGKTEVKIGAKTSVIR 288
QY 232 EKDGLVTGKDKENGSSSTDEGGLVTAKEVIDAVNKAARMKTTTANGOTGADKEETV 291
    |||
DB 289 EKDGLVTGKDKENGSSSTDEGGLVTAKEVIDAVNKAARMKTTTANGOTGADKEETV 348
QY 292 TSGTNTFASGKTATVSKDDOGNTVTMDVNVGDLNVNQLONGSNLDSKAVAGSSG 351
    |||
DB 349 TSGTNTFASGKTATVSKDDOGNTVTMDVNVGDLNVNQLONGSNLDSKAVAGSSG 408
QY 352 KVISGVSPSKGMDFTVINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTL 411
    |||
DB 409 KVISGVSPSKGMDFTVINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTL 468
QY 412 VDGD-ALNVGSKDKNKPVRTTNVAPGVKEGDVTNVQOLKGAONLNNRIDNVGNAAGI 470
    || : |||
DB 469 VDDEGALNVGSKDKNKPVRTTNVAPGVKEGDVTNVQOLKGAONLNNRIDNVGNAAGI 528
QY 471 AQAIAATAGLAQAVLPKSKMAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHF 530
    |||
DB 529 AQAIAATAGLAQAVLPKSKMAIGGTYRGEAGYAIGYSSISDGNMIIKGTASGNSRGHF 588
QY 531 GASASVGYOW 540
    |||
DB 589 GASASVGYOW 598

```

RESULT 15

ID AAU06177 standard; Protein; 598 AA.

XX AC AAU06177;

DT 24-OCT-2001 (first entry)

DE N. meningitidis H15 surface antigen Nhma polypeptide sequence.

KM Surface antigen Nhma; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain H15.

XX FH Location/Qualifiers

FT 1..50 /label= C1

FT /note= "Conserved region 1"

FT 51..104 /label= V1

FT /note= "Variable region 1"

FT 105..116 /label= C2

FT /note= "Conserved region 2"

FT 117..130 /label= V2

FT /note= "Variable region 2"

FT 131..194 /label= C3

FT /note= "Conserved region 3"

FT 195..216 /label= V3

FT /note= "Variable region 3"

FT 217..235 /label= C4

FT /note= "Conserved region 4"

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 ; Search time 14.4407 Seconds
(without alignments)
1582.188 Million cell updates/sec

Title: US-09-771-382-33

Perfect score: 2757

Sequence: 1 NNEQEYLYLHPVQRTAV.....TASGSRGHFGASVGYQW 540

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2727	98.9	591	3	US-09-377-155-21
2	2727	98.9	591	4	US-09-669-974-21
3	2720	98.7	591	3	US-09-377-155-11
4	2720	98.7	591	4	US-09-669-974-11
5	2695.5	97.8	592	3	US-09-377-155-2
6	2695.5	97.8	592	4	US-09-669-974-2
7	2512	91.1	594	3	US-09-377-155-9
8	2512	91.1	594	4	US-09-669-974-9
9	2493	90.4	594	3	US-09-377-155-7
10	2493	90.4	594	4	US-09-669-974-7
11	2478	89.9	598	3	US-09-377-155-5
12	2478	89.9	598	4	US-09-669-974-5
13	2478	89.9	598	4	US-09-669-974-5
14	2478	89.9	598	4	US-09-669-974-13
15	2430.5	88.2	599	3	US-09-377-155-15
16	2430.5	88.2	599	4	US-09-669-974-15
17	2321	84.2	592	3	US-09-377-155-17
18	2321	84.2	592	4	US-09-669-974-17
19	2241.5	81.3	589	3	US-09-377-155-19
20	2241.5	81.3	589	4	US-09-669-974-19
21	1033.5	37.5	2411	4	US-09-268-347-36
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24	1031.5	37.4	2353	4	US-09-669-974-33
25	1030.5	37.4	2354	4	US-09-268-347-47
26	1019.5	37.0	607	1	US-08-409-995-6
27	1019.5	37.0	607	3	US-08-685-467-6

28	1019.5	37.0	607	3	US-08-913-942-6	Sequence 6, Appli
29	1019.5	37.0	1912	1	US-08-409-995-4	Sequence 4, Appli
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31	927	33.6	1094	4	US-09-268-347-32	Sequence 32, Appli
32	908	32.9	1098	1	US-08-409-995-2	Sequence 2, Appli
33	908	32.9	1098	3	US-08-685-467-2	Sequence 2, Appli
34	908	32.9	1098	3	US-09-377-155-32	Sequence 32, Appli
35	908	32.9	1098	3	US-08-913-942-2	Sequence 2, Appli
36	908	32.9	1098	4	US-09-669-974-32	Sequence 32, Appli
37	908	32.9	1098	4	US-09-268-347-44	Sequence 44, Appli
38	890	32.3	658	1	US-08-409-995-5	Sequence 5, Appli
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41	809.5	29.4	679	3	US-08-913-942-15	Sequence 15, Appli
42	809.5	29.4	679	4	US-09-268-347-26	Sequence 26, Appli
43	598.5	21.7	1004	4	US-09-268-347-30	Sequence 30, Appli
44	593.5	21.5	1104	4	US-09-268-347-28	Sequence 28, Appli
45	593.5	21.5	1104	4	US-09-268-347-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1

US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377.155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match	98.9%	Score 2727;	DB 3;	Length 591;
Best Local Similarity	99.3%	Pred. No. 3.2e-203;		
Matches 536;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	NNEQEYLYLHPVQRTAVVLVNSDKGAGEKEKVEENSDWVYFNEKGVLTAREITLK	60	
Db	52	NNEQEEDLLDPQRTAVVLVNSDKGEGEKEKVEENSDWVYFNEKGVLTAREITLK	111	
Qy	61	AGDNLKIQKNGTNYTSLKKDLTDLTSVGTSEKLSFSAHGNKNVNTSDTKGLNFAKETAGT	120	
Db	112	AGDNLKIQKNGTNYTSLKKDLTDLTSVGTSEKLSFSAHGNKNVNTSDTKGLNFAKETAGT	171	
Qy	121	NGDTTVHLNGIGSTLTDTLLTGATTTVNDVNDDEKRAASVKVNLNAGWNKGVKPG	180	
Db	172	NGDTTVHLNGIGSTLTDTLLTGATTTVNDVNDDEKRAASVKVNLNAGWNKGVKPG	231	
Qy	181	TTASDNDVDFVRYTDTVEFLSADTKTTVNVNVEKDKGKTEVKGAKTSVLEKDKGLVTG	240	
Db	232	TTASDNDVDFVRYTDTVEFLSADTKTTVNVNVEKDKGKTEVKGAKTSVLEKDKGLVTG	291	
Qy	241	KDKGENSSDEGEGLVTAKEVIDAVNKGARMKTTTTANGQTGQADFEFTVTSCTNYTFA	300	
Db	292	KDKGENSSDEGEGLVTAKEVIDAVNKGARMKTTTTANGQTGQADFEFTVTSCTNYTFA	351	
Qy	301	SGKGTATVSKDDOGNITVMYDVGALNVQNLQNSGWNLDKAVAGSSGSKVTSNGVSP	360	

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Qy 361 SKGKMDETVNTNAGNNIEITRNGKNIDTATSWTQFSSVSLGAGADAPTLSDVDGALNVG 420
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Qy 421 SKKDNKPVRTNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGDNARAGIAQAATAGLV 480
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Qy 481 QAYLPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 540
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RESULT 2

US-09-669-974-21
; Sequence 21, Application US/09669974
; Patent No. 6333173

; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 98.9%; Score 2727; DB 4; Length 591;
Best Local Similarity 99.3%; Pred. No. 3.2e-203;
Matches 536; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db 52 NNEQEEEDLYLDPVRLTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAAREITLK 111
Qy 61 AGDNLKIKQNGTNTFTYSLKKDLTDLTSVGTSEKLSFSAHGKNVNTSDTKGLNFAKETAGT 120
Db 112 AGDNLKIKQNGTNTFTYSLKKDLTDLTSVGTSEKLSFSAHGKNVNTSDTKGLNFAKETAGT 171
Qy 121 NGDITVHLNGIGSTLTDFTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGNNIKGVKPG 180
Db 172 NGDITVHLNGIGSTLTDFTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGNNIKGVKPG 231
Qy 181 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKDKNGKKEVIGAKTSVIEKDGKLVG 240
Db 112 AGDNLKIKQNGTNTFTYSLKKDLTDLTSVGTSEKLSFSAHGKNVNTSDTKGLNFAKETAGT 171
Qy 121 NGDITVHLNGIGSTLTDFTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGNNIKGVKPG 180
Db 172 NGDITVHLNGIGSTLTDFTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGNNIKGVKPG 231
Qy 181 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKDKNGKKEVIGAKTSVIEKDGKLVG 240
Db 232 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKDKNGKKEVIGAKTSVIEKDGKLVG 291
Qy 241 KDKGENGSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 300
Db 292 KDKGENGSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 351
Qy 301 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQIQLNSGWNLDKAVAGSSGKVTSGNVSP 360
Db 232 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKDKNGKKEVIGAKTSVIEKDGKLVG 291
Qy 241 KDKGENGSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 300
Db 292 KDKGENGSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 351
Qy 301 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQIQLNSGWNLDKAVAGSSGKVTSGNVSP 360
Db 352 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQIQLNSGWNLDKAVAGSSGKVTSGNVSP 411
Qy 361 SKGKMDETVNTNAGNNIEITRNGKNIDTATSWTQFSSVSLGAGADAPTLSDVDGALNVG 420
Db 412 SKGKMDETVNTNAGNNIEITRNGKNIDTATSWTQFSSVSLGAGADAPTLSDVDGALNVG 471

Qy 421 SKKDNKPVRTNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGDNARAGIAQAATAGLV 480
Db 472 SKKDNKPVRTNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGDNARAGIAQAATAGLV 531
Qy 481 QAYLPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 540
Db 532 QAYLPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 591

RESULT 3

US-09-377-155-11
; Sequence 11, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11

Query Match 98.7%; Score 2720; DB 3; Length 591;
Best Local Similarity 99.1%; Pred. No. 1.1e-202;
Matches 535; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NNEQEEYLYLHPVORTVAVLIVNSDKEGAGEKEKEVEENSDWAVYFNEKGVLTAAREITLK 60
Db 52 NNEQEEEDLYLDPVRLTVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAAREITLK 111
Qy 61 AGDNLKIKQNGTNTFTYSLKKDLTDLTSVGTSEKLSFSAHGKNVNTSDTKGLNFAKETAGT 120
Db 112 AGDNLKIKQNGTNTFTYSLKKDLTDLTSVGTSEKLSFSAHGKNVNTSDTKGLNFAKETAGT 171
Qy 121 NGDITVHLNGIGSTLTDFTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGNNIKGVKPG 180
Db 172 NGDITVHLNGIGSTLTDFTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGNNIKGVKPG 231
Qy 181 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKDKNGKKEVIGAKTSVIEKDGKLVG 240
Db 232 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKDKNGKKEVIGAKTSVIEKDGKLVG 291
Qy 241 KDKGENGSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 300
Db 292 KDKGENGSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 351
Qy 301 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQIQLNSGWNLDKAVAGSSGKVTSGNVSP 360
Db 352 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQIQLNSGWNLDKAVAGSSGKVTSGNVSP 411
Qy 361 SKGKMDETVNTNAGNNIEITRNGKNIDTATSWTQFSSVSLGAGADAPTLSDVDGALNVG 420
Db 412 SKGKMDETVNTNAGNNIEITRNGKNIDTATSWTQFSSVSLGAGADAPTLSDVDGALNVG 471
Qy 421 SKKDNKPVRTNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGDNARAGIAQAATAGLV 480
Db 472 SKKDNKPVRTNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGDNARAGIAQAATAGLV 531
Qy 481 QAYLPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 540
Db 532 QAYLPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 591

RESULT 4
US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11

Query Match 98.7%; Score 2720; DB 4; Length 591;
Best Local Similarity 99.1%; Pred. No. 1.1e-202;
Matches 535; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 NNEEQEYLYLHPVORTVAVLIIVNSDKGAGEKEKEVEENSQWAVYFNEKGVLTAREITLK 60
DB 52 NNEEQEEDLYLDPVLTAVVAVLIIVNSDKGEGTGEKEVEENSQWAVYFNEKGVLTAREITLK 111
QY 61 AGNLIKIQNGTFTSLKDLTDLTSVGTGTEKLSFSAHGKVNITSDTKGLNFAKETAGT 120
DB 112 AGNLIKIQNGTFTSLKDLTDLTSVGTGTEKLSFSAHGKVNITSDTKGLNFAKETAGT 171
QY 121 NGDTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPG 180
DB 172 NGDTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPG 231
QY 181 TTASDNVDFVRTYDVTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVGT 240
DB 232 TTASDNVDFVRTYDVTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVGT 291
QY 241 KDKGESSSTDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTGOADKFETVTSQTNVTF 300
DB 292 KDKGESSSTDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTGOADKFETVTSQTNVTF 351
QY 301 SGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKSAVAGSSGKVISGNVSP 360
DB 352 SGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKSAVAGSSGKVISGNVSP 411
QY 361 SKGKMDETVINAGNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGDLNVG 420
DB 412 SKGKMDETVINAGNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGDLNVG 471
QY 421 SKKDNKPVRTNVPAGVKEGDTVNTVAQLKGVAQNLRNDVGNARAGIAQAIATAGLV 480
DB 472 SKKDNKPVRTNVPAGVKEGDTVNTVAQLKGVAQNLRNDVGNARAGIAQAIATAGLV 531
QY 481 QAYLPCKSMAIAGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYOW 540
DB 532 QAYLPCKSMAIAGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYOW 591

RESULT 5
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 97.8%; Score 2695.5; DB 3; Length 592;
Best Local Similarity 98.2%; Pred. No. 8.9e-201;
Matches 531; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
QY 1 NNEEQEYLYLHPVORTVAVLIIVNSDKGAGEKEKEVEENSQWAVYFNEKGVLTAREITL 59
DB 52 NNEPRKKDLYLDPVORTVAVLIIVNSDKGEGTGEKEVEENSQWAVYFNEKGVLTAREITL 111
QY 60 KAGDNLIKIQNGTFTSLKDLTDLTSVGTGTEKLSFSAHGKVNITSDTKGLNFAKETAG 119
DB 112 KAGDNLIKIQNGTFTSLKDLTDLTSVGTGTEKLSFSAHGKVNITSDTKGLNFAKETAG 171
QY 120 TNGDTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVK 179
DB 172 TNGDTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVK 231
QY 180 GTTASDNVDFVRTYDVTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLV 239
DB 232 GTTASDNVDFVRTYDVTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLV 291
QY 240 GKDKGESSSTDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTGOADKFETVTSQTNVTF 299
DB 292 GKDKGESSSTDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTGOADKFETVTSQTNVTF 351
QY 300 ASGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKSAVAGSSGKVISGNVS 359
DB 352 ASGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKSAVAGSSGKVISGNVS 411
QY 360 PSKGMDETVINAGNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGDLNV 419
DB 412 PSKGMDETVINAGNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDGDLNV 471
QY 420 GSKKDNKPVRTNVPAGVKEGDTVNTVAQLKGVAQNLRNDVGNARAGIAQAIATAGL 479
DB 472 GSKKDNKPVRTNVPAGVKEGDTVNTVAQLKGVAQNLRNDVGNARAGIAQAIATAGL 531
QY 480 QAYLPCKSMAIAGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYO 539
DB 532 QAYLPCKSMAIAGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYO 591
QY 540 W 540
DB 592 W 592

RESULT 6
US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

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; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2

Query Match
Best Local Similarity 97.8%; Score 2695.5; DB 4; Length 592;
Matches 531; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 NNEE-QEYLXHPVQRTAVVLVNSDKEGAGEKEKEVEENSQWVYFNEKGVLTAREITL 59
Db 52 NNERPRKKDLYLDPVQRTAVVLVNSDKEGAGEKEKEVEENSQWVYFNEKGVLTAREITL 111

Qy 60 KAGDNLKITQNGTFTYSLKDLTDLTSVGTSEKLSFSAHGKNVITSDTKGLNFAKETAG 119
Db 112 KAGDNLKITQNGTFTYSLKDLTDLTSVGTSEKLSFSAHGKNVITSDTKGLNFAKETAG 171

Qy 120 TNGDPTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVP 179
Db 172 TNGDPTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVP 231

Qy 180 GTTASDNVDVFRYDTVFEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDGKLV 239
Db 232 GTTASDNVDVFRYDTVFEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDGKLV 291

Qy 240 GKDKGENSSDDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFEFVTSGTNTVF 299
Db 292 GKDKGENSSDDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFEFVTSGTNTVF 351

Qy 300 ASGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKAVAGSSGKVISGNVS 359
Db 352 ASGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKAVAGSSGKVISGNVS 411

Qy 360 PSKGKMDETVINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLISVDGDLNV 419
Db 412 PSKGKMDETVINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLISVDGDLNV 471

Qy 420 GSKKDNKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDVGNARAGIAQAIATAGL 479
Db 472 GSKKDNKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDVGNARAGIAQAIATAGL 531

Qy 480 VQAYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASVGYQ 539
Db 532 VQAYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASVGYQ 591

Qy 540 W 540
Db 592 W 592
```

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RESULT 7
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
```

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; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match
Best Local Similarity 91.1%; Score 2512; DB 3; Length 594;
Matches 501; Conservative 13; Mismatches 20; Indels 8; Gaps 3;

Qy 6 BEYLHPVQRTAVVLVNSDKEGAGEKEKEVEENSQWVYFNEKGVLTAREITLAKGDNL 65
Db 54 DDDLYLEFPVQRTAVVLVLSFRSDEGTGEKE-VTEDSNMGVYFDDKGVLTAGTITLAKGDNL 112

Qy 66 KIKQ-----NGTFTYSLKDLTDLTSVGTSEKLSFSAHGKNVITSDTKGLNFAKETAG 119
Db 113 KIKQNTNENTNASSFTYSLKDLTDLTSVGTSEKLSFSAHGKNVITSDTKGLNFAKETAG 172

Qy 120 TNGDPTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVP 179
Db 173 TNGDPTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVP 232

Qy 180 GTTASDNVDVFRYDTVFEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDGKLV 239
Db 233 GTTASDNVDVFRYDTVFEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDGKLV 292

Qy 240 GKDKGENSSDDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFEFVTSGTNTVF 299
Db 293 GKDKGENSSDDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFEFVTSGTNTVF 352

Qy 300 ASGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKAVAGSSGKVISGNVS 359
Db 353 ASGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKAVAGSSGKVISGNVS 412

Qy 360 PSKGKMDETVINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLISVDGD-ALN 418
Db 413 PSKGKMDETVINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLISVDGDGALN 472

Qy 419 VGSKKDNKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDVGNARAGIAQAIATAG 478
Db 473 VGSKKDNKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDVGNARAGIAQAIATAG 532

Qy 479 LVQAYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASVGY 538
Db 533 LVQAYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASVGY 592

Qy 539 QW 540
Db 593 QW 594
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```

RESULT 8
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
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; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match      90.4%; Score 2493; DB 4; Length 594;
Best Local Similarity 91.6%; Pred. No. 4.4e-185;
Matches 500; Conservative 9; Mismatches 29; Indels 8; Gaps 3;

Qy 2 NEEOEYLHPVORTVAVLVNSDKGAGKEKEKVEENSQWAVYFNKGVLTAREITLKA 61
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 50 NATDDDLYLEPVORTAVLVNSDKGEGTGEKEDT-SNNAVYFDEKRVLKAGAITLKA 108

Qy 62 GDNLKIKQ-----NGTNYTSLKDLTDLTSVTEKLSFSAHGKNVITSDTKGLN 111
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 109 GDNLKIKQNTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLN 168

Qy 112 NFAKETAGTNGDTTVHLNGIGSTLDTLLNTGATTNVTNDVDEKRAASVKDVLNAG 171
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 169 NFAKETAGTNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVDEKRAASVKDVLNAG 228

Qy 172 WNIKGVPGTTASNDVDFVRYDVEFLSADTKTTVNVEKDKGKTEVIGAKTSVIK 231
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 229 WNIKGVPGTTASNDVDFVRYDVEFLSADTKTTVNVEKDKGKTEVIGAKTSVIK 288

Qy 232 EKDGKLVTKDCKGSGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFTV 291
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 289 EKDGKLVTKGKGSGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFTV 348

Qy 292 TSGTNTVTFASGKGTATTATVSKDDQGNITVMYDVNVDALNVQLNSGWNLDKAVAGSSG 351
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 349 TSGTKVTFASGNGTTATVSKDDQGNITVMYDVNVDALNVQLNSGWNLDKAVAGSSG 408

Qy 352 KVISGNSVSPKGMDETVNINAGNIEITRNGKNIDTATSMTPFSSVSLGAGADAPTLS 411
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 409 KVISGNSVSPKGMDETVNINAGNIEITRNGKNIDTATSMTPFSSVSLGAGADAPTLS 468

Qy 412 VDGG-ALNVGSKDKNPVRIITNAPGVKEGDTNVAQLKGVQNLNRRIDNVDGNARAGI 470
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 469 VDDEGALNVGSKDKNPVRIITNAPGVKEGDTNVAQLKGVQNLNRRIDNVDGNARAGI 528

Qy 471 AQATATAGLVQAYLPGKSMAIGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHF 530
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 529 AQATATAGLVQAYLPGKSMAIGGTYRGEAGYAGYSSISDGTGCMVVIKGTASGNSRGHF 588

Qy 531 GASASVGYQW 540
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 589 GTSASVGYQW 598

RESULT 12
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377.155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

Query Match      89.9%; Score 2478; DB 3; Length 598;
Best Local Similarity 90.2%; Pred. No. 6.5e-184;
Matches 496; Conservative 11; Mismatches 31; Indels 12; Gaps 3;

Qy 2 NEEOEYLHPVORTVAVLVNSDKGAGKEKEKVEENSQWAVYFNKGVLTAREITLKA 61
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 50 NATDDDLYLEPVORTAVLVNSDKGEGTGEKEDT-SNNAVYFDEKRVLKAGAITLKA 108

Qy 62 GDNLKIKQ-----NGTNYTSLKDLTDLTSVTEKLSFSAHGKNVITSDTKGLN 111
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 109 GDNLKIKQNTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLN 168

Qy 112 NFAKETAGTNGDTTVHLNGIGSTLDTLLNTGATTNVTNDVDEKRAASVKDVLNAG 171
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 169 NFAKETAGTNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVDEKRAASVKDVLNAG 228

Qy 172 WNIKGVPGTTASNDVDFVRYDVEFLSADTKTTVNVEKDKGKTEVIGAKTSVIK 231
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 229 WNIKGVPGTTASNDVDFVRYDVEFLSADTKTTVNVEKDKGKTEVIGAKTSVIK 288

Qy 232 EKDGKLVTKDCKGSGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFTV 291
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 289 EKDGKLVTKGKGSGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFTV 348

Qy 292 TSGTNTVTFASGKGTATTATVSKDDQGNITVMYDVNVDALNVQLNSGWNLDKAVAGSSG 351
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 349 TSGTKVTFASGNGTTATVSKDDQGNITVMYDVNVDALNVQLNSGWNLDKAVAGSSG 408

Qy 352 KVISGNSVSPKGMDETVNINAGNIEITRNGKNIDTATSMTPFSSVSLGAGADAPTLS 411
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Db 409 KVISGNSVSPKGMDETVNINAGNIEITRNGKNIDTATSMTPFSSVSLGAGADAPTLS 468

Qy 412 VDGG-ALNVGSKDKNPVRIITNAPGVKEGDTNVAQLKGVQNLNRRIDNVDGNARAGI 470
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Db 469 VDDEGALNVGSKDKNPVRIITNAPGVKEGDTNVAQLKGVQNLNRRIDNVDGNARAGI 528

Qy 471 AQATATAGLVQAYLPGKSMAIGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHF 530
   : : ||| ||| ||| ||| ||| : : ||| ||| ||| ||| |||
Db 529 AQATATAGLVQAYLPGKSMAIGGTYRGEAGYAGYSSISDGTGCMVVIKGTASGNSRGHF 588

Qy 531 GASASVGYQW 540
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Db 589 GTSASVGYQW 598

RESULT 11
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377.155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5
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QY 2 NEEQEEYLYLHPVQRTAVVLVNSDKGAGEKEVEENSDWAVYFNEKGVLTAIREITLKA 61
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Db 50 NATDDDDLYLEPVQRTAVVLSFRSKDEGTGEGTEGD-SNWAVYFDEKRVLKAGAITLKA 108
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QY 62 GDNLKTKQ-----NCTNTYSLKLDLTDLTSGTEKLSFSAHGNKVNITSDTKGL 111
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QY 112 NFAKETAGTNGDTTVHLNGIGSLTDLTLLNTGATTNTNDVDDDEKKRAASVKDVLNAG 171
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Db 169 NFAKETAGTNGDPTVHLNGIGSLTDLTLLNTGATTNTNDVDDDEKKRAASVKDVLNAG 228
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
QY 172 WNIKGVPKGTASDNVDFVRYDTVEPLSADTKTTTVNVESKONGKTEVKIGAKTSVIK 231
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
Db 229 WNIKGVPKGTASDNVDFVRYDTVEPLSADTKTTTVNVESKONGKTEVKIGAKTSVIK 288
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QY 232 EKDGKLVTKDGKENGSSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKPEV 291
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
Db 289 EKDGKLVTKDGKENGSSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKPEV 348
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
QY 292 TSGTNTVFASGKGTATVSKDDGNTVMYDVNVGDALNVQNSGNWLDKRAVAGSSG 351
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Db 349 TSGTKVTFASGNGTTATVSKDDGNTVMYDVNVGDALNVQNSGNWLDKRAVAGSSG 408
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QY 352 KVISGNVSPSKGMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLS 411
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Db 409 KVISGNVSPSKGMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLS 468
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
QY 412 VDGD-ALNVGSKDKNPVRITNVAPGVKEGDTNVNVAQLKGAQNLRNDRIDVGNARAGI 470
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QY 471 AQAIATAGLVAQVLPKGSMAIGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHF 530
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Db 529 AQAIATAGLAQVLPKGSMAIGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHF 588
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QY 531 GASASVGYQW 540
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Db 589 GASASVGYQW 598
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RESULT 13
US-09-669-974-5

; Sequence 5, Application US/09669974
; Patent No. 633173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; CURRENT FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; TYPE: PRT

; LENGTH: 598

; ORGANISM: Neisseria meningitidis

US-09-669-974-5

Query Match 89.9%; Score 2478; DB 4; Length 598;

Best Local Similarity 90.2%; Pred. No. 6.5e-184;

Matches 496; Conservative 11; Mismatches 31; Indels 12; Gaps 3;

QY 2 NEEQEEYLYLHPVQRTAVVLVNSDKGAGEKEVEENSDWAVYFNEKGVLTAIREITLKA 61

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QY 62 GDNLKTKQ-----NCTNTYSLKLDLTDLTSGTEKLSFSAHGNKVNITSDTKGL 111
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Db 109 GDNLKIKONTNENTNDSSFTYSLKDLTDLTSTVETEKLSFGANGKVNITSDTKGL 168
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QY 112 NFAKETAGTNGDTTVHLNGIGSLTDLTLLNTGATTNTNDVDDDEKKRAASVKDVLNAG 171
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
Db 169 NFAKETAGTNGDPTVHLNGIGSLTDLTLLNTGATTNTNDVDDDEKKRAASVKDVLNAG 228
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
QY 172 WNIKGVPKGTASDNVDFVRYDTVEPLSADTKTTTVNVESKONGKTEVKIGAKTSVIK 231
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
Db 229 WNIKGVPKGTASDNVDFVRYDTVEPLSADTKTTTVNVESKONGKTEVKIGAKTSVIK 288
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QY 232 EKDGKLVTKDGKENGSSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKPEV 291
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
Db 289 EKDGKLVTKDGKENGSSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKPEV 348
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
QY 292 TSGTNTVFASGKGTATVSKDDGNTVMYDVNVGDALNVQNSGNWLDKRAVAGSSG 351
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Db 349 TSGTKVTFASGNGTTATVSKDDGNTVMYDVNVGDALNVQNSGNWLDKRAVAGSSG 408
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QY 352 KVISGNVSPSKGMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLS 411
   : : ||| ||| ||| ||| ||| ||| : : ||| ||| ||| ||| ||| |||
Db 409 KVISGNVSPSKGMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLS 468
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QY 412 VDGD-ALNVGSKDKNPVRITNVAPGVKEGDTNVNVAQLKGAQNLRNDRIDVGNARAGI 470
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Db 469 VDDEGALNVGSKDKANKPVRITNVAPGVKEGDTNVNVAQLKGAQNLRNDRIDVGNARAGI 528
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QY 471 AQAIATAGLVAQVLPKGSMAIGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHF 530
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Db 529 AQAIATAGLAQVLPKGSMAIGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHF 588
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Db 589 GASASVGYQW 598
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RESULT 14

US-09-669-974-13

; Sequence 13, Application US/09669974

; Patent No. 633173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; CURRENT FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; TYPE: PRT

; LENGTH: 598

; ORGANISM: Neisseria meningitidis

US-09-669-974-13

Query Match 89.9%; Score 2478; DB 4; Length 598;

Best Local Similarity 90.4%; Pred. No. 6.5e-184;

Matches 497; Conservative 10; Mismatches 31; Indels 12; Gaps 3;

QY 2 NEEQEEYLYLHPVQRTAVVLVNSDKGAGEKEVEENSDWAVYFNEKGVLTAIREITLKA 61

Db 50 NATDDDDLYLEPVQRTAVVLSFRSKDEGTGEGTEGD-SNWAVYFDEKRVLKAGAITLKA 108

Qy	62	GNLKI KO-----NGNFYYSUKKOLDTLDTSVGTBEKLSFSAHGKNKVITSDTKGL	111
Db	109	GNLKI KONTNENTNENTNDSSFTYSUKKOLDTLDTSVETEKLSFGAGKNKVITSDTKGL	168
Qy	112	NEFAKETAGTNGDTPVHLNGIGSTLTDLLNTGATTNVTNDVTTDDEKKRAASVKDVLNAG	171
Db	169	NEFAKETAGTNGDTPVHLNGIGSTLTDLLNTGATTNVTNDVTTDDEKKRAASVKDVLNAG	228
Qy	172	WNKGVKPGTTRASDNVDPRYDTRVEFLSADTKTTTVNVESKONGKKTEVKIGAKTSVIK	231
Db	229	WNKGVKPGTTRASDNVDPRYDTRVEFLSADTKTTTVNVESKONGKKTEVKIGAKTSVIK	288
Qy	232	EXDKGLVTGKDKGEGSSSTDEBGLVTAKEVIDAVNKAGWRMKTITTANGTGTGQADKFETV	291
Db	289	EXDKGLVTGKDKGEGSSSTDEBGLVTAKEVIDAVNKAGWRMKTITTANGTGTGQADKFETV	348
Qy	292	TSGTNVTRFASGKGTATVSKDDQGNITVMYDVNVGVDALNVQLQNSGWNLDSKAVAGSSG	351
Db	349	TSGTKVTRFASGNGTATVSKDDQGNITVKYDVNVGVDALNVQLQNSGWNLDSKAVAGSSG	408
Qy	352	KVYISGNVSPSKGMDETVNIAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLS	411
Db	409	KVYISGNVSPSKGMDETVNIAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLS	468
Qy	412	VDGD--ALNVGSKDKNKPVRTNVPAPGVKEGDTVNTVAOLKGAQNLANNRIDNVGDNARAGI	470
Db	469	VDEGALANVSGSKDANKPVRTNVPAPGVKEGDTVNTVAOLKGAQNLANNRIDNVGDNARAGI	528
Qy	471	AQAIATAGLQAQYLPKGSMMIAIGGTVRGEAGYAIGYSSISDGGNMI IKGTASGNSRGHF	530
Db	529	AQAIATAGLQAQYLPKGSMMIAIGGTVRGEAGYAIGYSSISDGGNMI IKGTASGNSRGHF	588
Qy	531	GASASVGYQW 540	
Db	589	GASASVGYQW 598	

RESULT 15

US-09-377-155-15
; Sequence 15, Application US/09377155

; GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm

APPLICANT: JENNINGS, Michael paul

; APPLICANT: MOXON, E. Richard

INVENTOR: MONROE E. RICHARDSON
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

FILE OF INVENTION: NOVEL 3
; FILE REFERENCE: 065064/0128

FILE REFERENCE: 003004/0120
CURRENT APPLICATION NUMBER: US/09/377,155

; CURRENT AFFILIATION NUMBER: 03/0
 ; CURRENT FILING DATE: 1999-08-19

: CURRENT FILING DATE: 1999-08-19
 : PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR APPLICATION NUMBER: PCT/
 : PRIOR FILING DATE: 1998-12-14

; PRIOR FILING DATE: 1998-12-14
 : PRIOR APPLICATION NUMBER: GB 9726398 2

; PRIOR APPLICATION NUMBER: GB
 : PRIOR FILING DATE: 1997-12-12

; PRIOR FILING DATE: 1997-12
 : NUMBER OF SEQ ID NOS. 33

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: BioEdit version 3.0

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; SOFTWARE: PatentIn Ver.
; SEQ ID NO 15

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; SEQ ID NO 15
: 1 ENCTII: 500

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; LENGTH: 50
TYPE: PAPER

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; TYPE: PRT
;

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; ORGANISM: NE:

Query Match

Query Match
Best Local similarity 88.28; score 2430.3; DB 3
Best Local similarity 88.68; Pred No 3 1e-180.

BEST LOCAL SIMILARITY 88.6%; Pred. NO. 3, IE-180;
Matches 488: Conservative 14: Mismatches 34:
Indels 15: Cans 4:

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QY I NNEEQEEI LIDH FVQRI VAVLIVNSDREGAGERKEKVEENS DWAVIFN ERGVLTARETLK 60

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109 AC0NI K I KANTNKNTNENTNDCSEETVSI VKDI ETOTI TQVETETVI SECACNCNZNINTTSCMYC 160

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Db	169	LNF	A	K	E	T	A	G	T	I	N	G	L	T	D	P	L	L	N	G	A	T	N	T	N	D	N	V	T	D	D	E	K	K	R	A	A	S	V	K	D	V	L	N	A	228														
Qy	171	G	N	I	K	G	V	K	P	G	T	A	S	D	N	V	D	F	V	T	D	V	B	F	L	S	A	D	T	K	T	T	T	V	N	E	S	K	D	G	K	K	T	E	V	I	K	A	G	T	S	V	I	230						
Db	229	G	N	I	K	G	V	K	P	G	T	A	S	D	N	V	D	F	V	T	D	V	B	F	L	S	A	D	T	K	T	T	T	V	N	E	S	K	D	G	K	K	T	E	V	I	K	A	G	T	S	V	I	288						
Qy	231	K	E	D	G	K	L	V	T	G	K	D	G	E	N	S	T	D	E	G	E	L	V	T	A	K	E	I	D	A	V	N	K	A	G	W	R	M	K	T	T	T	A	N	G	O	T	G	A	D	K	F	E	T	290					
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Qy	291	V	T	S	T	N	T	F	A	S	G	K	T	T	A	T	S	K	D	O	G	N	I	T	V	M	V	D	N	V	G	D	A	L	N	V	N	O	L	N	G	N	L	D	S	K	A	V	A	G	S	350								
Db	349	V	T	S	T	N	T	F	A	S	G	K	T	T	A	T	S	K	D	O	G	N	I	T	V	M	V	D	N	V	G	D	A	L	N	V	N	O	L	N	G	N	L	D	S	K	A	V	A	G	S	408								
Qy	351	G	K	V	I	S	G	N	V	S	P	S	G	K	M	D	E	T	V	N	I	N	A	G	N	N	I	E	I	T	R	N	G	K	N	I	D	I	A	T	S	M	T	P	O	F	S	S	V	S	L	G	A	G	A	D	A	P	L	410
Db	409	G	K	V	I	S	G	N	V	S	P	S	G	K	M	D	E	T	V	N	I	N	A	G	N	N	I	E	I	T	R	N	G	K	N	I	D	I	A	T	S	M	T	P	O	F	S	S	V	S	L	G	A	G	A	D	A	P	L	468
Qy	411	S	V	D	G	-	D	A	L	N	V	G	S	K	D	N	K	P	V	R	I	T	N	V	A	P	G	V	K	E	G	D	V	T	N	V	A	O	L	K	G	V	A	O	N	L	N	R	I	D	N	V	D	G	N	A	R	A	G	469
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Qy	470	I	A	O	A	I	A	T	A	G	L	V	A	Y	L	P	G	K	S	M	A	I	G	G	T	V	R	G	E	A	G	Y	A	I	G	S	S	I	S	D	G	G	N	W	I	I	K	T	A	S	G	N	S	R	G	H	529			
Db	529	I	A	O	A	I	A	T	A	G	L	V	A	Y	L	P	G	K	S	M	A	I	G	G	T	V	R	G	E	A	G	Y	A	I	G	S	S	I	S	D	G	G	N	W	I	I	K	T	A	S	G	N	S	R	G	H	588			
Qy	530																																																											

Search completed: October 6, 2003, 09:35:53

Job time : 16.4407 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 15.4576 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-33

Perfect score: 2757

Sequence: 1 NNEQEYLYLHPVQRTAV.....TASGNSRGHFGASASGYQW 540

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2212	80.2	592	2 A81888	probable surface f
3	451	16.4	298	2 I64138	adhesin homolog HI
4	393	14.3	2059	2 D82671	surface protein XF
5	369.5	13.4	1107	2 AC0976	probable autotrans
6	365.5	13.3	1190	2 A82615	surface protein XF
7	358	13.0	1588	2 A86036	probable adhesin z
8	358	13.0	1588	2 H91188	probable adhesin E
9	331.5	12.0	658	2 AH0110	probable surface p
10	228.5	8.3	1536	2 A43855	high-molecular-wel
11	212	7.7	2020	2 C48399	ABC-type transport
12	209	7.6	2273	2 T09083	hemagglutinin/hemo
13	207	7.5	1910	2 AF0394	probable adhesin h
14	206.5	7.5	4919	2 T31105	hypothetical prote
15	203	7.4	936	2 I40711	sapB protein - Cam
16	200.5	7.3	1477	2 B43855	high-molecular-wel
17	199.5	7.2	5291	2 F90696	hypothetical prote
18	198.5	7.2	1109	2 A56143	surface-array prot
19	195	7.1	585	2 F90961	flagellin [importe
20	195	7.1	585	2 F85809	hypothetical prote
21	195	7.1	1004	2 C82672	surface-exposed ou
22	195	7.1	1461	2 E90696	hypothetical prote
23	194.5	7.1	1035	2 AD3203	autotransporter pr
24	193	7.0	5188	2 B85547	probable RTX famil
25	192.5	7.0	1428	2 AC2224	hypothetical prote
26	192	7.0	1635	2 A10452	hemolysin [importe
27	191	6.9	1461	2 A85547	hypothetical prote
28	189	6.9	2249	2 A41477	190K surface anti
29	188.5	6.8	4152	2 T31102	filamentous hemagg

RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masiangani, V.; Pizza, M. Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: G81133

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <TET>

A:Cross-references: GB:AE002450; GB:AE002098; NET:g7226229; PIDN:AAF1395.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match 98.9%; Score 2727; DB 2; Length 591;

Best Local Similarity 99.3%; Pred. No. 4.6e-133;

Matches 536; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNEQEYLYLHPVQRTAVLIIVNSDKEGAGEKEKEVEENSDWAYVFNEKGVLTAREITLK 60

Db 52 NNEQEEDLYDPVQRTAVLIIVNSDKEGTGEKEVEENSDWAYVFNEKGVLTAREITLK 111

Qy 61 AGDNLKTQNGTNTFTYSLKKDLTDTSVGTEKLSFSAHGNKVNITTSDTKGLNFAKETAGT 120

Db 112 AGDNLKTQNGTNTFTYSLKKDLTDTSVGTEKLSFSAHGNKVNITTSDTKGLNFAKETAGT 171

Qy 121 NGDPTVHLNGTSTLTDTLLNTGATTNTVNDVNDDEKRAASVKDVLNAGNWKGVKPG 180

Db 172 NGDPTVHLNGTSTLTDTLLNTGATTNTVNDVNDDEKRAASVKDVLNAGNWKGVKPG 231

Qy 181 TTASDNVDVFTVDTVEFLSADTKTTTVNVESKDKKKTEVKIGAKTSVKEKDGKLVGT 240

Db 232 TTASDNVDVFTVDTVEFLSADTKTTTVNVESKDKKKTEVKIGAKTSVKEKDGKLVGT 291

Qy 241 KDKGESSDDEGEGLVTAKEIDAVNKAGRMKTTTANGOTGADKFETVTSCTNVTFA 300

Db 292 KDKGESSDDEGEGLVTAKEIDAVNKAGRMKTTTANGOTGADKFETVTSCTNVTFA 351

Qy 301 SGKGTATVSKDDGNTVMYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSP 360

Db 352 SGKGTATVSKDDGNTVMYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSP 411

Qy 361 SKGMDETVMINAGNNIEITRNKGNIDATSMTPQFSSVLGAGADAPTLISVDGDLNVG 420

Db 420 SKGMDETVMINAGNNIEITRNKGNIDATSMTPQFSSVLGAGADAPTLISVDGDLNVG 420

Db 412 SKKMDETVNNIAGNBIETIRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGDLNVG 471

Qy 421 SKDKNKPVRITNVAPGVKEGVDVTVNAQLKGVAQNLNNRIDNVGDNARAGIAQAATAGLV 480

Db 472 SKDKNKPVRITNVAPGVKEGVDVTVNAQLKGVAQNLNNRIDNVGDNARAGIAQAATAGLV 531

Qy 481 QAYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIIGKTPASNSRGRHFGASASVGQW 540

Db 532 QAYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIIGKTPASNSRGRHFGASASVGQW 591

RESULT 2

A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.

A:Reference number: A81775; MUID:20223556; PMID:10761919

A:Accession: A81888

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-592 <PAR>

A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989

A:Experimental source: serogroup A, strain 22491

C:Genetics:

A:Gene: NMA1200

Query Match 80.2%; Score 2212; DB 2; Length 592;

Best Local Similarity 82.9%; Pred. No. 1.4e-106;

Matches 456; Conservative 28; Mismatches 46; Indels 20; Gaps 8;

Qy 1 NNEQEEYLYLHPQRTVAVVLIVNSDKGAGEKEKVE-ENSDWAVYFNEKGVLTAREITL 59

Db 53 DEDEEEE---LESVQRSV-VGSIQASMEGSGELETISLSMTNDSKEFDYPIV---VTL 104

Qy 60 KAGDNLKIQ-----NCTNFTYSLKDLTDLTSVGTLEKLSFSAHGNKVNITSDTKGLNF 113

Db 105 KAGDNLKIQNTNENTNASSFTYSLKDLTGLINVELEKLSFGANGKVNITSDTKGLNF 164

Qy 114 AKETAGTNGDTTVHLNGIGSTLTDTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGWN 173

Db 165 AKETAGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWN 222

Qy 174 IKGVKPGTTA--SDNVDFVRYDTVEFLSADTKTTTVNVEKDKNGKKEVKGAKTSVIK 231

Db 223 IKGVKGTGTGQSENVDFVRYDTVEFLSADTKTTTVNVEKDKNGKKEVKGAKTSVIK 282

Qy 232 EKDKGLVTGDKGNGSSTDEGGLVTAKEVIDAVNKAQWRMKTTTANGQTGQADKPETV 291

Db 283 EKDKGLVTGDKGNGSSTDEGGLVTAKEVIDAVNKAQWRMKTTTANGQTGQADKPETV 342

Qy 292 TSGTNVTPASGKGTATATYKDDQGNITVMYDQVNDALNVQLNSGNWNLDSKAVAGSSG 351

Db 343 TSGTNVTPASGKGTATATYKDDQGNITVMYDQVNDALNVQLNSGNWNLDSKAVAGSSG 402

Qy 352 KVISGNVSPSGKMDETVNIAGNNIETIRNGKNIDTATSMTPQFSSVSLGAGADAPTLS 411

Db 403 KVISGNVSPSGKMDETVNIAGNNIETIRNGKNIDTATSMTPQFSSVSLGAGADAPTLS 462

Qy 412 VDGD--ALNVGSKDKPKVRITNVAPGVKEGVDVTVNAQLKGVAQNLNNRIDNVGDNARAGI 470

Db 463 VDDEGALNVGSKDKPKVRITNVAPGVKEGVDVTVNAQLKGVAQNLNNRIDNVGDNARAGI 522

Qy 471 QAATATAGLVQAYLPKGSMAIGGTYRGEAGYAGYSSISDGGNWIIGKTPASNSRGRH 530

Db 523 QAATATAGLVQAYLPKGSMAIGGTYRGEAGYAGYSSISDGGNWIIGKTPASNSRGRH 582

Qy 531 GASASVGQW 540

Db 583 GASASVGQW 592

RESULT 3

164138

adhesin homolog HI1732 - *Haemophilus influenzae* (strain Rd KW20)

C:Species: *Haemophilus influenzae*

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997

C:Accession: I64138

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.B.; Fuhmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: I64138

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-298 <TIGR>

A:Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:HI1732

Query Match 16.4%; Score 451; DB 2; Length 298;

Best Local Similarity 48.2%; Pred. No. 2e-16;

Matches 106; Conservative 31; Mismatches 67; Indels 16; Gaps 6;

Qy 47 NEKGVLTARE-ITLKAGDNLKIK--QNGTNTYSLKKDL-----TDLTSVGTLEKLSFS 96

Db 76 NKNQALKAGDTLTLKAGKNLAKLDQGGKSVTFALAKDVKTAKVSDTLTIGGNTPAAG 135

Qy 97 AHGNKVNITSDTKGLNFPAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATNTVNDVTD 156

Db 136 GATPKVSTSTADGKLAK---GTNGDTAVHLNGLASTLPDVTNTGASTSVT-FSPSDI 191

Qy 157 EKRAASVKDVLNAGWIKGVKPGTASDNDVFTVTVFEFLSADTKTTTVNVEKDKNG 216

Db 192 EKTRAATIKDVLNAGWIKGVKAGVAGNTENVDLVAGDVNVEITGDKNLTDLVLTAKENG 251

Qy 217 KKEVTKGAKTSVIKEDKGLVTGKD--KGNGSSTDEGE 254

Db 252 KTEVKTPTKTSVIKDNNGKLLTGKQLKDANTGATNATE 291

RESULT 4

D82671

surface protein XF1529 [imported] - *Xylella fastidiosa* (strain 9a5c)

C:Species: *Xylella fastidiosa*

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: D82671

R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82671

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2059 <STM>

A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN A:Experimental source: Strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovskij-Almeida, S.; Vettore, A.L. A:Reference number: A59328

A;Contents: annotation
C;Genetics:
A;Gene: XF1529

Query Match	14.3%;	Score 393;	DB 2;	Length 2059;		
Best Local Similarity	23.9%;	Pred. No. 2.2e-12;				
Matches	170;	Conservative 95;	Mismatches 217;	Indels 230; Gaps 30;		
QY	21	LIVNSDKEGAGEKEKVEENS	DAVYFNE-KGVLTARE----	ITLKAGDNLKIKQNGT--- 72		
DB	1386	VIWNGGKIGSVTAGTEETD--	AVNFSQLKSISTAVDQGWTLT	FASGANGSKVASGGTVDL 1443		
QY	73	-----NFTYSLKKDLTDLT	-----SYG-----	-----TEKLSFSA 97		
DB	1444	KNTDGNLTISKSGSDNDVFN	LSBLLKEKSITVGTQLDKDG	VKVSSVLLDSNELVITS 1503		
QY	98	HGNKVNTISDTKGLNFAKET	A---GTNGDTTVHLNGI-----	GSTLDTLNTGA--T 145		
DB	1504	HSSTSSYKTLANGESVYVNR	TVVAGDGVNIDVVVVVNDLGL	SVIGGASLTLSGINAGSHKI 1563		
QY	146	TNVT-----NDNVTDD	EKKRAASVKVNLNAGWNI-----	-KGVPGTTASDNVD--- 188		
DB	1564	TNVTAGTEDDVAVNF	SOLK---SVSEAVDKGWL	TASGANGKVVSGCTVDLNTDGNLA 1620		
QY	189	---FVRTYDVFEL	SADTK-----TTTVN	VESKONGKKTEVKIGATSVI	KEKDGKLV 238	
DB	1621	ISKSGSDNDVFNLSKDF	KVDEVTAGTVNTDGV	KVG---SDVSLGAMGLFI	ANGPSVTA 1678	
QY	239	TGRDKGEN-----	GSSTDEGGLVTAKEVID	AVANKAGWRMTT-----	ANGQ 281	
DB	1679	SGFNAGDKVISHVAVG	MADTDVAVNSOLKQAV	QSVTVKATRYYSTNDGGT	QGGNYDGDGA 1738	
QY	282	TGO---ADKPE	TVTSGTNV-----TF	ASCKGTTA-----	--- 307	
DB	1739	TGSKAIAGVGTQASG	GEAAAVSGGAASCKGST	AIGRNAIASADGSVAL	CDGAKDGGRG 1798	
QY	308	-----TVS-----	KDDOGNIITVMDVNYG-	DALNYNQL-----Q	NSGWN 340	
DB	1799	AESYTGKYGQVNN	TVGTVSGVDAAKG	ETRSISNVADAKEAMD	AVNLRLDQDAV	AKSNLQ 1858
QY	341	LDS-----	-----KAVAGSSG	KVIGSNVSPSGKKM	DETVNIN 372	
DB	1859	TDDMRHEINNIED	VFKITTKGDSASSV	KMGVNMAMIGTNA	AVSGTESVALGK---N	TNVS 1915
QY	373	AGNNIETRNGKNID	IATSMTPOFSSVSL	GACAGADAPTL	SVDDGALNVGSKKDN	KPVRIITN 432
DB	1916	ADNAVAI-GNG-----	SVADRANSVSGG-----	-----GSER-----	QVTN 1947	
QY	433	VAPGVKEGDVTN	VNAQLKGAQN	LNNRIDNDGNAR----	AGIAQATATAGL	QAYLPGKS 488
DB	1948	VAAGTADTDVAVNS	QLNGLITAKQYTDG	MVGNLRLRETSG	VGAAAIATANL	PQAYVOGRG 2007
QY	489	MMAIIGGTYRGE	AGYATGYSSISD	GGNWIITGTASGN	SRGHFGASV	GYQW 540
DB	2008	MTSVSSYQCGQA	IAVGVSAVSG	SHWFKFSGSANT	RSHVGVGAGV	QYQW 2059

RESULT 5

AC0976

probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0976

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.;...
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, M.;...
S.; Moulé, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;...
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar...
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0976
A>Status: preliminary

A: Molecule type: DNA
A: Residues: 1-1107 <PAR>
A: Cross-references: GB:AL513382; PIDN:CAD03303.1; PID: g16504923; GSPDB:GN00176
C: Genetics:
A: Gene: sapB

Query Match	13.4%	Score 369.5	DB 2	Length 1107
Best Local Similarity	21.6%	Pred. No. 1.6e-11		
Matches 164	Conservative 100	Mismatches 211	Indels 283	Gaps 28
Qy	34	KEVEENSQWAVYFNEKCVLTAREITLKAGDNLIKONGT--NFTYSLKKXDLTDLTSGVT	90	
Db	382	EKVDQNI-----TDTAANTNITQNSTAIENLNTSVSDINITSITGLTD	424	
Qy	91	EKL-----SFSAH--GNKVNTISDTKGLNFAKETAGTNG---DFTVHLNGIGSGTLTD	137	
Db	425	NALLWDSBTDGAFSANHGGSTSKITNVAAGALSESDTDAVNGSOLYETYNQKVDQNTSAID	484	
Qy	138	TLNLTGATTNVTNDVTDDEKKRAASYKVDVLNAGWNILKGVKPGTASDNVDV--RTYD	194	
Db	485	--INT-SITNLGTDALSDDDEGAFSASHGTSGTNKITNVAAGIAISDSYDAINGSOLYE	541	
Qy	195	T-----VEPLSADTKTTTIVN-----VESKDNGKKTVEKIGAKTSVIEKDKG	236	
Db	542	TNMLISQYNESISOLAGDTSITYITENGTVGVKIIRTNDNGLEGQ-----DAYATCNGA	594	
Qy	237	LVTGKKK-----GENSGSTDEG-----EGLV-----	257	
Db	595	TAVGYDAVASGAGCALGQSSSSIEGSIAGLGGSTSNRAITTTGIRETSATSDGVWIGYN	654	
Qy	258	-TAKEVIDAVNKA---GWRMKTTTANGQTQ-----ADKPEYTVSG	294	
Db	655	TTDRELGLALSLGTDGESYRQITNVADGSEQAQNAVTVRQLQNAIGAVTTPTKYYHANST	714	
Qy	295	TNVTFSAGKGTTA---TVSKDDQG-----NITVMYDVNVYGDALNVN-----	332	
Db	715	EEDSLAVGCTDSLAMGAKTIIVNADAGIGIGLNTLVMAIDAINGAIGSNARANHANSIAMGN	774	
Qy	333	-----QLONSGWNLDSK-----AVAGSSGKVIISGNVSPSKGKMDVTVNINAG---	374	
Db	775	GSQTRGAQTDYTAYNMDTTPNSVGEFSVSGEDGQRQITNVAAGSADTDA---VNVGOLK	831	
Qy	375	NNIEITRNKNI-----DIATSMTPQF-----	396	
Db	832	VTDAQVSRNTQTSITNLNTQVSNLDRVTNTIENGIGDIVTGGTKYFKYKNTDGDADANAQGA	891	
Qy	397	SSVSLGAGADAP-----TLSDVGDALNVGSKKDNKPKVRTITNVAPGVKEGDVTNVA	446	
Db	892	DSVAIGSGSIAAAENSVALGTGNSVADEANTVSVSGSTQQR--RITNVAAGVNNNTDAVNVA	949	
Qy	447	QLK-----GVAQ-----	453	
Db	950	QLKASEAGSVRYETNADGSVNYSVLNLGDSGGTTRIGNVSAAVNDTDAVNYAGLKRVSVE	1009	
Qy	454	-----NLNRRINDVNGNARAGIAQAIATAGLVQAYLPCKSHMAIGGGYRGEAG	502	
Db	1010	EANTYTDQKWEENSKLKGIEKNKSGGSIASMANAGLPQAYAPCANNTSTAGGTFNGESA	1069	
Qy	503	YAIGYSSISDGGNWIIKGTASGNSRGRHFGASASVGYOW	540	
Db	1070	VAIGVSWVSGGWVYKQGTSSNGQSYSAIAGAGFOW	1107	

RESULT 6

A82615
surface protein XF1981 [imported] - *Xylella fastidiosa* (strain 9a5c)
C:Species: *Xylella fastidiosa*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82615
R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: A82615; MUID:20365717; PMID:10910347

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1588 <H
A;Cross-references: G
A;Experimental source
C;Genetics:
A;Gene: ECs4480

Query Match	13.0%;	Score 358;	DB 2;	Length 1588;
Best Local Similarity	24.5%;	Pred. No. 1e-10;		
Matches 144;	Conservative 79;	Mismatches 228;	Indels 136;	Gaps 22;

Qy		70	NGTNTYSLKDDLTDLTSVGTSEKLPSAHGKNVN-ITSDTKGLNFAKETAGNGDITVVHL	128
			: : : : : : : :	
D _b		1022	NATNMITEQNQTIIINQLAGNTDATYIOENGAGINYYRTNDGDAFNDSAQGVGAIGY	1081
			: : : : : : : :	

Qy	129	NCI	-----GSTLTDTLNLTGA-TTNVTNDNV-----	TDDE	157
			! : : : : ! : : : ! : : ! : !		
Db	1082	NSVAKGDSVAIGQGSYSVDVFIAGLSSSVSRVIAKGRSDTSITENGWVICYDTDTGGE			1141

Qy	158	KKRAASVKD-----	VLNAGNIKGVKPGTTASDNDFVVRTYDTVEFLSADPKTTTVNVE	211
Db	1142	LLGALSIGDGGKYRIQIIN-----	-VADGSEAHDAVT--VROLQNAIGAVATPTTKYEHAN	1193

Qy	212	SKDNGK	----	KTEVKIGAKTSYIKEK	----	-----	DGKLVTGDKDGE	-----	245
Db	1194	STEEDSLAVGTD	SLAMGAKT	IVNGDKIGIGY	GVYDANALNGA	IGSN	AOVTHVNSTAI	1253	

Qy	246	-NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGO-----TGADKFETVTSGTN	297
		: : :	
Db	1254	GNGSTTRGAOTNYTAYNMDAPONSVCFEFSGSADGROITNVAAAGSAD-----TDVNV	1308

QY	298	TFASGGKTTATVSKDDQGNITVM-----YDVNVGDAL-----	-----NVNQL	334
Db	1309	--GOLKYTDAQVSONTO-SITNIDNRVTNIDSRVTNITFNGIGIVTNGSTKYKFTNDCV	-----	1365

QY	335	QNSGWNLDKAVAGSSKVISGNVSPKGM---	DETVNINAGNNIETRN---	GKN---	385
Db	1366	DSAAOGKDSVATGSGTAAADNSVALCTGSA	TEFTNISVGSSTNOBPITVNAAGKATD	1425	

QY 386 - IDIATSMTPQSSVSLGAGADAPTLTSDGDALNVGSKKDKNPVRIRINVPAGVKEGDVTN 444
::: |
Dd 1426 ANVAOLIKSSRAGGVVDTKRGD--STDVSNTIGC-CNGCGTRPISNYSCVNNNDVYN 1491

QY 445 VAQLKGVQ-----NLNNRIDVNGNARAGIAQAATATAGLVAQYLPGKSMMMAIG 493
|||||
Dh 1482 VAQLKGVQGVGVTGGDDVVNDKTSKSTPSTSCCTCSNMAMTCTDQNYMTCSSMGIC 1543

[illegible]

RESULT 9

probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

R: Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, D.A.; Deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; El, M.; Rucherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.;

A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0110

A: Molecule type: DNA
A: Residues: 1-658 <KOR>
A: Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:gl5978974; GSPDB:GN00175

A; Gene: YFO902

Query Match 12.0%; Score 331.5; DB 2; Length 658;
Best Local Similarity 25.2%; Pred. No. 7.7e-10;
Matches 132; Conservative 74; Mismatches 204; Indels 113; Gaps 22;
QY 50 GVLTAAREITLTKAGDNLKIKQNGTFNFYSLLKKDLTDLTSVGTETKLSFSAHGNKVNITSQK 109
||||:||||:||||:
Db 217 GAVTSCAANSTALG-AASINTVGAQSSVSAAVATAPQASVGFGLGIG-TALGNP-KITGVAA 273

Qy	110 G L N F A K E T A G T N G D T T V H L N G I G S T I T D T L L N T G A T N V T N -- D N V T D D E R K K R A A S V K D V 167
Db	274 G ----- S A S D A N V N A Q L T A G D Q V Q O N ----- T A N I T S L G G R V T T I E --- G S M A S I 317

Qy	168	LNAGWNIKGVPGTTASDNVDVFRTYDVEFLSADTKTTTVNESKDGKKT-----EV	221
Dd	318	ANGG-GVKYFHNSTDPDS-----ASGTNSVAITCPASLASNLAASGAGV	364

Qy	222 -KIGAKTSVIKEKDGLVTKDKGENGSSSTDEGEGLTAKEVIDAVNKAGWRMKT	281
<div style="text-align: center;"> : :</div>		
Db	365 AIG--GCAASADGSVAIGOCSDNGRVENIG-----KYSNASNTS	405

Qy	282	TGQADKFEVTSGTNNVTFASCKGTATATSVSKDDQGNTITVMYDYNVGDAALNVQLQNSGNL	341
	:	: :	:
	:	TVSGNTAT---	GETRVSNAVDG-----
Db	406	SG-----	442
	:	TVSGNTAT---	GETRVSNAVDG-----
	:	TSVSGNTAT---	LOATAVNRLDGG----

QY 342 DSKAVAGSSGVIISGVNVSPPSKGKMDETVINAGNNI-EITRNGKNIDI--EATSMTPQFSS 398

Dh 443 ----TAAATVVENNVNVSGLONGTCGMFOVNNSSGGIAPKPSATGANSATGGAGSVASGNNNS 497

```
QY      VSLGAGADAP-----TLSVDGDALNVGSKKDNKPVRITNVPAGVKEGDVTINVAQL 448
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dh     498 TAFGCGAKATAAANSAAIGANSVADRANSVSGSVGNRP--OTTNPAPATOCGTDAVNFDOL 555
```

QY 449 KGVAQN---LNNRIDNVDGNAR-----AGIAQAATATAGLVQAYLPKGSMMIAIGGTY 497

DB 556 KTSISNOTNVAVNPQYSEFKODIPKONSVI SGCIASMSMSASTQDPTYSGSMTTIGASV 615

QY 498 RGEAGYAIGYSISDGGNWIILKGTASNGSRGHFGASASVGYQM 540
||||| : ||||| : ||||| : ||||| : ||||| :
DB 616 PGCAATSLGVSTSDGCBWFWYLONSGTODFECYVCVGYQM 558
||||| : ||||| : ||||| : ||||| : ||||| :

RESULT 10
N4395

high-molecular-weight surface-exposed protein HMW1 - Haemophilus influenzae
C:Species: Haemophilus influenzae
C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999

R: Barenkamp, S. J.; Leininger, E.
Infect. Immun. 60, 1302-1313, 1992
A: Title: Cloning, expression, and DNA sequence analysis of genes encoding non-

A:Reference number: A43855; PMID:92192797; PMID:1548058
A:Accession: A43855
A>Status: preliminary

A;Residues: 1-1536 <BAR>
A;Cross-references: GB:U08876; GB:M84616; NID:g475770; PIDN:AAA20527.1; PID:g475770
A;Note: sequence inconsistent with the nucleotide translation

Query Match	8.3%	Score 228.5	DB 2	Length 1536
Best Local Similarity	22.1%	Pred. No. 0.00044		

	QY	51 VLTAREITLKGADNLKIKONGTNTFT-YSLKKDLTLDTLSVGTKEKLFSFSAHGN-----100 : :: : : : : : : : : : : : : : 126; CONSERVATIVE 83; MISMATCHES 413; INDELS 145; GAPS 20;
--	----	---

DD	760	VINSKIFNVSTGSSLRKFISSIKIGFSLDEL-LNAIGNMLIQVEGIDMIGKGV	824
QY	101	-KVNITSDTKGLNFAKETAGT--NGDITVHLNG---IGSTL-----TDLLNTG	143

DD . 825 AKNNLTFEGGNLTFUSKRAVTELEGNVINNNANVLJGSDFNHUKPLTKDKVJLNSG 884

QY 144 ATT---NVTN--DNVTDDEKKRAASKVDVLNAGWNIKGV-----KPGTTASD- 185

Db 885 NLTAGGNIVNAGNLTVESN---ANFRATNFTENVGGLFDNKGNSNISIAKGARPKDI 941
Qy 186 -----NVDFVRYTDFEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIKEKDKGL 237
Db 942 DNSKNLSITNSSSTYRTIISGNTNKNGLDNLNITNE--GSDTEMOIGGDVS---QKEGNL 996
Qy 238 VTGRDK-----GENGSSTDEGEGLVTAKEVIDAVNKAQWRMKTTFANGQTQAD 286
Db 997 TISSDKINIKITIKAGVDGNSDS-----DATNNANLTIKT----- 1034
Qy 287 KFETVTSQNTVTFASGKGTATYVSKDDQGNITVMYDYNVGDALNV-----NOLQNSGNL 341
Db 1035 KELKLTQDLNI---SGFNKAEITAKD--GSDLTIGNTSADGNTNNAKVTENQVQKDSISA 1089
Qy 342 DSKAVAGSSGKVISGNVSPSKGKDETVNINAGNNIETTRNGKNIDIASMTPOFSSVSL 401
Db 1090 DGHKVTLHKSVEVSGSNNTEDSSD-----NNAGLTIDAKNVTYNNNIT-SHKAVSI 1140
Qy 402 GAGADAPTLSDGALNVGSKKKNKPVRTNVPVK--EGDVTNVAQLKGVAQNLNRI 459
Db 1141 SATSGETTKT-GTTINATTGNVEITATGTSILGIESSGSVTLTATEGALA-----V 1193
Qy 460 DNVDGNARAGIAQAIATAGLVOALPKGSMMAIG-----GGYRGEAGTAIGVSSISDG 513
Db 1194 SNISGNTVTVTNSGALTTLAGSTIKGTSVTTSSQSGDGGTISGTVYKATESLTQ 1253
Qy 514 GNWLIK-----GTASGNS 526
Db 1254 SNSKIKATTEANVTSATGIGGTISGNT 1282
RESULT 11
C48399
ABC-type transport protein ydbA.2 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 19-Nov-1993 #sequence_revision 16-Oct-1998 #text_change 01-Mar-2002
C:Accession: C48399; D64891; H64891
R:Moszer, I.; Glaser, P.; Danchin, A.
Biochimie 73, 1361-1374, 1991
A:Title: Multiple IS insertion sequences near the replication terminus in Escherichia coli
A:Reference number: A48399; MUID:92190338; PMID:1665988
A:Accession: C48399
A:Molecule type: DNA
A:Residues: 464-2020 <MOS>
A:Cross-references: GB:D85081; NID:g3041754
A:Experimental source: strain K-12
A:Note: sequence inconsistent with the nucleotide translation
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cro
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: D64891
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-839, 'LDLPLYFQTSVIT' <BLA1>
A:Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74483.1; PID:g1787668;
A:Experimental source: strain K-12, substrain M61655
A:Accession: H64891
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 'M', 915-2020 <BLA2>
A:Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74487.1; PID:g1787672;
A:Experimental source: strain K-12, substrain M61655
C:Genetics:
A:Gene: ydbA.2
A:Start codon: GTG
Query Match 7.7% Score 212; DB 2; Length 2020;
Best Local Similarity 24.28; Pred. No. 0.0044;
Matches 160; Conservative 70; Mismatches 216; Indels 216; Gaps 37;

Qy 17 TVAVLIVNSDKEGAGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNTFY 76
Db 195 TVALGVSAD--GA-----TKWOYNHNGELVIT-----GDNATVNNNG----- 230
Qy 77 SLKDKLFDLSVSGTE-----KLSFSAHGNKVNTISDT-----KG----- 110
Db 231 --KTTVDGKDSGTGEINGNNGKVIQDGLDVGSGGHGIDITGDSATVDNKGTMVTVDOPES 288
Qy 111 -----LAFKATAGTNGDTTVHLNG-----IGSTLTDLTLLNTGATTNVNDN 152
Db 289 MGIOIDGKAIIVNNEGESTITNGGTGTQINGDDATANNNGKTTVDGKDSGTGEINGNNGK 348
Qy 153 VTDEKKRAASVKDVLNAGWNKGVKPGCTASDNVDFRVTVDFEF--LSADTKTTTNNVE 211
Db 349 VIQD-----GDLVSGGGHGI--DITGDSATVDNKGTMVTVDPEISIGIQVDGQAVVNE 401
Qy 212 SKD-----NGKKEVTKIGAKTSVIKEKDGKLVTKD-KGENG----- 247
Db 402 GESAITNGGTGTQINGDDATANNNGKTV-----DGKDSGTGTEIAGNNGKVIQDGLDVG 457
Qy 248 -----SSTDGEGGLVTAKG-----VIDA-----VNKAGWRMKTTFANGOTGQADK 287
Db 458 GGHGIDITGDSATVDNKGTMVTVDPEISIGIQDQQAIVNNEG---ESTITNGGTG--- 510
Qy 288 FETVTSQNTVTFASGKGTATYVSKDD-----QGNITVMYDYNVGDALNV-----NOLQNSG 338
Db 511 --TQINGNDAT--ANNSGKTTVDGKDSGTGKIAGNIGI---VNLDSLTVTGGAGHVENIG 564
Qy 339 WN--LDSK-----AVAGSSKVISGNVSPSKGKDETVNINAGNNIETTRNGKNIDIAS 391
Db 565 DNGTVNNKGDIVVSDTSGISGVLINGEGATVSNITGDVNVV--NEATGFSITTTNSGKVSLAGS 623
Qy 392 M-TPQFS-----SVSLGA-----GADAPTLSDGALNV---GSKKDNKPVRT 431
Db 624 MQVGDFSTGVDLNGNNSVTLAAKDLKVGGKATGIVNSGDANTVNTGVNVLVDKDKTAD 683
Qy 432 NVA-----PGV-----KEGDTNVAQLKGVAQN--LNNRIDNV--DGNARAGIAQAIATAG 478
Db 684 NAAEYFFDPSPGVINGVSDNNVTLDGKLTVVVSDSEVTSRQSNLFDGSAE-----KTSQ 736
Qy 479 LV-----QAYLPCKSMATGGGTGYREAGYAT-----GYSSISDGGNWII 518
Db 737 LVVIGDGTVMNMGLELIGEKNALADGSQVTSURTGYSTVTSVIVSGESSVYLNGLDGTI 796
Qy 519 KG 520
Db 797 SG 798
RESULT 12
T09083
hemagglutinin/hemolysin-related protein NMB1214 [imported] - Neisseria meningitidis (N)
N:Alternate names: probable secreted protein
C:Species: Neisseria meningitidis
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 19-Jan-2001
R:Simpson, N.J.; Spratt, B.G.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z16558
A:Accession: T09083
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2273 <SIM>
A:Cross-references: EMBL:AF030941; NID:g2623257; PID:g2623258
A:Experimental source: strain 44/76
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masiugnani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: B81109
A:Molecule type: DNA
A:Residues: 1-2273 <TEXT>
A:Cross-references: GB:AE002469; GB:AE002098; NID:g7226446; PIDN:AAF41596.1; PID:g722645
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: pspA; NMB1214

Query Match 7.6%; Score 209; DB 2; Length 2273;
Best Local Similarity 20.8%; Pred. No. 0.0073;
Matches 132; Conservative 78; Mismatches 238; Indels 188; Gaps 26;

QY 47 NEKGVLTAIREITLKAGDNLIKQ---NGTNYFSLKDLTDLTSVGTSEKLSFSAHGNKYN 103
DB 1002 NRGGLIAGREALILNAQNIKNLQGLQGNFAAGSDITNTGSICAEALLKASNNIE 1061
QY 104 ISTDPKGLNFAKTAGTNGDIT-VHLNG--IGSTLTD---LLATGATTNTNDNVTD 156
DB 1062 SRSETRSNQNEGSRVNRIGRVAGIYLTGRQNSVLLDAGNNIVLTASELTNSEDGQT-- 1119
QY 157 EKKRAASVKDVLNAGNIVGVPGTTASDNVDF-----VRYTDVTF- 198
DB 1120 -----VLNAGDIRSDTIGISRNQNTIFDSNYYVIRKEQNEVGSTIRTNLSLN 1169
QY 199 LSADPKTTTVNVEKDNGK-----TEVKIGAKTSVKEKDKGLVTGKD----- 242
DB 1170 AKGDIRIRAAEYVSGEQLKLAAGRDIKVEAGKAHTETEDALKYTGSRGGGIKQKMRHL 1229
QY 243 KGENSSSTDGEGLYTAKEVIDAVNKAGWRMKTITANGOTGOADKFEFVTSCTNYTF--- 299
DB 1230 KNQNGQAV---SGTLDGREIILVSG-----RDIIVTGSNIADNHTILSAKNIVLKAA 1280
QY 300 -----ASGKGTATVSKDDQGN--ITVMYDVNVDALVNOLQNSG 338
DB 1281 ETRSRSAENKKEKSLGSGGIGFTAGSKKDTQNRSETSVSTESVVGSLNGNTLISAG 1340
QY 339 WNLDSKAVAGSGKVIYSGNVSFSGKMDTVNINAGN-----IETRNKKNIDIATSM- 392
DB 1341 KHYTQ---TGSTISSPGQDVGISGK-----ISIDAAQNRYSQESQVYEQKGVTAISVP 1393
QY 393 -----TPQFSSVSLGAGADAPTLSDV-----GDAL 417
DB 1394 VYNTVMGAVDAVKAVQTGKSNRNVMAAANALNKGVDSGVALYNAARNPKAAGQGI 1453
QY 418 NV-----GSKKNKPVRIITNAPGVKGDVT----- 443
DB 1454 SVSVTYGEQKNFSERIKGTQ--VQEGKITGGKVSLSLTASGAKDSRITITGSDYVGKG 1511
QY 444 -----NVAQLKGVQNLNRIDNDGNARAGIAQAIATAGLVQAYLPKSM-MAITGG- 495
DB 1512 TRLKAENAVQIEAARQTHOERSENKSNAGFAGVATAI-NKGISFGFTAGANYGKGYNGD 1570
QY 496 --TYR-GEAGYAIQYSSISDGNWIIKGPASNSRG 528
DB 1571 ETAYRNHSHGKDSQTAIESGGDTVIKG---GOLKG 1603

RESULT 13
AF0394
Probable adhesin hmwA [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0394
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175
C:Genetics:
A:Gene: hmwA

Query Match 7.5%; Score 207; DB 2; Length 1910;
Best Local Similarity 23.1%; Pred. No. 0.0074;
Matches 126; Conservative 67; Mismatches 180; Indels 172; Gaps 27;

QY 49 KGVLTAREITLKAGDNLIKQKQNTFYSLKDLTDLTSVGTSEKLSFSAHGNKVNITS-- 106
DB 803 KGIWISGKTNLASGNVNLHGVTTSAYA-----CADAIKISGNSSNNVNITAGG 853
QY 107 --DTKGLNPAKETACT-----NGDTTVHLNGI-GS---TLTDLTLLNTGATNTYT 149
DB 854 HISLIAVNGGKEIGSTSVSDYANIATKAGDFENLITGMKSGSPENNATITANNISMGNIT 913
QY 150 -NDNV--TDDEKKRAASVKDVLNAGNVIKGV---KPGTTASDNVDFTYDTVEFLSAD 202
DB 914 ANDAVLMTFTLTAKGDIKTDLT--PTKGLMFRGNGMTAANNILLVAN-----STSS 965
QY 203 TKTITTVNVEKDKNGKKTEVKIGAKTSVKEKDKGLVTGDKGKNGSGSTDEGEGLVTAKEV 262
DB 966 GETVKINASSN-----KNITAGKDISIIAGNSKTATGPNIN----- 1003
QY 263 IDAVNKAGWRMKT---TANGOTGOADKFEFVTSCTNYT-----PASGKGTATVSKDD 313
DB 1004 IENVN-----IETNNGNFTNGIT-----STWLSGVNVSVANGVDITSNSTGTGGVLDN 1052
QY 314 QGNITVMYDVNV-----GDALNVNOLQNSGNLDSKAVAGSSK-----VISGNVSPS 361
DB 1053 TWILFTVVGDIINTVTVNSSKGVIKSNSTLNS--NKDITLVGSAGONEGVIIQSGSDAS 1110
QY 362 KCKMDETVNI---NAGN-----NIEITRNKKNIDIATSMTPQFSSVSLGAGAD 406
DB 1111 RNNISAGQNTILIKMGNGSGQSHLINLGNVLSITSSGRNIDNGS-----SAGTG-- 1160
QY 407 APTLSVDGALNVGSKKDKNPVRITNVAPGVKGDVTNVQAQLGVQAQNLNRIDNDVGN- 465
DB 1161 -----DVYFTNVELNATAGNVSIVAEKTKALTSLTSLNAVLSGGNN 1200
QY 466 ---ARAGIAQAIATAGLVQAYLPKGSMAIGGTGTYRGEAGYAIQY---SSISDGNWIIK 519
DB 1201 STKAQNG-----WLIQKA-----FNTQOGAGIGFRANSSLSVDGNIIILK 1239
QY 520 GTASG 524
DB 1240 GETEG 1244

RESULT 14
T31105
hypothetical protein 2 - Haemophilus ducreyi
C:Species: Haemophilus ducreyi
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T31105
R:Ward, C.K.; Lumley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A:Reference number: Z20984; MUID:99030326; PMID:9811662
A:Accession: T31105
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4919 <WAW>
A:Cross-references: EMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AAC79761.1
C:Genetics:
A:Gene: lspa2

Query Match 7.5%; Score 206.5; DB 2; Length 4919;
Best Local Similarity 22.1%; Pred. No. 0.026;
Matches 147; Conservative 73; Mismatches 213; Indels 231; Gaps 32;

QY 48 EKGVLTAIREITLKAGDNLIKQKQNTFYSLK-KDLTDLTSVGTSEKLSFSAHGNKVNITS 106
DB 48 EKGVLTAIREITLKAGDNLIKQKQNTFYSLK-KDLTDLTSVGTSEKLSFSAHGNKVNITS 106

```
Db 477 DKASVLAHKLTNISNDVSLNOSKLSANNLKKIKYVRDLNLNSE---LSANNLTNTSN 533
Qy 107 DTKGLNFAKETAGT---NGDTTVHLNGIGSTLTDTLINTGATTVNT-----149
Db 534 NITLKNKSFAGNMVLTNNVTLNN-DSELAANLTLNVTKNVTLNDASKLSANKL 592
Qy 150 --NDNVTDDKKRAAS-----VKDV-----LNAGWNKGVKPGCTTASDN 186
Db 593 NVTDNVTLNSKLSAGELTFKKVKVNTLNDSELAANLNLNASHNVTLLNNKSKLSAQ 652
Qy 187 VDF---VRTYDVEFL--SADTKTTTVNVVESDNGKTKTEVKIGAKTSVIKEDGKL---237
Db 653 ADIKAVNLINDTELTAKNLDINSTIIT---NNGTIACIPANITEKLNNEKALILA 708
Qy 238 -----VTGDKD-----GENGSTDEGEGLVTAKEVIDAVNKAQWRMK 274
Db 709 EQNLNFTVNGSHYENKGDIVSKDKATVTFKSNDSFTSNGSKLYNAQN-----QLK 758
Qy 275 TTTANGOTGQADKFETVTSNTWTF-ASGKGTATVSKDDOGNITVMYDVNVGDALNVNQ 333
Db 759 VMYNNFTISQGD---DITLIGNVTLNASGTF-----NSGNLTVTKTLDDVGDIQFTN 808
Qy 334 LON---SGWNLDSKAVAGSGKVIS-----GN---357
Db 809 KGNLTGVEDLHIKSKYKITNDGKLISIKNLNISSEADFINNGFLILGIEALKIATKGNFTN 868
Qy 358 -----VSPSKGKMDVTN---INAGNNIEITRNGK--NIDIATSMT-PQFSS 398
Db 869 KEKAILASLLDISVAEGK--RTFNNGTIESCKNLNITNGAFLNVDNATISFGVLNI 926
Qy 399 VSLGAGADAPTLSDGDALNVGSKKONKPVRTNVPAG-----VKEGDVTN---444
Db 927 TSTGNVSNNGTL-ISNERLNITS-----AANFTNESNGTVMSNGLNLIITAKOGNITMKNL 980
Qy 445 -----VAQLKGVAQNLRNDVGNARAGIAQIATAGLV-----QAVLPG-----486
Db 981 IASRQQLNTAVADNITN-----DSNISNKIA-VLHSLGNISLNSKDDVYNLGEIYAGNN 1034
Qy 487 -----KSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHEGASA 534
Db 1035 ISVKAHQKNDVKLMGDMITTKREGQASYKLYQAS-----NGGHEGNDG 1078
Qy 535 SVGY 538
Db 1079 SSGY 1082

RESULT 15
I40711
sapB protein - Campylobacter fetus
C:Species: Campylobacter fetus
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
C:Accession: I40711
R:Dworkin, J.; Tummuru, M.K.; Blaser, M.J.
J. Biol. Chem. 270, 15093-15101, 1995
A:Title: Segmental conservation of sapA sequences in type B Campylobacter fetus cells.
A:Reference number: A56999; MUID:95318069; PMID:7797493
A:Accession: I40711
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-936 <RES>
A:Cross-references: EMBL:U25133; NID:g801999; PIDN:AAA79683.1; PID:g802000
C:Genetics:
A:Gene: sapB

Query Match 7.4%; Score 203; DB 2; Length 936;
Best Local Similarity 22.8%; Pred. No. 0.0048;
Matches 130; Conservative 77; Mismatches 244; Indels 120; Gaps 27;

Qy 25 SDKEGAGE-----KEKVEENSDWAVYFNKEKGVLTAREITLKAGDNLKIKONGTNTFTYSLK 79
Db 281 SDETSQDFVFNKGVKVG-----FNVLGDIAS--FATDASKSVNVEITGT-----323
```

```
Qy 80 KDLTDITSVGTEKLSAHSAGNKVNITSDTK---GLNFAKET---AGTNGDTTVHLNGIGS 133
Db 324 --ITAFTAAGTGVDDVVA-GKITALTADSATSYNLTATNDITLTLSANAATSYNLKTSGA 380
Qy 134 TLTDTLLNTGATTVND-----NVTDDKKRAASVKDVLNAGWNKGVKPGTTASDNVD 188
Db 381 AKSATITSAANAANIITIDATGVAAVTSATAVENLTVKHATNVTLAGNMDKLAIVTLDNAA 440
Qy 189 F-----VRTYDVEFLSADTKTTTVNVESKD-----NGKKEVKGIGA-----KTSVIKEK 233
Db 441 LTAADIKSASTLNLINSSVNGHNISSTAADVTVHLSSAAKVKLNTTAATDQTVTLKAN 500
Qy 234 --DGKLVTKDKGKENGSSDDEGEG---LVTAKEVIDAVNKAQWRMKTTTAN-----GQ 281
Db 501 ATDNSLEFDSGTAKTTSVTASGSGKTLIVKGAESVETLVN-----IDTAFNGAADVSFGK 555
Qy 282 TGOADKFETVTSCTNVTFFASGKGTATVSK--DDQGNITVMYDVNVGDALNVQLNOLNSG 339
Db 556 DAOSGRF-SVKTGTGDDKIEFVGTTLTTEGVIDGAGNDTIAMKSAALTSANFTWIKNIE- 613
Qy 340 NL---DSKAVAGSGKVISGNVSPSKGKMDVTNINAGNNIEITR-----381
Db 614 NVAISDAVATADLSSSAFKNIITTKEAADTLTINKDQVINFTAADRGSVKLITVKLND 673
Qy 382 -NGKN--IDIATSMTPQFSSVSLGAGADAPTLSDG--DALNVGS-KKDNKPVRTNVP 435
Db 674 VTGANDVVKTVLDAARAKDASIALGTEATDKALVIDTGTETLNTISLVKATSPENTANTV- 732
Qy 436 GYKEGDTVNAQLKGVAQNLRNDVGNARAGIAQIATAGLVQAYLPKGSMAIGGG 495
Db 733 NAKLTDVTSII-----IDGDAKITLGHGA-GTAGTDYSKVSMDIARAL---773
Qy 496 TYRGEAGYAIGYSSISDGGNWIKGTASGNS 526
Db 774 ----KAGLTFDASAITLGANATIKGSGADS 800
```

Search completed: October 6, 2003, 09:33:28
Job time : 18.4576 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 8.33898 Seconds
(without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-33

Perfect score: 2757

Sequence: 1 NNEQEYLYLHPVQRTVAV.....TASGNSRGHFGASVGYQW 540

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	212	7.7	2003	1	YDBA_ECOLI	P33666 escherichia
2	189	6.9	2249	1	OMPA_RICRI	P15921 rickettsia
3	187.5	6.8	1953	1	BIGA_SALTY	P25927 salmonella
4	185	6.7	1654	1	OMPB_RICRI	Q53047 r outer mem
5	183.5	6.7	1608	1	HLXA_SERMA	P15320 serratia ma
6	182.5	6.6	1039	1	AG43_ECOLI	P39180 escherichia
7	182.5	6.6	1577	1	HLXA_PROMI	P16466 proteus mir
8	181.5	6.6	1645	1	OMPB_RICTY	P96989 r outer mem
9	177.5	6.4	1007	1	Y741_CHLMU	Q9P1t6 chlamydia m
10	177	6.4	917	1	HXA3_HAEIN	P45355 haemophilus
11	177	6.4	1655	1	OMPB_RICCN	Q9kka3 r outer mem
12	176.5	6.4	1569	1	YPUA_ECOLI	P52143 escherichia
13	174	6.3	1567	1	ICEN_YANCT	P18127 xanthomonas
14	173.5	6.3	2334	1	WAPA_BACSU	Q07833 bacillus su
15	173	6.3	933	1	SLAP_CAMFE	P35827 campylobact
16	170.5	6.2	1656	1	OMPB_RICJA	O06653 r outer mem
17	170.5	6.2	2021	1	OMPA_RICCN	Q52657 rickettsia
18	169.5	6.1	928	1	HXA2_HAEIN	P45354 haemophilus
19	169	6.1	918	1	YMBJ_CAEEL	P34487 caenorhabdi
20	167	6.1	1643	1	OMPB_RICPR	Q53020 r outer mem
21	163.5	5.9	1861	1	APU_THETU	P38536 t amylopull
22	162	5.9	2660	1	YEJF_ECO57	P08877 escherichia
23	161.5	5.9	1286	1	AIDA_ECOLI	Q03155 escherichia
24	161	5.8	550	1	FLIC_SHIFL	Q08960 shigella fl
25	161	5.8	1148	1	ICBK_PSESX	O30611 pseudomonas
26	160	5.8	1300	1	120K_RICRI	P14914 rickettsia
27	159.5	5.8	642	1	FLID_CAMJE	Q9phw6 campylobact
28	159.5	5.8	2358	1	YEJF_ECOLI	P76347 escherichia
29	158.5	5.7	1025	1	SLAP_CAUCR	P35828 caulobacter
30	157.5	5.7	3178	1	YS99_CAEEL	Q09624 caenorhabdi
31	157	5.7	737	1	ALYS_ENTFA	P37710 enterococcu
32	157	5.7	928	1	PM10_CHLPN	Q9rb65 chlamydia p
33	157	5.7	1153	1	PVDB_PLAKN	P50493 plasmodium

RESULT 1

ID	YDBA_ECOLI	STANDARD;	PRT;	2003 AA.
AC	P33666;	P76087;	P76856;	P76857;
DT	01-FEB-1994	(Rel. 28, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Hypothetical protein ydbA.			
GN	YDBA OR B1401/B1405.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=97426617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:1453-1474(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=97251357; PubMed=9097039;			
RA	Aiba H., Baba T., Fujita K., Hayashi K., Isono K., Itoh T.,			
RA	Kasai H., Kashimoto K., Kimura S., Kitagawa M., Kitagawa M.,			
RA	Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,			
RA	Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,			
RA	Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,			
RA	Takekoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;			
RT	"A 570-kb DNA sequence of the Escherichia coli K-12 genome			
RL	corresponding to the 28,040.1 min region on the linkage map.";			
RN	DNA Res. 3:363-377(1996).			
RN	[3]			
RP	SEQUENCE OF 464-2003 FROM N.A.			
RC	STRAIN=K12;			
RX	MEDLINE=92190338; PubMed=1665988;			
RA	Moszer I., Glaser P., Danchin A.;			
RT	"Multiple IS insertion sequences near the replication terminus in			
RL	Escherichia coli K-12.";			
RL	Biochimie 73:1361-1374(1991).			
CC	-1- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYS8 (AC P25928).			
CC	-1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION: THE GENE CODING FOR			
CC	THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT			
CC	BETWEEN AMINO ACIDS 839 AND 840.			
CC	-----			
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P04949 escherichia
O33479 pseudomonas
P06620 pseudomonas
Q06974 salmonella
P44969 haemophilus
P45384 haemophilus
Q06968 salmonella
P18481 streptococ
P15345 caulobacter
Q48253 helicobacte
P32051 escherichia
P46949 saccharomyc

```
CC EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -: NOT_ANNOTATED_CDS.
DR EcoGene; EG11307; ydbA.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

Query Match
Best Local Similarity 7.7%; Score 212; DB 1; Length 2003;
Matches 160; Conservative 70; Mismatches 216; Indels 216; Gaps 37;

QY 17 TVAVLVNSKEGAGEKEVEENSDWAVYNEKGVLTAREITLKAGDNLKIKONGINFTY 76
Db 195 TVALEGVSD--GA-----TKWYNHNGELVIT-----GDNATVNNNG-----230

QY 77 SLAKDITLTSVTE-----KLSFSAHGKKNVITSDT-----KG-----110
Db 231 --KTVVDGKDTGTEINGNNGKVIQDGLDVSOGGHCIDITGSAVDNKGTVTDPES 288

QY 111 -----LNPAGETAGTNGDTTVHLNG-----IGSTLTDLTLLNTGATNTVNDN 152
Db 289 MGIIQIDGKAIVNNEGESTITNGTGTQINGDDATANNNGKTVTDGKDSGTGTEINGNNGK 348

QY 153 VTDEKRAASVDNLNAGNINIKVPGTASNDVDFVRYDVPEF--LSADTKTTVNVVE 211
Db 349 VIQD-----GDLDSVGGHGI--DITGDSATVNDKGTMTVDPESIGIQDVGQAVVNE 401

QY 212 SKD-----NGKTEVKIGAKTSVIKEKDKLVTKGD--KGEG-----247
Db 402 GESAITNGTGTQINGDDATANNKTTV-----DGRDSTGTEAGNNGKVIQDGLDVS 457

QY 248 -----SSTDEGEGLVTAKE-----VIDA-----VNKAGWRKTTTANGOTGOADK 287
Db 458 GGHGIDITGDSATVDNKGTVTDPESIGIQDQDAIVNNEG---ESTITNGTG-----510

QY 288 FEVTSCTNTVFASGKGTATVSKDD-----QGNITVMYDVNVGDALNV---NQLQNSG 338
Db 511 --TQINGDAT--ANNSKTTVDGKDTGTGKIAGNIGI---VNLDSGLTVTGGAGHVENIG 564

QY 339 WN--LQSK-----AVAGSSGKVISGNVSPSKMDETVNIAGNIIETIRNGKNIDIATS 391
Db 565 DNGTVNKGDIIVSDTGSIGVLINGEGATVNSNGDVNSV-NEATGFSITNSGKVSLAGS 623

QY 392 M-TPOFS-----SVSLGA-----CADAPTLVSVDGALNV-----GSKDNKPVRI 431
Db 624 MQVGDFSTGVDLNGNNSVTLAAKDLKVVGGQKATGINVSGDANTVNTITGNVLVDKDKTAD 683

QY 432 NVA-----PGV-----KEGDVTNVAQLKGAON--LNNRITDNV--DGNARAGIAQATATAG 478
Db 684 NAAEYFDPSPVGVINGVSDNNVTLGKLTIVSSEVTSROSNFLDGSAE-----KTS 736

QY 479 LV-----QAYLPKGMMAIGGTYRGEAGYAI-----GYSSIDGGNWII 518
Db 737 LVVIGDGTNTVMNGGLELKEKNALADGSQVTSIRTCYSYTSIVVSGESSVYLNGDTTI 796

QY 519 KG 520
Db 797 SG 798

RESULT 2
OMPA_RICRI
ID OMPA_RICRI STANDARD; PRT; 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DF 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
```

```
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
GN antigen) (rOmpA).
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly
RL repeated, near-identical sequences.";
RL Infect. Immun. 58:2760-2769(1990).
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- PTM: GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC -----
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CC -----
EMBL; M31227; AAA26380.1; -
DR PIR; A41477; A41477.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRFAMs; TIGR01414; autotrans_barl; 3.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 358 B (TYPE I).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D646C089DF087 CRC64;

Query Match
Best Local Similarity 6.9%; Score 189; DB 1; Length 2249;
Matches 122; Conservative 64; Mismatches 208; Indels 152; Gaps 25;

QY 57 ITLKAGDNLKIKONGTN---FTYSLKKDLTDLTSVGTEKLS-----FSAHGKNVNI 105
Db 134 VTLNAGKSLFL--NGNNAVAANGFDAPADNYTGLGNIALGGANAALIQAAPSKITLA 191

QY 106 S--DTRGLNFAKETAGTNGDTTVHLNGIGSTLTDLTLLNTGATNTVNDNV---TDDEKKR 160
Db 192 GNIDGGGIITVKDAAINGT-----IGNTNALATVNVGAGTATLGAVIKATTKLTN 244

QY 161 AASVKDVLNAGNWKGVKPGCTTASDNVDFVTRTDTVEFLSADTKTTTVNVESKNGKTE 220
Db 245 AASVLTITNANAVLTGAIDNTTGGDNGVNLNAGALSQVTDIGT-----NSLAT- 295

QY 221 VKTCAKT-----SVIKEKDKLVTKGDKGNGSGTDSGEGLVTAKEVIDAVNKGWRMKT 275
```

Db 296 ISVGACTATLGGAVIKATTTKLT-----DAASAVKFTNPVVVTGAIDNTGNANNGIYV 348
QY 276 TTAN-----QOTGOAKFETVIGTGTNTVFASG---KGTATVSKDDOGNITVMYDVNVGDA 328
Db 349 FTGNSVTGCVGNATATVNVGAGLLQVGGVVKANTINLT-DNASAVTFNPPVVVTGA 407
QY 329 LNVNQLNSGWNLDKAVAGSSGKVISGWNVSPSKGMDTETVINAG-----374
Db 408 ID-----NRTG-NANNGIYFTGNSVTGTDIGNTNAL--ATVNVGAGTATLGGAVIKATTT 459
QY 375 -----NNIEITRNGKNIDIAT-----SMTPOFSSVSLGA 403
Db 460 KITNAASVLTNLNANAVLTGAIDNTGGDNVGNLNLNGALSVQVTGNIGNTSLATISVGA 519
QY 404 GADAPTSLVDGDAIYVSKKDKNKPVRITNVAPGVKEGDTNVNAQLKGVAQNLNRRIDNVD 463
Db 520 G-----TATLGGAVIKATTTK-----LTDAAASAVK---FTNPVVVTGA-----IDNT- 558
QY 464 GNARAGIAOAIATAGLVQALYLPKSKMAITGGTYRGEAGYATGYSSISDG-----GNMI 517
Db 559 GNANNGI-----VTFGTGNSVTGTDIGNTNSLATISVGAAGTATLGGAV 600
QY 518 IKTAS 523
Db 601 IRATTT 606

RESULT 3
BIGA_SALTY STANDARD; PRT; 1953 AA.
AC P25927; P25928; O9XCQ3;
DT 01-MAY-1992 (Rel. 22, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative surface-exposed virulence protein bigA precursor.
GN BIGA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 14028;
RA Stojiljkovic I., Valentine P., Heffron F.;
RT "Salmonella typhimurium rhs homolog.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE-21534948; PubMed-11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
RN [3]
RP SEQUENCE OF 1-765 FROM N.A.
RC STRAIN-LT2;
RX MEDLINE-91100301; PubMed-19871123;
RA Wu J.Y., Siegel L.M., Kredich N.M.;
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:
RT requirement for a cloned cysE plasmid to overcome limiting siroheme
RT cofactor.";
RL J. Bacteriol. 173:325-333(1991).
CC -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
CC in positions 414 and 732.
CC -----
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CC -----
DR EMBL; AF133696; AAD39458.1; -;
DR EMBL; AF000859; AAL22340.1; -;
DR EMBL; M64606; AAA27042.1; ALT_FRAME.
DR EMBL; M64606; AAA27043.1; ALT_FRAME.
DR StyGene; SG10437; bigA.
KW Virulence; Repeat; Signal; Complete proteome.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 1953 PUTATIVE SURFACE-EXPOSED VIRULENCE
FT PROTEIN BIGA.
FT DOMAIN 101 252 15 X 11 AA TANDEM REPEATS.
FT REPEAT 101 103 1 (INCOMPLETE).
FT REPEAT 104 113 2 (INCOMPLETE).
FT REPEAT 114 122 3 (INCOMPLETE).
FT REPEAT 123 133 4.
FT REPEAT 134 144 5.
FT REPEAT 145 155 6.
FT REPEAT 156 166 7.
FT REPEAT 167 177 8.
FT REPEAT 178 188 9.
FT REPEAT 189 199 10.
FT REPEAT 200 210 11.
FT REPEAT 211 221 12.
FT REPEAT 222 232 13.
FT REPEAT 233 243 14.
FT REPEAT 244 252 15 (INCOMPLETE).
FT CONFLICT 207 207 D -> DRGDDVTPDD (IN REF. 1).
FT CONFLICT 514 514 A -> R (IN REF. 3).
FT CONFLICT 1698 1698 D -> N (IN REF. 1).
FT CONFLICT 1795 1798 OYLE -> ITLO (IN REF. 1).
FT CONFLICT 1836 1837 SA -> T (IN REF. 1).
SQ SEQUENCE 1953 AA; 200150 MW; 611B3FC954D91AE CRC64;
Query Match 6.8%; Score 187.5; DB 1; Length 1953;
Best Local Similarity 23.1%; Pred. No. 0.049;
Matches 126; Conservative 63; Mismatches 195; Indels 161; Gaps 29;
QY 62 GDNLIKQNGTFTYSLKKDLTLTSVGTSEKLSFSAHGKNVNTSDTKGLNFAKETAGTN 121
Db 447 GDNATIKNTGTS-----DISGAGTGT-----VIDGNRNARNYND-----480
QY 122 GDTTVHLNGTSLT-DTLL--NTGATT-----NTNDNVNTDDEKKRAASVDVLN 169
Db 481 GDMTITGGTGHTGDNVVIDNAGSTTVSGADATALLYEGDNAL-----VIN 528
QY 170 AG-WNIKGVKPGTASDNDFVRYDTVEFLSADTKTTTVNVESKDKKTEVKIGAKTS 228
Db 529 EGNQTTSGGAVGTRIDG-----DAHTTNTGDTAVDGAGSAAVII-----568
QY 229 VIKEDGKLVTKDKGENSSSTDEGEGLVT--AKEVI--DAVNKAGWRMKTNTTANGQTGQ 284
Db 569 -----NGDNGSLTQAGDLVLTGDMAGIITYGTGNEA-----KNTGNATVRD 609
QY 285 ADKFETVTSCTNVTF-----ASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNS 337
Db 610 ADSVGFVAGEKNTFRNKGDIDVSLNGTICALVS-GDMSQVTLDCDINV---VSVQDSEGV 665
QY 338 GWNLDKAVAGSSGKV-ISGNVSPS-----KGMDETVMINAGNIEITRNGK-NI 386
Db 666 FSSATGVSVDGSDSNAVDITGNVNISADYGDDDLAAGAPPLTGTVGVGNGTIVLNGALNI 725
QY 387 ---DIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVAPGVKEGDTV 443
Db 726 DNDLSATGGQYLDVVVGLSVTGDNDVDEIDG-GINITHSED--PLDCTS-----ADIT 775
QY 444 NVAQLKGVAQNLNRRIDNVDGNARAG---IAQAIATAGLV-----QAALP-----485
Db 776 GISVSGNSTVTLNGH-STIDTNTVGGHVVLARNNGGSLILGDDSVVDVNVSVIPTGY 834

```

QY 486 --GKSMAIGGTYRGEAG-----YAI-----GYSSISDGGNWIILKGTASGSRGHGA 532
Db 835 TYNALLMADGEGTSIENKGDITSHGVYSVRADNGSEVSGDILVTATSSNSSEDAAI 894
QY 533 SASVG 537
Db 895 TRASG 899

RESULT 4
OMP_B_RICRI
ID OMP_B_RICRI STANDARD; PRT; 1654 AA.
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptidel.
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia
rickettsii is encoded by an unusually long open reading frame:
evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R;
RX MEDLINE=50136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
120 kDa surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
LAYER WITH HEXAGONAL SYMMETRY.
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
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CC -----
DR EMBL; X16353; CAA34403.1; -.
DR PIR; S18227; S18227.
DR InterPro; IPR005315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRfams; TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 kDa SURFACE-EXPOSED PROTEIN.
FT CHAIN 1334 1654 32 kDa BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 6.7%; Score 185; DB 1; Length 1654;
Best Local Similarity 22.5%; Pred. No. 0.054;
Matches 147; Conservative 77; Mismatches 255; Indels 174; Gaps 30;

```

```

QY 14 VORTVAVLIIVNSDKEGAGEKEKVEENSQWAVYFNEKGVLTAREITLKAGDNLKIKONGTN 73
Db 156 VQNNNGAIDNNDLKGVG---RIDFGAPASTLVFNLANPTQKAPLILGNVAVI-ANGVN 211
QY 74 FTYSLKKDLTDLT--SVGTEKLSFSAHGNKVNTISDTKGLNFAKETAGTNGDITVHLNGI 131
Db 212 GTLVNTNGFIQVSNKSFATVKAINIADGGQIIFENTDANNANTLNQA---GGTTINFTGT 268
QY 132 GSTLTDTLLNTGATVNTNDNVTDDEKKRAASKVDVNLNAGWNKIKGVKPGTGTASDNDVDFVR 191
Db 269 DGTGRLVLLSKHAA--ATNENITG-----SLGNNLKGVIETFTVA-----VD 308
QY 192 TYDTVEFLSADTKTTVN-----VESKDNGKKTVEV--KIGAKTSVIEKDGKLVTKG 241
Db 309 GQLTANAGAAANAVIGNNGAGRAAGFVSVNDNGKVATIDQVIAKDWIUSAN---ATGQ 365
QY 242 -----DKGENS-----STDEGEGLVTAKEVIDAV----- 266
Db 366 VNFRIHVDVGADCTTAFKTAASKVTITQDSNFGNTDFG-NLAAQIKVPNAITLTGFTG 424
QY 267 -----NKAGWRMKTTHANG--QTQADKFTVTSCTNVTTFASGKT-----TAVVSKD 312
Db 425 ASNPNGTAG--VITFDANGTLESASADANVAVTNITAIASAGVYVQLSGTHAAELRLG 482
QY 313 DOGNITVMYDVNVGDALN--VNOLQSGWNLDKAVAGSSGKVTISGNVSPSKGM----- 365
Db 483 NAGSIFKLAD---GTVINGKVNOTALVGGALAAAGTITLDGSATITDIGNAGAAALQRI 539
QY 366 -----DETVINIA--GNIEITRNKNI-----DIATSMTPQFSSV 399
Db 540 TLANDAKKTLTGLGANIIGAGGTIDLQANGGTIKLTSTONNIWVDFDLAIA-TDQTGVV 598
QY 400 SLGAGADAPTLSVDG-----DALNVSCK---DNKPVRTNVAPGVKEGDV-- 442
Db 599 DASSLTNAOPLTINGIKTIGANNKTLGQFNIGSSKTVLSNGVAINELVIG-NDGAVQF 657
QY 443 -----TNVAOLKGVANLNLRIDNVGNARAGIAQAIATAGLVQAYLPK-----SMM 490
Db 658 AHTYLTITRTNNAAGOKIIFNPVNVNGTTLAAGTILGSAITNPLAEINFSGKGVNDVTVL 717
QY 491 AIGGGTYRGEAGYA-----IGYSSISDGGNWIILKGTASGSRGHFGASA 534
Db 718 NVCEGVNL-----YATNITTTDANVGSEVFNAGCTNIVSGTVGGQGGKFNNTVA 766

RESULT 5
HLVA_SERMA
ID HLVA_SERMA STANDARD; PRT; 1608 AA.
AC P15320;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN SHLA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
RC STRAIN=SN8;
RX MEDLINE=88257037; PubMed=3290200;
RA Poolie K., Schiebel E., Braun V.;
RT "Molecular characterization of the hemolysin determinant of Serratia
marcescens.";
RL J. Bacteriol. 170:3177-3188(1988).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA
REQUIRES SHLB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.

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EMBL; AE000291; AAC75061.1; ALT_INIT.
DR EMBL; D90838; BAA15825.1; ALT_INIT.
DR EMBL; D90839; BAA15832.1; ALT_INIT.
DR EMBL; U24429; ABA47869.1; -
DR HSP; P07505; LSRO.
DR EcoGene; EGI2686; flu.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR InterPro; IPR004899; Pertactin.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF03212; Pertactin; 1.
DR TIGRfams; TIGR01414; autotrans_bar1; 1.
KW Outer membrane; Signal; Complete proteome.
FT SIGNAL 1 52
FT CHAIN 53 551 ANTIGEN 43 ALPHA CHAIN.
FT CHAIN 552 1039 ANTIGEN 43 BETA CHAIN.
FT VARIANT 2 2 K -> N (IN STRAIN ML 308-225).
FT VARIANT 41 42 SL -> FF (IN STRAIN ML 308-225).
FT VARIANT 46 46 T -> K (IN STRAIN ML 308-225).
FT VARIANT 157 157 W -> L (IN STRAIN ML 308-225).
FT VARIANT 188 188 V -> F (IN STRAIN ML 308-225).
FT VARIANT 303 305 ATN -> STI (IN STRAIN ML 308-225).
FT VARIANT 320 320 A -> T (IN STRAIN ML 308-225).
FT VARIANT 372 372 N -> Q (IN STRAIN ML 308-225).
FT VARIANT 493 493 E -> V (IN STRAIN ML 308-225).
FT VARIANT 497 497 S -> N (IN STRAIN ML 308-225).
FT VARIANT 585 585 H -> Y (IN STRAIN ML 308-225).
FT VARIANT 709 709 E -> K (IN STRAIN ML 308-225).
FT VARIANT 721 721 M -> T (IN STRAIN ML 308-225).
FT VARIANT 751 753 GHL -> SHF (IN STRAIN ML 308-225).
FT VARIANT 803 803 S -> P (IN STRAIN ML 308-225).
FT VARIANT 815 815 A -> V (IN STRAIN ML 308-225).
FT VARIANT 824 824 C -> S (IN STRAIN ML 308-225).
FT VARIANT 829 835 LNLVHTS -> MNLVNA (IN STRAIN ML 308-225).
FT VARIANT 845 847 QGT -> LGA (IN STRAIN ML 308-225).
FT VARIANT 855 855 S -> T (IN STRAIN ML 308-225).
FT VARIANT 888 888 Q -> L (IN STRAIN ML 308-225).
FT VARIANT 1025 1025 S -> I (IN STRAIN ML 308-225).
FT CONFLICT 61 63 ETV -> TTT (IN REF. 5).
SQ SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEBE0 CRC64;

Query Match 6.6%; Score 182.5; DB 1; Length 1039;
Best Local Similarity 23.7%; Pred. No. 0.041;
Matches 116; Conservative 68; Mismatches 154; Indels 151; Gaps 32;

QY 98 HGKVNITSDTKGLNFAK-----ETAGNGDTTVHLNGI-----GSTL 135
DB 71 HDNQI-VFGTNGWTISTGLEYPDNEANTGGWQDGGTANTTTSGLQVRNPGGSV 129
QY 136 TDTLLTNGATFN-----TNDNVTDDEK---KRAASVKDVLN-AGWNKGVKPGTASDNV 187
DB 130 SDTVISAGGGSQLOGRAVNTTLNGGEQWHEGAIATGTVINDKGQV--VKPGTVATDTV 187
QY 188 DFVRT-----VDTFEFLSADTKTTNVNESKDNKKTEVKIG-AKTSVKEKDGK 236
DB 188 --VNTGAEGPDPAENGDTGQFVRGDAVRTTIN--KNGRQIVRAEGTANTTVV----- 235
QY 237 LVTKGDKGNGSSTDE---GEGLV-----TAKEVIDAVNKAGWRM-----KTTTANGQ 281
DB 236 -YAGGQTVGHCHALDTTLNGGYVHNGGTASTV--VNSDGGWQIVKNGGVAGNTTVN-Q 291
QY 282 TQADKFEVTSTGNTVTFASG---KGTTFATSKDQD--NITVMYDVNVGDALNQLQN 336
DB 292 KGRU-QVDAGGTATNTVLKQGGALVTSTAATVT---GINRLGAFSVVEGKADNV-VLEN 345
QY 337 SGWNLDSKAVAGSSGKVISGNVSPSKGMDKDETVINAGNNIETIRNGKNIDIIATSWTPQF 396

346 GG-RLD-----VLTGHTATN-----TRVDDGGTLDV-RNG-----GTATTT--- 378
QY 397 SSVSLGAGADAPTLSDVDGALNVGSKDKNPVRITNVAPGVKGDVTNVAQLKGVAQNLN 456
DB 379 --VSMNGG---VLLADSGAAVSGTRSDGK-----AFSIGGQADALMLEKGSFTLN 426
QY 457 NRIDNVDGNARAGIAQIATAGLVQAYLPCKSMMAIGGGTYRGEAGYAIQYSSISDGNW 516
DB 427 -----AGDTATDTT-----VNGGLFTARGGTLAGTTTLNNGAIL 460
QY 517 IIKGTASGN 525
DB 461 TLSGKTVNN 469

RESULT 7
HLVA_PROMI STANDARD; PRT; 1577 AA.
ID HLVA_PROMI
AC PI6466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN=Isolate 477-12;
RA MEDLINE=90170827; PubMed=2407716;
RA Upjohn T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
CC -----
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DR EMBL; M30186; AAA25657.1; -
DR PIR; A35140; A35140.
DR Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.6%; Score 182.5; DB 1; Length 1577;
Best Local Similarity 22.7%; Pred. No. 0.068;
Matches 139; Conservative 71; Mismatches 229; Indels 173; Gaps 30;

QY 32 EKEKVE-----ENSDWAVYFNKGLVLTAREITLKAGDNLKIKQNGTNTFTYSLKDLTDL 85
DB 383 EKEQIQIGSQIDAKNNATLTATKGDVTLDAKINAGNNLAINAN-----KDI 430
QY 86 TSVG-TEKLSFSAHKNKNITS-----DTKGLNFAKETAG----- 119

[illegible]

RESULT 8

Query Match	Best Local Similarity	6.6%	Score 181.5	DB 1	Length 1645
Matches 138	Conservative 67	Mismatches 220	Indels 189	Gaps 32	
Qy	53	TAREITLKAGDNLKIKONGTNTFTYSLKK	---	DLTDLTSTVCTEKLSTSAHKNKVNITSDRK	109
Db	192	TTOEAPITLGDNAKI-VNGANGILNITNGEVKVSDDKTFAGIK	-----	TINI-GDNO	240
Qy	110	GLNFAKETAGTN-----GDTTVHLANGIGSTLTDLLNTGATTNTVNDVNTDDEKKRAAS	163		
Db	241	GLMNTTPDAANALNLGGGGTINFNGRDG--TGKLVLSKNGNATEFNVTG	-----	290	
Qy	164	VKDVLNAGWNIKV-PPGTTA-----SDN-----VDFVRYDTVFELLS	200		
Db	291	-----SLGGNLKGVIEFDTTAAAGKLIANGAANAVIGTDNGAGRAAGFIVSYD	-----	340	
Qy	201	ADTKTTTVNVESKD-----NGKKT-----EVKIGAKTSVKEKDGKLVTKGDKGKENG	247		
Db	341	GNAATISGGQVIADIVIQSANAGGQVTFEHLVDVGLGGKTN-FRTADSKVII	-----	395	
Qy	248	S--STDEG-----EGLVTAKEVIDAVNR---AGWRMKTTTANGQ--TGQADKFET	290		
Db	396	SFGSTDFGNLAVQIVVPPNNKILTNFGIDAKNNGTAG--VITFNANGTLVSGNTDPNIV	453		
Qy	291	VTS-----GTNVTFASG-----KGTATVTSKDDQGNITVMYDVNVGDDALNVNQLON	336		
Db	454	VTNIKATEVEGAGIVQSGIHGAELRLGNAGSIFKLADGTV-INGPVMQNPLVNNNALAA	512		
Qy	337	SGWNLDKAVAGSGGKVIQSNVSPSKGKMDET-----VNINAGNNIET	380		
Db	513	GSIQLDGSAII--TGDI--NGGAVNALQDITILANDASKILTLUSGANIIGANAGGAIHFQ	568		
Qy	381	RNGKNIDIAATSM-----TPQFSSVSLGAGADAPTLSDVGD	-----	416	


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FT DOMAIN 24 38 3 X 5 AA TANDEM REPEATS.
FT REPEAT 24 1-1.
FT REPEAT 29 33 1-2.
FT REPEAT 34 38 1-3.
FT DOMAIN 111 668 6 X 6 AA APPROXIMATE REPEATS.
FT REPEAT 111 116 2-1.
FT REPEAT 203 208 2-2.
FT REPEAT 277 282 2-3.
FT REPEAT 399 404 2-4.
FT REPEAT 624 629 2-5.
FT REPEAT 663 668 2-6.
FT DOMAIN 159 170 2 X 6 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 159 164 3-1.
FT REPEAT 165 170 3-2.
SQ SEQUENCE 917 AA; 100148 MW; 7FF39BB8C046539D CRC64;

Query Match 6.4%; Score 177; DB 1; Length 917;
Best Local Similarity 21.1%; Pred. No. 0.067;
Matches 118; Conservative 93; Mismatches 223; Indels 124; Gaps 23;

QY 14 VQRTAVLVNSDKGAGEKEKVE--ENSDWAYVFNEKGVLTAREITLKGADNLKI---K 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 INQTSKQVQINHSFSDIGQKVEFKQPSSENSVAYNRVTGGNASQIQGLTANGKQVLAN 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 69 QNGTNTYSLKDLTDLTSGTEKLSFSAHGKVNITSDTKGLNFAKETAGTN-----GD 123
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 PNGVIITGAEINAVGALLATTKDLQIENSNSYQFTRKTKQDVVKEGVINEGEITAK 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 TVHLNGIGSTLDTLLNGTATNTVDNDVDEKKRAASVKDVLNAGNNIKGVKPGTTA 183
   ||| ||| : : : : : : : : : : : : : : : : : : : : : :
Db 179 DFVVLNG-----DEVINKG-----NINV---EKNSTNGKVKYLSGGYNFT-----FTL 218
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 SDNVDFVRYTYDFELFSADTKTTVN--VESKDNKGKTEVKIGAK----- 226
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 219 SDS-----GISVALEDNTVRGIVQNEGSIKAGEITLSAKGRKEALDSLVMNGV 267
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 227 --TSVTKEDKGLVTKDKE--NGSSTDEGEGLVTAKEVIDAVNKAGRWKMTTANGQTG 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 268 LEATKVSNRNGKVLVSADNVQLNNSNIRKEIVNFGTEVTSNEDK---KLKITSKTSKV 324
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 284 QADKFETVSGTNTVTSAGKGTATVSKDDQGNITVMDVNVGDALNVQNLQ--SGWNLD 342
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 325 TSPKINFKGSVNINGNFNGSGTHYNEERKTLNTEVNDVDPGAENIRIADDKNTETD 384
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 343 S-----KAVAGSGKV-----ISGNVS-----PSKGMKD--ETVNIINA 373
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 385 SFIQTEALSSLLANCKVNLKNDVNLISGNINIDSPFGTDSLKLTLNQGHINIDHADINS 444
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 374 -GNNEITRNGKNIDTATSTPQFSSVSLGAGADAPTLSDVDGALNVGSKDNKPVRIT- 431
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 445 KGRLFVVTSLQNDVDVFKSNITITDTSKINLNGAMGLRSVYNNEDDYATRWKRAEKSQRKF 504
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 432 NVAPGVKGGDTVNVQALKGVAQNLNRRIDNV---DGNARAGIAQATATAGLVQAYLPGKS 488
   || : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 505 NV-----DMRNV-----VFNQVDEVILAGGFEKVLNLDKIVAT-----GQT 539
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 489 MMAIGGTYRGEAGYAG 506
   ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 540 NFYIDGGVSRNNSRYEYG 557
   ||| : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
OMP_R1CCN
ID OMPB_R1CCN STANDARD; PRT; 1655 AA.
AC O9KKK3: O9KK98; O9XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sc55) (rOmpB)
DE (rOmp B) [contains: 120 kDa surface-exposed protein (Surface protein
  antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR RC1085.
```

```
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
  gene coding the outer-membrane protein rOmpB (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
  australis, the most divergent rickettsia of the spotted fever group.";
RL Submitt (MAY-1999), to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
  STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
  VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
  SIMILARITY).
CC -I- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
  (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
  LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE008659; AAL03623.1; -
DR EMBL; AF123721; AAF34124.1; -
DR EMBL; AF123726; AAF34129.1; -
DR EMBL; AF149110; AAD39533.1; -
DR PIR; E97835; E97835.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRfams; TIGR01414; autotrans_barl; 2.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.
FT CHAIN 1335 1655 32 kDa BETA PEPTIDE.
FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 353 354 KD -> GH (IN REF. 3).
FT CONFLICT 776 F -> S (IN REF. 3).
FT CONFLICT 1159 1159 E -> D (IN REF. 3).
FT CONFLICT 1177 1177 G -> S (IN REF. 3).
FT CONFLICT 1492 1492 H -> R (IN REF. 3).
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;
```

Query Match	6.4%; Score 177; DB 1; Length 1655;
Best Local Similarity	23.9%; Pred. No. 0.13;
Matches	142; Conservative 71; Mismatches 265; Indels 116; Gaps 30;
QY	14 VORTVAVLVNSDKEGEKEKEKEVEENSQWVYFNEKGLVTAREITLKGONLAK--IKONG 71
DB	256 LQANGATTFFNG--TDGTRGLVLLSKNAA--ATDFNVTGSL-----GGNLKGIIEFNT 304
QY	72 TNYFTSLKDL--TDLTSVSGTEKLSFSAHGKNVNI-----TSDTKGLNPAK----ETAGTNG 122
DB	305 VAVNGQLKANAGANAAVIGTNNAGRAAGFVVSVDNGKVATIDGQVYAKDWIQSANAVG 364
QY	123 DTT-----VHLNIGIGTGLTDLTLLNGATTNNVNDVDEKRAASVKD-----VLNAGWNK 175
DB	365 QVNFRIHVDVGTGDTAFKTAASKVAITQNSFGTDTFGLNLAQIIVPNTMTLNGNFTGD 424
QY	176 GYKPGCTASDNVDFVRYD---TVEFLSADPKTTTVN-----VESKDNG-----KTEV 221
DB	425 ASNPNTAG-----VITFDANGTLASADANAVTNNITAIEASGAGVYVOLSSTHAAEL 479
QY	222 KIGAKTSVKEKDKGLVTGDKG-----ENGSSSTDEGEGLVTAKEVIDAVNKAGWRM 273
DB	480 RLGNAGSVFKLADGTVINGKNVQYALVCGALAAAGTILDGSAITG-----DIGNAGG--- 532
QY	274 KTTTANGOTQADKFEVTV-----SGTNVTFASGKGTTPVSKDDQGNITVMYDV- 323
DB	533 -AAALQGITLANDATKTLTGLGANGITANGGTINFQANGGTIKLTS--TQNNIVDFDLA 589
QY	324 -----NVGDALNVNLQNSGNLDSKAVAGSSKGVISGNVSPSKGM--DETNNIN---A 373
DB	590 IATDQTGVVDASSLTNAQTLTINGKIGTVGANNKTLGQFNIGSSKTVLSDGDVAINELVI 649
QY	374 GNN--IEITRNGKNIDIATSTMPQ-----FSSV-----SLGAGADAPTLSDGDALNVGSK 422
DB	650 GNGAVQFAHNYLITPTNAGQKGIIFNPVNNVTTLATGNLGSATPLAEINFGSK 709
QY	423 KDNKPVRTINVAPGYKEGDVTNVNQLKGVAQNLNRRIDNVG--NARAGIAQATATAGLVQ 481
DB	710 GAANDVTVLNVGKGVNL--YATNITTTDA---NVGSFIFNAGGTVIVSG-----TVGGQ 759
QY	482 -----AYLPKSKMAITGGTYGCEAGYAGYSSISDGGNWIIGKTASGNSRG 528
DB	760 GNKFNTVALDNGTTVKFLGNATFNNGNTTIAAN--STLQIGGNYTADFVASADGTG 812
RESULT 12	
YPJA_ECOLI	
ID	YPJA_ECOLI STANDARD; PRT: 1569 AA.
AC	P52143; P76610; P77017; P77019;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Hypothetical outer membrane protein ypja.
GN	YPJA OR B2647.
OS	Escherichia coli.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Escherichia.
OX	NCBI_TaxID=562;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=K12 / MG1655;
RC	MEDLINE=97426617; PubMed=9278503;
RX	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA	Mau B., Shao Y.;
RT	"The complete genome sequence of Escherichia coli K-12.;"
RL	Science 277:1453-1474(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=K12;
RX	MEDLINE=97349980; PubMed=9205837;
RA	Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,

Qy 479 LVOAYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWI--KGTASGNS 526
Db 815 -----ANNILLANGCVLTVESDTSKDTQVNMGGREIVKTRATATGTT 857

RESULT 13

ID ICEN_XANCT STANDARD; PRT; 1567 AA.
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=343;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=X56S;
RX MEDLINE=91080859; PubMed=2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
Xanthomonas campestris pv. translucens.";
RL Mol. Gen. Genet. 223:163-166(1990).
CC -|- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CRYSTALLIZATION IN SUPERCOOLED WATER.
CC -|- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -|- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC -|- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -|- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
FAMILY.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL; X52970; CAA37140.1; -;
CC HSP; P06620; IINA.
CC InterPro: IPR000258; Ice.nucleatn.
CC Pfam; PF00818; Ice.nucleation; 81.
CC PRINTS; PR00327; ICENUCLEATN.
CC PROSITE; PS00314; ICE_NUCLEATION; 57.
KW Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;

Query Match 6.38; Score 174; DB 1; Length 1567;
Best local similarity 21.58; Pred. No. 0.18;
Matches 120; Conservative 69; Mismatches 246; Indels 122; Gaps 23;
Qy 29 GAGEKEKVEENSDWAVYFNEKGVLTAREITLKAG-----DNLKIKQNGTNYTSLK 79
Db 605 GYSTQTARGSDVTAGYGTGTAGAG--DSTLIAGYGTQTSGSDSSLTAGYGTQTARKG 663
Qy 80 KDLT-----DLTSVGTKELSFSAHGKNVNTSD---TKGLNFAKETA-----G 119
Db 664 SDVTAGYGTGTAGADSTLIAGYGTQTSGSDSSLTAGYGTQTARKGSDVTAGYGTG 722
Qy 120 TNGDTFVHLNGIGSTLTDTLLNCGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKP 179
Db 723 TAGADSTLIAGYGTGT-----SGSDSSLTAGYGTQTARKGSDV-----TAGYGTG--- 770
Qy 180 GTTASDNVDFRVTYDFEFLSADTKTTVNVESKDKGKTEVKIGAKTSVIKEDGKLVT 239
Db 771 --TAGADSTLIAGYGTQTSGSDSSLTAGYGTGTQTARKGSDITAGYGTGTAGADSTLIA 828

Qy 240 GKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFFETVTSGTNVTF 299
Db 829 G-----YGSTQTS-----DSSLTAGYGTQTAREGSDVTAGYGTGTAGADSTL 874
Qy 300 ASGKGTATVSKDDQGNITVNY-----DYNVGDALNVNQLQNSGNWLDKAVAGS 349
Db 875 ISGYGSTQTAGSD--SSLTAGYGTQTARKGSDVTAG-----YGSTGTAGA 918
Qy 350 SGKVISGNVSPSKGMDETVINAGNNIETRNCKNIDIIATSMTPQFSSVSLGAGADAPT 409
Db 919 DSTLIAGYGTQTSGSDSSLTAGYGT--QTARKG-----SDMTAGYGTGT--AGADSTL 970
Qy 410 LSYVDGALNVGSKKDNKPNRITNVAPGVKEGDVTNVAQLKGVAQNLRNNDVNDGNARAG 469
Db 971 IAGYGTQTSGSD-----SSLTAGY-----GSTQTAREGSDVTAGYGTG 1010
Qy 470 IQAA-----IATAGLVQAYLPGKSMMAIGGGTYRGEAGYAI--GYSSISDGG--NWIKGT 521
Db 1011 TAGADSTLIAGYGTQTAGSDSSLTAGYGTQTAROGSDVTAGYGTGTAGADSTLIAGY 1070
Qy 522 ASGNSRGHFGASASVGY 538
Db 1071 GSTQTAGS--DSSLTAGY 1086
RESULT 14
ID WAPA_BACSU STANDARD; PRT; 2334 AA.
AC Q07833;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Wall-associated protein precursor.
GN WAPA OR N17G.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=93302506; PubMed=8316082;
RA Foster S.J.;
RT "Molecular analysis of three major wall-associated proteins of
Bacillus subtilis 168: evidence for processing of the product of a
gene encoding a 258 kDa precursor two-domain ligand-binding
protein.";
RL Mol. Microbiol. 8:299-310(1993).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=95219088; PubMed=7704263;
RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis
genome containing the hut and wapa loci.";
RL Microbiology 141:337-343(1995).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=97124196; PubMed=8969509;
RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
RT "Sequencing of a 65 kb region of the Bacillus subtilis genome
containing the lic and cel loci, and creation of a 177 kb contig
covering the gnt-sacXY region.";
RL Microbiology 142:3113-3123(1996).
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borliss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Fritsch C., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritsch C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klarr-Blandhard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maul C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara K., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scalan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zumbstein A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
CC -!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
CC MOTILITY, SECRETION OR DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
CC INTO THE MEDIUM.
CC -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE
CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE
CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
CC MOTIF REPEATED 31 TIMES.
CC -!- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
CC SIMILARITY TO THE REPEAT IN E.COLI RBS GROUP OF PROTEINS (RBSA-D).
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; L05634; AAA22883.1; -;
CC EMBL; D31856; BAA06656.1; -;
CC EMBL; D29985; BAA06260.1; -;
CC EMBL; D83026; BAA11683.1; -;
CC EMBL; Z99124; CAB15959.1; -;
CC PIR; S32920; S32920.
CC Subtilisin; BG10797; wapa.
CC InterPro; IPR003305; CBM_CenC.
CC InterPro; IPR006530; YD.
CC Pfam; PF02018; CBM_4_9; 1.
CC TIGRFAMs; TIGR01643; YD_repeat_2x; 17.
KW Cell wall; Repeat; Signal; Complete proteome.
FT SIGNAL 1 28
FT CHAIN 29 2334
FT DOMAIN 504 869
FT REPEAT 504 605
FT REPEAT 636 736
FT REPEAT 769 869
FT DOMAIN 1021 2139
FT REPEAT 1021 1040
FT REPEAT 1042 1061
FT REPEAT 1063 1082
FT REPEAT 1083 1102
FT REPEAT 1109 1128
FT REPEAT 1129 1148

FT REPEAT 1150 1169 2-7.
FT REPEAT 1174 1193 2-8.
FT REPEAT 1199 1218 2-9.
FT REPEAT 1219 1238 2-10.
FT REPEAT 1249 1268 2-11.
FT REPEAT 1269 1288 2-12.
FT REPEAT 1289 1308 2-13.
FT REPEAT 1309 1328 2-14.
FT REPEAT 1329 1348 2-15.
FT REPEAT 1349 1368 2-16.
FT REPEAT 1369 1388 2-17.
FT REPEAT 1389 1408 2-18.
FT REPEAT 1409 1428 2-19.
FT REPEAT 1429 1448 2-20.
FT REPEAT 1449 1468 2-21.
FT REPEAT 1469 1488 2-22.
FT REPEAT 1489 1508 2-23.
FT REPEAT 1509 1528 2-24 (APPROXIMATE).
FT REPEAT 1529 1548 2-25.
FT REPEAT 1549 1568 2-26.
FT REPEAT 1569 1588 2-27.
FT REPEAT 1589 1608 2-28.
FT REPEAT 1609 1628 2-29.
FT REPEAT 1629 1648 2-30.
FT REPEAT 1649 1668 2-31.
SQ SEQUENCE 2334 AA; 258329 MW; B75138CCD278BAA3 CRC64;

Query Match 6.3%; Score 173.5; DB 1; Length 2334;
Best Local Similarity 23.1%; Pred. No. 0.3;
Matches 110; Conservative 63; Mismatches 169; Indels 135; Gaps 23;

Qy 33 KEKVEENSDWAVYENKGVLTAREITLKAGDNLKIKONGNTYSLKDLFDLTSVGTGK 92
Db 1001 KTKDQTN-----YENKGGKQLKVV-----GHN-----NATVYTNKQLTAITDASGRK 1048
Qy 93 LSFSS--AHGNKVNITS--DTKGLNFAKETAGTNGDTTVHLNGIGSLTDFDFTLLTWTGATNVT 149
Db 1049 LTFTYDENGHVTSITGPKNKVITYSE-----NDLLKKVTDY---DGTVTSYD 1093
Qy 150 NDNVTDDEKRAASVKVDNLNAGWNIKGVKPGTTA-----SDNVDFVRYTDTV 196
Db 1094 YDSGRVLKQVSA-----NSTEAKPVFTYQYSGHLEKAINNAKKETIYVSYD-- 1141
Qy 197 EFLSADTKTTNVNYESKDNKKTEV---KIGAKTSVIKEKDKGLVT-----GKDKGNG 247
Db 1142 ----ADKKTLLM---TOPNGRKYQVGYNEAGNPIQVDDDAEGLKITTNTKVEGNVVEDV 1194
Qy 248 SSTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGOTGQADKEFTVTS-----GTNVTFASG 302
Db 1195 DPNDVGTGKAT-----ESYQYDKDGNVTYSVKDAYGTE-TVEYN 1231
Qy 303 KGTATATYSKDDOGNIT--VMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPS 361
Db 1232 KNNDVTNKKDTEGNVTDIAD-----GLDAVSETQSGKSSAAVYDK 1274
Qy 362 KG-KMDETVINAGNNIEITRNKKNIDIAATSMTPQFSVSLGAGADAPTLTSVDGDLNVG 420
Db 1275 YGNIQSSKDLASTN--ILKDG-----SFEAQKSGWNLTSKDRRKISVIADKSGVL 1325
Qy 421 SKDNKPVRTNVAPGVKEG--DVTNVAQLKGVAQNLNRRIDNVGDNARAGIAAIA 475
Db 1326 SGSKALEVLQSSTAGTHGYSSATQVLE-----PNTTYSLSGKIKTDLAKSRA 1376

RESULT 15
SLAP_CAME STANDARD; PRT; 933 AA.
ID SLAP_CAME
AC P35827;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE S-layer protein (Surface array protein) (SAP).
GN SAPA.

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Result No.	Query	Score	Query			ID	Description
			Match	Length	DB		
1	2727	98.9	591	2	Q9JPS7	Q9Jps7 neisseria m	
2	2727	98.9	591	16	Q9JRI8	Q9Jri8 neisseria m	
3	2720	98.7	591	2	Q93QY3	Q93qy3 neisseria m	
4	2695.5	97.8	592	2	Q9AQF0	Q9aqf0 neisseria m	
5	2624.5	95.2	590	2	Q9JPS3	Q9jps3 neisseria m	
6	2512	91.1	594	2	Q93QY4	Q93qy4 neisseria m	
7	2511	91.1	600	2	Q9JPS6	Q9jps6 neisseria m	
8	2501	90.7	594	2	Q9JPI3	Q9jpi3 neisseria m	
9	2501	90.7	594	2	Q9JPS2	Q9jps2 neisseria m	
10	2493	90.4	594	2	Q9JPH7	Q9jph7 neisseria m	
11	2491	90.4	598	2	Q9JPR9	Q9jpr9 neisseria m	
12	2478	89.9	598	2	Q9JPS0	Q9jps0 neisseria m	
13	2478	89.9	598	2	Q93QY5	Q93qy5 neisseria m	
14	2478	89.9	598	2	Q9JPT0	Q9jpt0 neisseria m	
15	2442.5	88.6	526	2	Q9JPS4	Q9jps4 neisseria m	
16	2440.5	88.5	530	2	Q9JPS1	Q9jps1 neisseria m	

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QY 61 AGDNLKIKQNGTNTFYSLKDLTDLTSVGTETKLSFSAHGKNVNTSDTKGLNFAKETAGT 120
DB 112 AGDNLKIKQNGTNTFYSLKDLTDLTSVGTETKLSFSAHGKNVNTSDTKGLNFAKETAGT 171
QY 121 NGDITVHLNGTSLTDLTLLNVTGATNTVNDVDEKKRAASVKDVLNAGWNKIGVKPG 180
DB 172 NGDITVHLNGTSLTDLTLLNVTGATNTVNDVDEKKRAASVKDVLNAGWNKIGVKPG 231
QY 181 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIEKDGKLVG 240
DB 232 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIEKDGKLVG 291
QY 241 KDKGSGSSTDEGEGLVTAKEVIDAVNKGAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 300
DB 292 KDKGSGSSTDEGEGLVTAKEVIDAVNKGAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 351
QY 301 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSP 360
DB 352 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSP 411
QY 361 SKGKMDETVNTNAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGDLNNG 420
DB 412 SKGKMDETVNTNAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGDLNNG 471
QY 421 SKKDNKPVRIITNAPGVKEGVDVTVNVAQLKGVAQLNNRDNVGNARAGIAQAATAGLV 480
DB 472 SKKDNKPVRIITNAPGVKEGVDVTVNVAQLKGVAQLNNRDNVGNARAGIAQAATAGLV 531
QY 481 QAYLPKGSMAIAGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFHGASVGYOW 540
DB 532 QAYLPKGSMAIAGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFHGASVGYOW 591
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RESULT 2

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Q9JUR18 PRELIMINARY; PRT; 591 AA.
ID Q9JUR18
AC Q9JUR18;
DC 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Outer membrane protein GNA992 (Adhesin) (NhaA outer membrane
protein).
GN GNA992 OR NMB0992 OR NHA.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B, B2169, B283, and H44/76;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Galeanducci M., Jennings G.F., Baldi L., Bartolini E., Capeocchi B.,
RA Ratti G., Santini L., Savino S., Marchetti E., Mora M., Nuti S.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tetelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
```

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RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226375; AAF42524.1; -
DR EMBL; AF002450; AAF41395.1; -
DR EMBL; AF226367; AAF42516.1; -
DR EMBL; AF226370; AAF42519.1; -
DR EMBL; AF226374; AAF42523.1; -
DR EMBL; AF157611; AAK68872.1; -
DR TIGR; NMB0992; -
DR InterPro; IPR005594; YadaA.
DR Pfam; PF03895; YadaA; 1.
KW Complete proteome.
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match 98.9%; Score 2727; DB-16; Length 591;
Best Local Similarity 99.3%; Pred. No. 1.2e-107;
Matches 536; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNEQEEVLYLHPQRTVAVLVNDSKEGACEKEKEVEENSDWAVYFNEKGLVTAREITLK 60
DB 52 NNEQEEEDLYLDPQRTVAVLVNDSKEGCEKEKEVEENSDWAVYFNEKGLVTAREITLK 111
QY 61 AGDNLKIKQNGTNTFYSLKDLTDLTSVGTETKLSFSAHGKNVNTSDTKGLNFAKETAGT 120
DB 112 AGDNLKIKQNGTNTFYSLKDLTDLTSVGTETKLSFSAHGKNVNTSDTKGLNFAKETAGT 171
QY 121 NGDITVHLNGTSLTDLTLLNVTGATNTVNDVDEKKRAASVKDVLNAGWNKIGVKPG 180
DB 172 NGDITVHLNGTSLTDLTLLNVTGATNTVNDVDEKKRAASVKDVLNAGWNKIGVKPG 231
QY 181 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIEKDGKLVG 240
DB 232 TTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIEKDGKLVG 291
QY 241 KDKGSGSSTDEGEGLVTAKEVIDAVNKGAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 300
DB 292 KDKGSGSSTDEGEGLVTAKEVIDAVNKGAGRMKTTTANGOTGQADKFEETVTSGTNTVFA 351
QY 301 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSP 360
DB 352 SGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSP 411
QY 361 SKGKMDETVNTNAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGDLNNG 420
DB 412 SKGKMDETVNTNAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGDLNNG 471
QY 421 SKKDNKPVRIITNAPGVKEGVDVTVNVAQLKGVAQLNNRDNVGNARAGIAQAATAGLV 480
DB 472 SKKDNKPVRIITNAPGVKEGVDVTVNVAQLKGVAQLNNRDNVGNARAGIAQAATAGLV 531
QY 481 QAYLPKGSMAIAGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFHGASVGYOW 540
DB 532 QAYLPKGSMAIAGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFHGASVGYOW 591

RESULT 3
Q93QY3 PRELIMINARY; PRT; 591 AA.
ID Q93QY3
AC Q93QY3;
DC 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Outer membrane protein.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
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GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AFI57606; AK68867.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;

Query Match 98.7%; Score 2720; DB 2; Length 591;
Best Local Similarity 99.1%; Pred. No. 2.3e-107;
Matches 535; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 NNEEQEYLHPVQRTVAVLIVNSDKGAGEKEKEVEENSDWAVYFNEKGVLTAREITLK 60
Db ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 52 NNEEQEEDLYLDPVLTAVLIVNSDKGEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLK 111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AGDNLKIKQNGTNYTSLKDKDLTSLVSGTEKLSFSAHGKNKVNITSDTKGLNFAKETAGT 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 112 AGDNLKIKQNGTNYTSLKDKDLTSLVSGTEKLSFSAHGKNKVNITSDTKGLNFAKETAGT 171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 NGDTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 172 NGDTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPG 231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TTASDNVDFVRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDGKLVG 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 232 TTASDNVDFVRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDGKLVG 291
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 KDKGSGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTNVTF 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 292 KDKGSGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTNVTF 351
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 SGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKAVAGSSGKVISGNVSP 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 352 SGKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKAVAGSSGKVISGNVSP 411
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 SKGKMDETVNIAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGDLNVG 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 412 SKGKMDETVNIAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGDLNVG 471
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 SKKDNKPVRTNTPVAPGKEDVTNVAQLKGVAQNLRNIDVGNARAGIAQAIATAGLV 480
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 472 SKKDNKPVRTNTPVAPGKEDVTNVAQLKGVAQNLRNIDVGNARAGIAQAIATAGLV 531
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 481 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASGYQW 540
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 532 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASGYQW 591
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
Q9AQF0 PRELIMINARY; PRT; 592 AA.
AC Q9AQF0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
```

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RC STRAIN=MC58;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AFI25375; AAK09243.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 97.8%; Score 2695.5; DB 2; Length 592;
Best Local Similarity 98.2%; Pred. No. 2.5e-106;
Matches 531; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 NNEEQEYLHPVQRTVAVLIVNSDKGAGEKEKEVEENSDWAVYFNEKGVLTAREITL 59
Db ||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 52 NNERPRKKDLYLDPVQRTVAVLIVNSDKGEGTGEKEKEVEENSDWAVYFNEKGVLTAREITL 111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 60 KAGDNLKIKQNGTNYTSLKDKDLTSLVSGTEKLSFSAHGKNKVNITSDTKGLNFAKETAG 119
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 112 KAGDNLKIKQNGTNYTSLKDKDLTSLVSGTEKLSFSAHGKNKVNITSDTKGLNFAKETAG 171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 120 TNGDITVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVK 179
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 172 TNGDITVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVK 231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 180 GTTASDNVDFVRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDGKLV 239
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 232 GTTASDNVDFVRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDGKLV 291
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 240 GKDKGSGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTNVTF 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 292 GKDKGSGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTNVTF 351
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 300 ASKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKAVAGSSGKVISGNVS 359
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 352 ASKGTATVSKDDQGNITVMYDVGDLNVLQNSGWNLDKAVAGSSGKVISGNVS 411
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 360 PSKGMDETVINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGDLNV 419
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 412 PSKGMDETVINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGDLNV 471
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 420 GSKDNKPVRTNTPVAPGKEDVTNVAQLKGVAQNLRNIDVGNARAGIAQAIATAGL 479
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 472 GSKDNKPVRTNTPVAPGKEDVTNVAQLKGVAQNLRNIDVGNARAGIAQAIATAGL 531
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 480 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASGYQ 539
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 532 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASGYQ 591
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 540 W 540
Db 592 W 592

RESULT 5
Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
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OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226379; AAF42528.1; -.
DR InterPro; IPR005594; YadaA.
DR Pfam; PF03895; YadaA; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 90.7%; Score 2501; DB 2; Length 594;
Best Local Similarity 92.1%; Pred. No. 3.9e-98;
Matches 499; Conservative 12; Mismatches 23; Indels 8; Gaps 3;

Qy 6 EBYLYLHPVORTVAVLIVNSDKGAGEKEKVEKNSDMWVYFNEKGVLTAREITLKAQDNL 65
Db 54 DDDLYLEPVORTAPVLSFHADSEGTGEKE-VTSDSNMGVYFDKKGVLTAQTITLKAQDNL 112
Qy 66 KIKO-----NGTNFTYSLKKDLTDLTSVTEKLSFSAHGNKVNITSDTKLNAFAKETAG 119
Db 113 KIKQNTDENTNASSFTYSLKKDLTDLTSVTEKLSFGANGKKNVITSDTKLNAFAKETAG 172
Qy 120 TNGDTTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVK 179
Db 173 TNGDTTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVK 232
Qy 180 GTTASDNVDFVRTYDVFELVSADTKTTNVNVEKDKGKTEVKIGAKTSVIKEKDKGLVT 239
Db 233 GTTASDNVDFVRTYDVFELVSADTKTTNVNVEKDKGKTEVKIGAKTSVIKEKDKGLVT 292
Qy 240 GKDKGENSSDDEGEGLVTAKEVIDAVNKAQWNRMTTANGQTQADKFFETVTSQVTF 299
Db 293 GKDKGENSSDDEGEGLVTAKEVIDAVNKAQWNRMTTANGQTQADKFFETVTSQVTF 352
Qy 300 ASGKGTATATVSKDDQGNITVMYDYNVGDALNVQLNSGWNLSKAVAGSSGKVISGNVS 359
Db 353 ASGNGTTATVSKDDQGNITVKYDYNVGDALNVQLNSGWNLSKAVAGSSGKVISGNVS 412
Qy 360 PSKGGKMDETVNNAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDG-ALN 418
Db 413 PSKGGKMDETVNNAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDGALN 472
Qy 419 VGSKKDNKPVRIITNAPGVKEGDTNVAQLKGVQNLNRRIDNVGDNARAGIAQAIATAG 478
Db 473 VGSKDNKPVRIITNAPGVKEGDTNVAQLKGVQNLNRRIDNVGDNARAGIAQAIATAG 532
Qy 479 LVQAYLPGKSMMAIGGTYRGEAGYAGYSGISDGGNWIIGKTASGNSRHFHGASVGY 538
Db 533 LVQAYLPGKSMMAIGGTYRGEAGYAGYSGISDGGNWIIGKTASGNSRHFHGASVGY 592
Qy 539 QW 540
Db 593 QW 594

RESULT 10
Q9JPH7 PRELIMINARY; PRT; 594 AA.
AC Q9JPH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
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QY	292	TSGTNTVTSASGKGTATATVSKDDQGNITVMDVNVGDALNVQNLQNSGWNLD	SKAVAGSSG	355
Db	349	TSGTKVTFASNGTGTATVSKDDQGNITVKYDVNVGDALNVQNLQNSGWNLD	SKAVAGSSG	408
QY	352	KVISGNVSPSKGKMDETVINAGNNIEITRNGKNIDIATSWTPOFSSVSLGAGADAPTLS	411	
Db	409	KVISGNVSPSKGKMDETVINAGNNIEITRNGKNIDIATSWTPOFSSVSLGAGADAPTLS	468	
QY	412	VDGD-ALNVGSKKDKNPVRIITNVPAGVKEGDVTVNAQLKGVAQNLRNIDNV	DGNARAGI	470
Db	469	VDEGALNVGSKDKANKPVRIITNVPAGVKEGDVTVNAQLKGVAQNLRNIDNV	DGNARAGI	528
QY	471	AQAATATAGLVQAYLPGKSMMAIGGGTGRGEAGYAIGYSSISDGGNWLIIKKTASGNSRGHF	530	
Db	529	AQAATATAGLAQYALPGKSMMAIGGGTGRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHF	588	
QY	531	GASASVGQYW	540	
Db	589	GASASVGQYW	598	
RESULT 13				
Q93QY5 PRELIMINARY; PRG; 598 AA.				
ID	Q93QY5			
AC	Q93QY5;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)			
DE	NhhA outer membrane protein.			
GN	NHHA.			
OS	Neisseria meningitidis.			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=487;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=B210;			
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;			
RT	"Identification and characterization of a gene encoding a novel outer			
RT	membrane protein of Neisseria meningitidis."			
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF157603; AAK68864.1;			
DR	InterPro; IPR005594; Yada.			
DR	Pfam; PF03895; Yada; 1.			
SQ	SEQUENCE 598 AA; 62687 MW; 18CEFFFE6410A15DF CRC64;			

Qy	352	KVISGNYSPSKGKMDETVNIAGNNIETIRNGKNIDIIATSMTPQPSVSLGAGADAPTLS	411
Db	409	KVISGNYSPSKGKMDETVNIAGNNIETIRNGKNIDIIATSMTPQPSVSLGAGADAPTLS	468
Qy	412	VDGD-ALNVGSKDKNPVRIITNVAPGYKEGDTVNAQLKGVAQNLNRRIDNVGNGRAGI	470
Db	469	VDDGALNVGSKDKNPVRIITNVAPGYKEGDTVNAQLKGVAQNLNRRIDNVGNGRAGI	528
Qy	471	AQATATAGLVQAYLPKGSMAAIGGTYRGEAGYAIIGSYISDSGGNWIKTGTASGNSRGHF	530
Db	529	AQATATAGLVQAYLPKGSMAAIGGTYRGEAGYAIIGSYISDSGGNWIKTGTASGNSRGHF	588
Qy	531	GASASVGYQW 540	
Db	589	GTSASVGYQW 598	

RESULT 14

Q9JPT0 PRELIMINARY; PRT; 598 AA.

AC Q9JPT0;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 22, Last annotation update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OC NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=2996.

RX MEDLINE=2017556; PubMed=10710308;

RA Pizzo M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappuoli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

FL Science 287:1816-1820(2000).

DR EMBL; AF226359; AAF42508.1; --

DR InterPro; IPR005594; Yada.

DR Pfam; PF03895; Yada; 1.

SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

QY	292	TSGETVTFASGKGTATVSKDDQGNITVMYDVNVGDALNVQLQNSGWNLDKSAVAGSSG	351
Db	349	TSCTKVTFAAGNGTTATVSKDDQGNITVKYDVNVGDALNVQLQNSGWNLDKSAVAGSSG	408
QY	352	KVISGNVSPSKGMDETVINAAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLS	411
Db	409	KVISGNVSPSKGMDETVINAAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLS	468
QY	412	VDCD-ALNVGSKDKDKPVRITNVAPGVKGGDVNTVAQLKGVAQLNNRINDNVGNARAGI	470
Db	469	VDEGALNVGSKDKDKPVRITNVAPGVKGGDVNTVAQLKGVAQLNNRINDNVGNARAGI	528
QY	471	AQAATAGLVQAYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNNWIIKGTASGNSRGHF	530
Db	529	AQAATAGLAQAYLPGKSMMAIGGTYRGEAGYAGYSSISDGTGNVWIKGTASGNSRGHF	588
QY	531	GASASVGYQW 540	
Db	589	GTSASVGYQW 598	
RESULT 15			
Q9JPS4 PRELIMINARY; PRT; 526 AA.			
AC	Q9JPS4		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)		
DE	Outer membrane protein GNA992.		
GN	GNA992.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
OC	Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=NG6788;		
RX	MEDLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,		
RA	Galeotti C.B., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.		
RT	*Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing.*;		
RL	Science 287:1816-1820(2000).		
DR	EMBL; AF226377; AAF42526.1; -.		
DR	InterPro; IPR005594; Yada.		
DR	Pfam; PF03895; Yada; 1.		
SQ	SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;		
Query Match 88.6%; Score 2442.5; DB 2; Length 526;			
Best Local Similarity 92.0%; Pred. No. 9.9e-96;			
Matches 483; Conservative 10; Mismatches 21; Indels 11; Gaps 2;			
QY	26	DREGAGEKEKEVENSQWVFNKGVLTAREITLKAGDNLKIQ-----NGTNET 75	
Db	3	DREGNGENEST-GNIGWSIYDHNHNTLHGATVTLKAGDNLKIKQNTKNTNENTNDSSET 61	
QY	76	YSLKDLTLTTSVTEKLSFSAHGKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 135	
Db	62	YSLKDLTLTTSVTEKLSFSGANGKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTL 121	
QY	136	TDLLNTGATNTVNDNDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRYDT 195	
Db	122	TDLLNTGATNTVNDNDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRYDT 181	
QY	196	VEFLSADTKTTTVNVESKNGKKTEYKIGAKTSVKEKDKLVTKGDKGENGSTDEGEG 255	
Db	182	VEFLSADTKTTTVNVESKNGKKRTEYKIGAKTSVKEKDKLVTKGDKGENGSTDEGEG 241	

QY	256	LVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSNTVTFASGKGTATVSKDDQG	315
Db	242	LVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSNTVTFASGKGTATVSKDDQG	301
QY	316	NITVMYDVNVGDALNVQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGMDETVINAAGN	375
Db	302	NITVKYDVNVGDALNVQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGMDETVINAAGN	361
QY	376	NIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDGDALNVGSKDKDKPVRITNVAP	435
Db	362	NIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDGDALNVGSKDKDKPVRITNVAP	421
QY	436	GVKEGSDVTNVAQLKGVAQLNNRINDNVGNARAGIAQAATAGLVQAYLPGKSMMAIGGG	495
Db	422	GVKEGSDVTNVAQLKGVAQLNNRINDNVGNARAGIAQAATAGLVQAYLPGKSMMAIGGG	481
QY	496	TYRGEAGYAGYSSISDGGNNWIIKGTASGNSRGHFASASVGYQW 540	
Db	482	TYRGEAGYAGYSSISDGGNNWIIKGTASGNSRGHFASASVGYQW 526	

Search completed: October 6, 2003, 09:30:47
Job time : 41.661 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 15.4863 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-34

Perfect score: 2735
Sequence: 1 TDEDEEELESVQSRVVGSI.....TASGNSRGHGASVGYQW 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2527	92.4	592	2 A81888	probable surface f
2	2330.5	85.2	591	2 G81133	adhesin NMB0992 fi
3	435.5	15.9	298	2 I64138	adhesin homolog HI
4	392.5	14.4	2059	2 D82671	surface protein XF
5	377	13.8	1588	2 A86036	probable adhesin Z
6	377	13.8	1588	2 H91188	probable adhesin E
7	368.5	13.5	1190	2 A82615	surface protein XF
8	363	13.3	1107	2 AC0976	probable autotrans
9	321.5	11.8	658	2 AH0110	probable surface p
10	231	8.4	1536	2 A43855	high-molecular-wel
11	225	8.2	1109	2 A56143	surface-array prot
12	220.5	8.1	1004	2 C82672	surface-exposed ou
13	214	7.8	1910	2 AF0394	probable adhesin h
14	212.5	7.8	4919	2 T31105	hypothetical prote
15	210	7.7	2249	2 A41477	190K surface anti
16	207	7.6	3705	2 AD0123	probable autotrans
17	206.5	7.6	1655	2 E97835	hypothetical prote
18	204.5	7.5	5188	2 B85547	probable RTX famil
19	203.5	7.4	5291	2 F90696	hypothetical prote
20	200	7.3	1238	2 AH0038	probable exported
21	198	7.2	2020	2 C48399	ABC-type transport
22	197.5	7.2	936	2 I40711	sapB protein - Cam
23	197.5	7.2	4152	2 T31102	filamentous hemag
24	197	7.2	1577	2 A35140	hemolysin A precu
25	197	7.2	3029	2 S76109	hypothetical prote
26	195	7.1	1477	2 B43855	high-molecular-wel
27	195	7.1	1651	2 JC1340	outer membrane pro
28	194	7.1	1275	2 T33369	hypothetical prote
29	193.5	7.1	2232	2 T34434	hypothetical prote

RESULT 1

A81888

probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C;Accession: A81888

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491

A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Accession: A81888

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-592 <PAR>

A;Cross-references: GB:AL157959; GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737

A;Experimental source: serogroup A, strain 22491

C;Genetics:

A;Gene: NMA1200

Query Match 92.4%; Score 2527; DB 2; Length 592;
Best Local Similarity 93.4%; Pred. No. 7e-121;
Matches 507; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

Qy	1	TDEDEEELESVQSRVVGSIQASMEGSGVELETISLSMTNDSKFEVDPIYVVTLKAGDNLK	60
Db	52	TDEDEEELESVQSRVVGSIQASMEGSGVELETISLSMTNDSKFEVDPIYVVTLKAGDNLK	111
Qy	61	IKQNTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKVKVNIISDTKGLNFAKETAGT	120
Db	112	IKQNTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKVKVNIISDTKGLNFAKETAGT	171
Qy	121	NGDFTVHLNGIGSTLTDMLLNTGATVNTDNDVDDKKRAASVKVDVNLGAWNTKGVKPG	180
Db	172	NGDFTVHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKVDNLGAWNTKGVKGT	229
Qy	181	TTA--SDNVDFVRYDVFELSDATKTTVNVESKDKNGKTEKVGAKTSVIREKDGKLV	238
Db	230	STTGQSENVDFRYDVFELSDATKTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKLV	289
Qy	239	TGKKGKENGSGTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSQTKVT	298
Db	290	TGKKGKENGSGTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFETVTSQTKVT	349
Qy	299	FASGNGTATVSKDDQCNITVYVDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNV	358
Db	350	FASGKGTTATVSKDDQCNITVYVDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNV	409
Qy	359	SPSKGKMDVFNINAGNNIETRNKKNIDTATSWTPOFSSVSLGAGADAPTLSVDDDEGAL	418
Db	410	SPSKGKMDVFNINAGNNIETRNKKNIDTATSWTPOFSSVSLGAGADAPTLSVDDDEGAL	469

Qy 419 NVGSKDANKPYRITNVAPVKEGDTNVNAQLKGYAQNLRNDRDNDVNGNARAGIAQATATA 478
Db 470 NVGSKDANKPYRITNVAPVKEGDTNVNAQLKGYAQNLRNDRDNDVNGNARAGIAQATATA 529
Qy 479 GLVQAYLPKSMMAIGGGTYRGEAGYAGYSSISAGGNWIIKGTASGSRGHFGASAVG 538
Db 530 GLVQAYLPKSMMAIGGGTYRGEAGYAGYSSISAGGNWIIKGTASGSRGHFGASAVG 589
Qy 539 YQW 541
Db 590 YQW 592

RESULT 2
G81133
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiagnani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755; PMID:10710307
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <TET>
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722623
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

Query Match 85.2%; Score 2330.5; DB 2; Length 591;
Best Local Similarity 86.8%; Pred. No. 6.3e-111; Indels 15; Gaps 6;
Matches 475; Conservative 22; Mismatches 35;

Qy 2 DEDEEEE--LESVORSV-VGSIQASMEGVSLEITSLSMTDSKEFVDPYIV---VTLK 54
Db 53 NEEQEEEDLYDPVQRTAVLVNSDKETGKEKVE-ENSDWAVYFNEKGVLTAREITLK 111
Qy 55 AGDNLKTKQNTNENTNASSFTYSLKDLTGLINVETKLSFGANGKKVNIISDTKGLNFA 114
Db 112 AGDNLKTKQ-----NGTFTYSLKDLTGLTSGTEKLSFGANGKKVNIISDTKGLNFA 165
Qy 115 KETAGTNGDTTVHLNGIGSTLMDLNTGATTNVDNVTDDKKRAASVKDVLNAGWNI 174
Db 166 KETAGTNGDTTVHLNGIGSTLMDLNTGATTNVDNVTDDKKRAASVKDVLNAGWNI 225
Qy 175 KGVKPGTTASDNVDFVRYTDFVEFLSADTKTTTVNVESKDKGKTKVIGAKTSVIREKD 234
Db 226 KGVKPGTTASDNVDFVRYTDFVEFLSADTKTTTVNVESKDKGKTKVIGAKTSVIREKD 285
Qy 235 KGLVTGKKGSGSSTDEGELVTAKEVIDAVNAGWRMTTANGQTGQADKFTVTSG 294
Db 286 KGLVTGKDKGSGSSTDEGELVTAKEVIDAVNAGWRMTTANGQTGQADKFTVTSG 345
Qy 295 TKVTFASNGPTATVSKDDQGNITVKYDVNVGDALNVNOLNSGWNLDLSKAVAGSGKVI 354
Db 346 TNVTFASGKGITATVSKDDQGNITVMDVNVGDALNVNOLNSGWNLDLSKAVAGSGKVI 405
Qy 355 SGNVSPSKGKMDETVNTNAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADPTLSVDD 414
Db 406 SGNVSPSKGKMDETVNTNAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADPTLSVDD 465
Qy 415 EGALNVGSKDKANKPYRITNVAPVKEGDTNVNAQLKGYAQNLRNDRDNDVNGNARAGIAQA 474
Db 466 D-ALNVGSKDKANKPYRITNVAPVKEGDTNVNAQLKGYAQNLRNDRDNDVNGNARAGIAQA 524
Qy 475 IATAGLVQAYLPKSMMAIGGGTYRGEAGYAGYSSISAGGNWIIKGTASGSRGHFGAS 534

Db 525 IATAGLVQAYLPKSMMAIGGGTYRGEAGYAGYSSISAGGNWIIKGTASGSRGHFGAS 584
Qy 535 ASVGQYQW 541
Db 585 ASVGQYQW 591

RESULT 3
I64138
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C:Accession: I64138
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: I64138
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <TIGR>
A:Cross-references: GB:U32846; GB:I42023; NID:gl574588; PID:gl574589; TIGR:HI1732

Query Match 15.9%; Score 435.5; DB 2; Length 298;
Best Local Similarity 48.0%; Pred. No. 2.6e-15;
Matches 106; Conservative 27; Mismatches 57; Indels 31; Gaps 7;

Qy 51 VTLKAGDNLKTKQNTNENTNASSFTYSLKDLTGLINVETKLS-----FGANG 99
Db 87 LTLKAGKNLKAKL----DQGGKSVTFALAKDL---DVKTAKVSDTLTIGGNTPAAGCAT 138
Qy 100 KKVNIISDTGLNFAKETAGTNGDTTVHLNGIGSTLMDLNTGATTNVDNVTDDKK 159
Db 139 PKVSTITADGLKLUAK---GTNGDTAVHLNGLASTLPDVTNTGASTSVT-FSPSDIEKT 194
Qy 160 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDFVEFLSADTKTTTVNYESKDNKKT 219
Db 195 RAATIKDVLNAGWNIKGAHVAGGNTENVDLVAGYDNVEFITGDKNTLDVLVTAKENGKTT 254
Qy 220 EVKIGAKTSVIREKDKLVTKG-----GKGNGS-STDE 252
Db 255 EVKFTPTSVIKDNGKLLTGKQLKDANTGTATNATEDTDE 295

RESULT 4
D82671
surface protein xfl529 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82671
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82671
A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: 1-2059 <SIM>
A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier
as-Neto, E.; Docena, C.; El-Dorri, H.; Pacinani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.M.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1529

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Query Match      14.4%  Score 392.5;  DB 2;  Length 2059;
Best Local Similarity 24.8%;  Pred. No. 4.7e-12;
Matches 173;  Conservative 98;  Mismatches 225;  Indels 201;  Gaps 32;

Qy  7  EELESVORSVVGSTQASMEGSVELETISLMTNDSKEFVDPYIVVTLKAGD-NLKIKONT 65
Db  1402 EETDAVNFSLKSTIAVD---QGWTLTASGANGSK--VASGGTVDLKNTDGNLTISKSG 1456

Qy  66 NENTNASSFYSLKDLTGLINVEKLSFGANGKKV--NTISDTKGLNFAKETAGT--- 120
Db  1457 DSNDDVFNLSDELKEKSIYVNTQLDK-----DGVKSSNVLLDSNELVTSHSSTSVK 1511

Qy  121 ---NGDPTVH---LNGIGSTLTDL-----LNTGA---TTNVT----- 149
Db  1512 TLANGESVNRVTVVGVDVNDLVVNDLGLSIVGCASLTLSGINAGSHKIINVTAGTE 1571

Qy  150 -NDNVTDEKKRAASVKDLNLNAGNI-----KGVKPGTTASDNVD-----FVRTY 193
Db  1572 DTDVNFSQLK-----SVSEAVDKWTLTASGANGSKVYSGTVDLKNLAIKSGSDSN 1628

Qy  194 DTVEFLSADTK-----TTTVNVESKDNGKKTEVKIGAKTSVTEKDKGLVTKGKGEN 246
Db  1629 DVVFNLSKDFKVDVNTAGTVNTDGVKVG--SDVSLGAMGLFTANGPSVTASGFNAGDK 1686

Qy  247 -----GSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTG-----QADKFETV 291
Db  1687 VISHVAVGMADTDVAVNVSQLKQAVSVTVKATRYISTNDGGTQGGNVDGSGATKAAIAA 1746

Qy  292 TSGTKVT-----FASGNGTT-----ATVSKD-----DQG-----NITVKY 321
Db  1747 GVGTQASGEGAAAVGSGAAASGKSTAIGRNAIASADSGVALGDGAKDGGRGAESEYTKY 1806

Qy  322 D-----VNVG-----DALNVNOL-----QNSGMNLD----- 343
Db  1807 SGVQNTVTVSVGDAAKGETRSISNVADAKEMADVNLKQLDVAOKSNLQTDMMRHEI 1866

Qy  344 -----KAVAGSGKVISGNVSPSKGMDETVNI-----GNIEITRN-----GKNIDI 388
Db  1867 NNIEDVFKITKGDSSASSVKG-----MGVNMAIGTNAAVSGTESVALGKNTNV 1914

Qy  389 ATSWTPQPFSSVSLGAGADAPTLSDVDDGALNVGSKDANKPVRITNVAPGKGVGDTNVQAQ 448
Db  1915 SAD-----NAVAIGNSVA-----DRANSVSVSGGSE--QVTNVAAGTADTDVAVNSQ 1962

Qy  449 LKGVQAQNLNRIDNVNGNAR---AGTAQAIAATAGLVOAYLPCKSMMAIGGTYLGEAGY 504
Db  1963 LNOGLITAKQYTDGWNGLNRRTSGGVAAAIATANLPQAYVQGRGMTSVGSSYQGOSAI 2022

Qy  505 AIGYSISAGNMIIKGTASGNSRGHFGASASVGYOW 541
Db  2023 AVGVSAVESGHWKVFSGSANTRSHVGVGAGVGYOW 2059
```

RESULT 5
A86036
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: A86036
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206351
A;Accession: A86036

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1588 <STO>
A;Cross-references: GB:AE0051174; NID:gl2518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z5029

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Query Match      13.8%  Score 377;  DB 2;  Length 1588;
Best Local Similarity 25.2%;  Pred. No. 2e-11;
Matches 155;  Conservative 88;  Mismatches 267;  Indels 106;  Gaps 21;

Qy  18 GSTQASMEGSVELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLKIKONT---NENTNAS 72
Db  987 GAYNASHDGKASIIITNVANGSISBSDAVNG-----SQLNATNMIEQNTQIINOLAGNT 1042

Qy  73 SFTYSLKDLTGLINVT---EKLSF-----GANGKKNIIISDTKGLNFAKETAGTNGDT 124
Db  1043 DATY-IOENGAGINIVRTNDDGLAFNDASAGGVGATAGYNSVAKGSSVAIGOGSYSDV 1101

Qy  125 TVHLNGIGSTLTDLMLNTGA--TTNVTNDNV-----TDDEKKRAASVKD-----VLNAG 171
Db  1102 DTGIALGSSSVSSRVIAKGSRTSITENGVIYDITDGLLGLALSICDDGKYQIIN-- 1159

Qy  172 WNITGVKPGTTASDNVDVRYDTVEFLSADTKTTTVNVESKONGK-----KTEVKIGAKT 227
Db  1160 -----VADGSEAHDAVT--VRQLQNAIGAVALTPPKYFHANSTEDSLAVGTDLSAMGAKT 1213

Qy  228 SVIKEK-----DGKLVTKGKGE-----NGSSTDEGEGLVTAKEVID 264
Db  1214 IVNGDKGIGIGYGAIVDANALGIAIGSNAQVIHVNIAIGNGSTTTTTRGAQTNTYATNMD 1273

Qy  265 AVNKAQWRMKTTTANGO-----TGQADKFETVTSKVTFSAGNGTTATVSKDDQ--- 314
Db  1274 APQNSVGEFSVGSADGQRIITNVAAAGSADTDVAVNVGQLKYTDQAVSQNTOSITNLDNRVT 1333

Qy  315 --GNITVKYDVNVGDAL-----NVNOLQNSGMNLDKSAVAGSGKVISGNVSPSK 362
Db  1334 NLDSRVNTNIEGIDIVTTGTSTKYFKTNTGDVDAQAQKSDVAIGSGSIAADNSVALGT 1393

Qy  363 GKM---DETVINAGNIEITRN--GKNIDIATSWTPQPFSSVSLGAGADAPTLSDVDEG 416
Db  1394 GSVAETEINTSVGSSTNORRITNVAAKNATDAVNAQLKSGVAGGVRYDTKADGSDYS 1453

Qy  417 ALNVGSKDANKPVRITNVAPGKGVGDTNVNAQLKGVQA-----NLNNRIDNVNG 465
Db  1454 NITLGGNGG--TTRISNVAGVNNNDVVNVAQLKQSVQETKQYTDQRMVEMDNKLSKTES 1512

Qy  466 NARAGTAQAIAATAGLVOAYLPCKSMMAIGGTYLGEAGYAGYSSISAGNMIIKGTASG 525
Db  1513 KLSGGIASAMAMTGLPQAYTPGASMASIGGTYNGESAVALGYSVMSANGRWVYKLGST 1572

Qy  526 NSRGHFGCASASVGYOW 541
Db  1573 NSQGEYSAAALGAGIQW 1588
```

RESULT 6
H91188
probable adhesin ECS4480 [similarity] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C;Accession: H91188
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H91188
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1588 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA837903.1; PID:gl33363955; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs4480

```
Query Match      13.8%; Score 377; DB 2; Length 1588;
Best Local Similarity 25.2%; Pred. No. 2e-11;
Matches 155; Conservative 88; Mismatches 267; Indels 106; Gaps 21;

Qy 18 GSIQASMEGSGVELET--ISLSMTNDSKEFVDPYIVVTLKAGDNLIKIKONT---NENTINAS 72
Db 987 GAYNASHDGKASIITNVANGSISESDTDAVNG---SOLNATNMIEQTOIINQLAGNT 1042

Qy 73 SFTYSLKDLNGLINVEF--EKLSP-----GANGKKVNIISDTKGLNFAKETAGTNGDT 124
Db 1043 DATY-IQENGAGINIVRTNDGLAFNDASAOQVGATAIGYNSVAKGSSVAIGOGSYSDV 1101

Qy 125 TVHLNGIGSTLDTMLNTGA--TTNVTNDNV-----TDDEKKRAASVKD-----VLNAG 171
Db 1102 DTGIALGSSSVSSRVIAGKSRDTSITENGVIIGVYDTTDDGELLGALSIGDGKRYQIIN-- 1159

Qy 172 WNIKGVKPGTTASDNVDFVRTYDFEFLSADTKTTTVNVESKDNGK----KTEVKIGAKT 227
Db 1160 ----VADGSEAHDAVT--VRQLQNAIGAVALTPTKYFPHANSTEEDSLAVGTDSLAMGAKT 1213

Qy 228 SVIKEK-----DGKLVTKGKGE-----NGSSTDEGEGLVTAKEVID 264
Db 1214 IVNGDKGIGIGYGAYVDANALNGIAIGSNAQVIHVNSTAIIGNSGTTRGAQNTYAYNMD 1273

Qy 265 AVNKGAWRMKTTTANGO-----TGQADKFETVTSFKTTFASGNGTATVSKDQO--- 314
Db 1274 APQNSVGEFSVGSADGQRQITNVAAGSADTDVAVNGQLKVTDQVSONTQBITNLNDRVT 1333

Qy 315 --GNITVKYDVNVDGAL-----NVNQLONGWMLNDSKAVAGSGSKVISGNVSPSK 362
Db 1334 NLDSRVNTNIENGIDVITVGTSTKYFKNTDGVDSAQGKDSVAIGSGSIAAADSVALGT 1393

Qy 363 GKM---DETVINAGNIEITRN---GKNIDIAITSMPTQFSSVSLGAGADAPTLISVDDEG 416
Db 1394 GSVATEENTISVGSSTNORRITNVAAGKNATDAVNVAQLKSSAGGVRYDTFKADGSIDYS 1453

Qy 417 ALNVGSKDANKPVRTITNVPAGVKEGDVTNVAQLKGVQA-----NLNNRIDNVNG 465
Db 1454 NITLGGNGG--TTRISNVSAQNNNDVVNYAQLKQSOETKQYTDQRKVENDKLSTES 1512

Qy 466 NARAGIAQAIATAGLVOAYLPKGSMAIIGGTYLGEAGYAIYSSISAGGNNIITKGTASG 525
Db 1513 KLSGGIASAMAMTGLPOAYTPGASMASIGGGTYNGESAVALGVSMVSAWGRWVYKLOGST 1572

Qy 526 NSRGHFGASASVGVQW 541
Db 1573 NSOGEYSAAALGAGIQW 1588
```

RESULT 7
A82615
surface protein xfl981 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82615
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1190 <SUM>
A:Cross-references: GB:AF004017; GB:AF003849; NID:G9107083; PIDN:AAF84783.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorriy, H.; Pacincañi, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
M.; Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1981

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Query Match      13.5%; Score 368.5; DB 2; Length 1190;
Best Local Similarity 23.9%; Pred. No. 3.8e-11;
Matches 153; Conservative 85; Mismatches 213; Indels 189; Gaps 25;

Qy 27 SVELE----TISLMTNDSKEFVDPYIVVTLKAGDNLIKIKONTNNTNASSFTYSLKKDL 82
Db 615 SVDLKNSDGNLLITKTTDSND-----VTENLATALKVDLSITTCNTAMTTDGTGTVGSNV 667

Qy 83 ----TGLI----NVETEKLSFGANGKVN1--ISDPKGLNEA----- 114
Db 668 TLGSTGLVITDGPVSTSGISAG-NQKITNVAAGTADTDVAVNSQLOQAVSSTASKGNMLL 726

Qy 115 -----KETAG-----TNGDITTVHLNGI 131
Db 727 ASGANSSNVAPGESVDLKNITDGNIVISKESNDVLFNLSSSLKDLKLTGDTVMTNGV 786

Qy 132 GSTLTDMLLNTGATNTVNDVTDDEKKRAASVKDLNAG-WNIKGVKPGTTASD----- 185
Db 787 ----TVSGSVTLGSMGLVITDGPVSTSGI-----NAGSOKITNVAAGTADTDVAVNLS 835

Qy 186 -----NVDFVRTYDFEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEK 233
Db 836 QLNLTAMAGSGAKSVHYIYSTYD-----GGTGGNYNGDGTGTSIAVGVTLASA----- 885

Qy 234 DGKLVTKGKGENG--SSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFETVT 292
Db 886 EGATAVSGSAAASCKGTAIGRNAVASADGSVALGD-GAKDGAESYTKYKSLQNNVT 944

Qy 293 SGTKVTASGNGTTATVSKDDQGNITVKYDVNVGDALNVNOL-----QNSGNWLSKAVAG 348
Db 945 VGTVSVGDASKGETRTVS-----NVADAKEAT--DAVNLRLDRAODANRYVDNKIESL 997

Qy 349 SSGKVISGNVSPSKKMDTETVINAGNIEITRNKKNIDIAITSMPTQFSSVSLGAGADA- 407
Db 998 SEGQTF-----VKVNSLNN-----SATPIAAGVDATAIGVGATAS 1032

Qy 408 -----PTLSVDDEGAL-----NVGSKDANKPVRTITNVPAGVKEGDVTN 445
Db 1033 GADSIAMGNKASASADNAVAIGNHNSVADRANTVSVGSAGSER--QVTNVAAGTADTDVAVN 1090

Qy 446 VAQLKGVQAQNLNNRIDNVNGAR-----AGTAAQTATAGLVOAYLPKGSMAIIGGTYLGE 501
Db 1091 VSQNLQGLITAKQYTDGVGVSLRRDITDGGVAAAIATANLPQAYIPGRGMTSVGVSSYRQG 1150

Qy 502 AGYAIQYSSISAGGNWIIKGTASGNSRGHFGASASVGVQW 541
Db 1151 SAIAVGSSVSESGRWVFKFSGSANTRSQVIGAGVGIQW 1190
```

RESULT 8
AC0976
probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova
C:Species: Salmonella enterica subsp. enterica serovar typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moule, S.; O'Gaora, P.

A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-1536 <BAR>

A:Cross-references: GB:U08876; GB:M84616; NID:g475770; PIDN:AAA20527.1; PID:g475771

A>Note: sequence inconsistent with the nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBI:89239)

Query Match 8.4%; Score 231; DB 2; Length 1536;
Best Local Similarity 23.4%; Pred. No. 0.00049;
Matches 142; Conservative 90; Mismatches 215; Indels 160; Gaps 33;

Qy 18 GSIOASMEGSELETSISLWTSNDKEFDVPIVITLK-----AGDNLKIKONTNENTNAS 72
Db 739 GNISVGGSGVDFTLLA-----SSSNVOTPGWINSKYFNYSSTGSLRFTSGTKTG-- 791

Qy 73 SFTYSLLKDLT-----GLINVETKLSFGANGK-----KVNTISDTKGLNFAKETAGT--N 121
Db 792 ---FSIEKDLPLNATGGNITLLQVEGTDGMIKGIVAKKNTFEGGNITFGSKRAVTEIE 848

Qy 122 GDTTVHLNG-----IGSTL-----TDLMLNTGATT-----NVTN--DNVTDDEKKRAA 162
Db 849 GNVTTNNANVTLLIGSDFDNHOKPLTIKKDVIINSGNLTAGGNIVNIAGNLTVESN--A 905

Qy 163 SVKDVNLNAGWIKGV-----KPGTTASD-----NVDVVRTYDVVEFLSA 201
Db 906 NFKAITFTFNVGGLFDNKGNSNISIAKGGARFKDIDNSKNLSITTNSSSTYRTIISGNI 965

Qy 202 DTKTTTVNVEKSKDKKTEVKIGAKTSVKEKDKGLVTGKCK-----GENG 247
Db 966 TNKNGDLNITNE--GSDTEMIIGDVS---QKEGNLISSDKINITKQITIKAGVDGENS 1020

Qy 248 SSTDEGEGLVPAK-----EVIDAVNKAQWRMKTITAN-----GOTQOADRFETVTSQK 296
Db 1021 DSDATNNANLTIKTKEKLTQDLNISGFNKAEITAKDGSDLTIGNTNSADG----TNAKK 1076

Qy 297 VTF-----ASNGTTATVSKDDQGNITVKDVNVGDALNVQNLQNSWNLDSKAVA 347
Db 1077 VTFNOVKDSKTSADGHKVLTHSKVETSGS-----NNNTEDSSD-----NNAGLTIDAKNV- 1126

Qy 348 GSSGKVISGNSVPSKGMDETVNINAGNNIEITRGNKNIDAT---SMTPOFSSVSLGAG 404
Db 1127 ----TVNNITSHK-----AVSISATSGEITTKTGTITNATTGNVEITAGTGSILGGIE 1176

Qy 405 ADAPTLSVD--DEGALNVGSKDANKPVRITNVAPGVKEGDVNTVA--OLKGV-AONLNNRI 460
Db 1177 SSSGSVTLTATGALAVSNISGN-----TVTVTANSGLTTLAGSTIKGPESVTTSSQS 1230

Qy 461 DNVGNARAGIAQAIAATAGLVOAYLPCKSMMAIGGTYLGEAGYALGYSSISAGNNWIK 520
Db 1231 GDIGGTISGGTVKVKATESLTT-----QSNKIKATT--GEANVT-----SATGT--IG 1275

Qy 521 GTASGNS 527
Db 1276 GTISGNT 1282

RESULT 11

A56143

surface-array protein homolog sapA2 - Campylobacter fetus (strain 82-40 LP3)

C:Species: Campylobacter fetus

C:Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999

C:Accession: A56143

R:Dworkin, J.; Tummuru, M.K.R.; Blaser, M.J.

J. Bacteriol. 177, 1734-1741, 1995

A:Title: A lipopolysaccharide-binding domain of the Campylobacter fetus S-layer protein

A:Reference number: A56143; MUID:95204338; PMID:7896695

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1109 <DWO>

A:Cross-references: GB:S76860; NID:g913763; PIDN:AAB33871.1; PID:g913764

A>Note: this gene appeared to be silent in strain 82-40 LP3

C:Genetics:

A:Gene: sapA2

Query Match 8.2%; Score 225; DB 2; Length 1109;

Best Local Similarity 25.0%; Pred. No. 0.00064;

Matches 152; Conservative 78; Mismatches 221; Indels 158; Gaps 35;

Qy 4 DEEELESVQSVSVGSIOASMEGSEVE-LETISLWTSNDKEFDVPIV-VTLKAGDNLKI 61
Db 330 DGSADVQNLKLVNGVGAASVAITADKTETELNLN--TTGSQSFVSADVASISVKGNANLSL 388

Qy 62 KONTNENT--NASSFTYSLLKDLTGLINVETKLSFGANGKKNVLIISDTKGLNFAKETAGT 120
Db 389 ATGAKTTTLTDLASSFGGALDADLTSASVTSIK---GGNGDKITIKDV-AVNVAID--GGA 443

Qy 121 NGDFTVHLNGIGSLTIDMLLNTGATTNVTNDNVTD---EKKRAASVKDVLNAGWNKGV 177
Db 444 GNDELVIKGSTADTLPQTLTN---IEKVTIDGNTKDLTSLKKAQSVTEL-----SPKNI 495

Qy 178 -KPGTTASDNVDVRYTYDVEFL--SADTKTTTVNVE-----KDNCKKTEVKIGA 225
Db 496 AKTVTESGNV-----ETVNLANATDKAVTINDESLKTIINFSVDVDDKG---ASVAA 545

Qy 226 KTSVIKEKDKGLVTGKCK-----GENGSSTDEGEGLVTAKEVID----- 264
Db 546 KGIIVADKATELTINSKNKVTLASDAVVOAANATKID----INAAKDTVGLTGLGVAKLTD 601

Qy 265 -AVNKAQWRMKTITANG-----OTQOADKFETVTS-----GTRVTFASG 302
Db 602 LTVNKG-AFALTGANATDLDVKNLSVNTGEGASIAATATSLKNNLNSLVGVSADLNSV 660

Qy 303 NGTTATVSKDDQ-----GNITVKYDV-----NVGDALNVQNLQNSWNLDSKAVA 347
Db 661 NVGTATLASLEANINVSGEFKLGTAKGDVDFNIENVG-ALTGAIITSTGNA-SVIIS 718

Qy 348 GSSGKVISGNSVPSKGMDETVNINAGNNIEITRGNKNIDATSMTPQFSSVSLGAGADA 407
Db 719 SATGNVTLGAVSATQGNL---TLNAGNTL-----GNITIGA-LKG 754

Qy 408 PTLSDVDEGALNVGSKDANKPVRITNVAPGVKEGDVT-----NVAQLKGA--ONLN 457
Db 755 DIVSDVLGGVLGTINSNANKVSITS-----NEVTYVGSSEIKNVVEITAAAGGTDLN 807

Qy 458 NRIDNVGNARAGIAQAIAATAGLVOAYLPCKSMMAIGGTYLGEAGYALGYSSISAGNNW 517
Db 808 AQ---VTGGAAADALTIIGKDTQTITASGD---LSGGTTLTTLTEATKLSLSDISG-- 859

Qy 518 IIKGTASGN 526
Db 860 -VKG-ITGN 866

RESULT 12

C82672

surface-exposed outer membrane protein Xfl1516 [imported] - Xylella fastidiosa (strain

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: C82672

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: C82672

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1004 <SIM>

A:Cross-references: GB:AE003981; GB:AE003849; NID:g9105543; PIDN:AAF84325.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
C;Genetics: annotation
A;Gene: XF1516

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Query Match      8.1% Score 220.5; DB 2; Length 1004;
Best Local Similarity 23.0%; Pred. No. 0.00096;
Matches 142; Conservative 76; Mismatches 236; Indels 163; Gaps 29;

QY 34 SLSTNDSKEFVDPYIVVTLKAGDNLKIKONTENTN-ASSFYSLKDLTGLINVTEK 92
Db 114 SLAIGFSKAFAPNAIAL-----GYNSSVTQSANNGVALGNSVVS-----GVNSVA 160
QY 93 LSFEGANGKKNYIISDTKGLNFAKETAGTNGDITVHLNGIGSTLTMLLNTGATNTVNDN 152
Db 161 LGAGSMASELNVISVGG-----DGVTPAVRRIVNVG-----DGIGNDAVNKSQLDG 209
QY 153 VTDEKKRAASVDVL-----NAGNKKGVKPGTTA-SDNVDFRVYDYTFEF- 198
Db 210 VTASVNDVAASVKTIALTNQVTGSSVASASGKESTAIGSAQAVADN-----TVAFG 261
QY 199 -----LSADP-----KTTTVNVEKSD-----NGKKEVTKGAK 226
Db 262 GRAIANAVGASALGDFSHAKGINTVTGTSVLSGQGVSLGYNSFVGECSFNGALGNS 321
QY 227 TSVIKERKGLVTGKG---KGNGSSTDEGGL--VTAKEVI-----DAVNRKAGWR 272
Db 322 SLVLQGVDSVALGSGSWASEPNVSVSGDGLRGPVRRIVNVGDIGNDAVNKSQLD 381
QY 273 MKTTTANGQGDADKFTV--TSGTKVTFASGNGTTAT-VSKDDQGNITVKYDYNVGDAL 329
Db 382 GVTASVNDVVASVKNIAGAQTGTSGVASVSGQDSTAAGASAAQAGDSSIA-----LGARS 437
QY 330 NVNOLONGWNLQ-----SKAVAGSSGVISGVNSPFSKGMDETNNAGNNIETRN 382
Db 438 RANAIGSALGVGDHALGANSTALGGQSTAISEGTSLSG---YNSFVGQSATNGIALGNS 494
QY 383 GKNIDIATSTPQFSSVSLGAGADAPTLISVDDGALNVGSKD-ANKPV--RITNVAPGVK 439
Db 495 -----AIVSGVNSVALGAGSVASELNV-----ISVGGDGVTPAVRRIVNVGDIG 541
QY 440 EGDVTNVQALKGVAQNLN--RIDNVNGNR--AGIAQAI---ATAGLVQAYLPKSM 490
Db 542 NNDVANKSOLDGVGTASVNDVAASVKIKVGTITQITGSGVASAIGKDSATGASAAQAGDSS 601
QY 491 MATG-----GGTYLGEAGYAGYSSISAGGNWLIK-----GTA 523
Db 602 VALGTRATANAIGSSVLGVDSRARGINSTALGRQSNAGIDGVSGLGFSNPFVROSGEHRVA 661
QY 524 SGNSRSHFGA-SASVGY 539
Db 662 LGTDAGVSGKDSIALGY 678
```

RESULT 13
AF0394
probable adhesin hmwA [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AF0394
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AF0394
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1910 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:q15981183; GSPDB:GN00175
C;Genetics:
A;Gene: hmwA

```
Query Match      7.8% Score 214; DB 2; Length 1910;
Best Local Similarity 22.1%; Pred. No. 0.0047;
Matches 141; Conservative 81; Mismatches 219; Indels 198; Gaps 31;

QY 27 SVELETI--SLSMTNDSKEFVDPYIVVTLKAGDNLKIKQ-----NTNENT-----N 70
Db 1166 NVELNATAGNVSIAETKLTALSTSLNAVLSLGNNSIKAQNGWLIGKAFNTTQAGATGCFR 1225
QY 71 ASFTYSLKDKLGLINLVETKLS-----FCAN-----GKVNIIISDTKGLNFAKE 116
Db 1226 ANS---SLSDVGNIIILKGETEGVGATRKGDIDFYGANTLNTIKGSQLLGENKG---AQD 1279
QY 117 TAGTNG-----DITVHLNGI-----GSTLTMLLNTGATNTVNDNVTDEKKRAASVK 165
Db 1280 TAGGNGISYTSLAKLTVNNNGSLKMEGRSTSGTGINFSSNNTLVFNGDGTLLIKGS-- 1337
QY 166 DVLNAGNWKIKVPGTPTASDNVDFRVYDT--VEFSLADTKTTTVNVESKDNKKTE---V 221
Db 1338 -VAGTGAASGVVNNSTGPMTEIGISTDGAGVHLFSAEHRIDRINV---TGSSTHAEBGL 1392
QY 222 KIGAKTSVIEKDKGLVTGKGKENGSGSTD-----EGEGLVTAKEVIDAVNKAQWMTT 277
Db 1393 RISGNAAIVD-----TTLTGKISNGSVKIDSLPGSSVVT-RSVLD-----NAT 1435
QY 278 ANGQTGQADRFETVTSCTKVTFASSNGTATATVSKDDQGNITVKYDYNVGDALNV----- 331
Db 1436 LNSGSSSGKGVETSDINGIHHSSINGTTGTG-----YCIDIGENSNTVTGSEA 1485
QY 332 -----NOLONGWNLDSKAVAG-----SSGKVISGNVS 359
Db 1486 DLLILOQVATTGTGTGIKLGNNDLSNT--SLNSSAVDGIADITGTPLANQGNVILNGTA 1543
QY 360 PSKG-----KDETIVNINAGNNIETRN----- 382
Db 1544 SSGIGAQVNSLSDSVVNGTSTNGIGVQINGSLKNSRINGISANGSGVKIDGESTLDNA 1603
QY 383 -----GKNIDIATSTPQFSSVSLGAGADAPTLISVDDGALNVGSKDANKPVRIYN 434
Db 1604 TLNGNSTEGKGVDLAANLNGHSGSVVHGTGIDVGRDVTLSGGTD--EPLTVSGN 1661
QY 435 APGVKEGDTVNVQALKGVAQNLNRI--VNGNARAGIAQAIATAGLVQAYLPKSMMA 492
Db 1662 ASGEKGTGV---QLGG-----NNTLDNTLISGNATDGHGVEI-----NSRLINNGNTT 1706
QY 493 IGGTYLGEAGYAGYSSISAGGNWLIKGTASGNSRGHF 531
Db 1707 INKGT--SDDGHVHINGAIGSGE--ING-HSDNSHGTV 1740
```

RESULT 14
T31105
hypothetical protein 2 - Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31105
R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A;Reference number: Z20984; MUID:99030326; PMID:9811662
A;Accession: T31105
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-4919 <WAR>
A;Cross-references: EMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AAC79761.1
C;Genetics:

A:Gene: lspA2

Query Match 7.8%; Score 212.5; DB 2; Length 4919;
Best Local Similarity 21.8%; Pred. NO. 0.019;
Matches 151; Conservative 85; Mismatches 248; Indels 209; Gaps 32;

QY 17 VGSTQASNE-CSVELETISLSMTNDSKEFVDPYIVVTLKAGD----- 57
DB 429 ISALNLTLENATVSAANLSFVTDTK--LNNLSKVSAARAADLQSGNLLDKASYLAHL 486
QY 58 NLKIKQNTNENTNASSFYSLKDLTGLINVEKESFGANGKKVNIISDTKGLNFAKET 117
DB 487 TLTNSDVLNQSKLSANNKIKKVRDLNLSLS--ANLTLTNSNTITLKNKSF 544
QY 118 AGT---NGDVTVHLNGIGSTLMLNTGATNTV-----NDNVTDDK 158
DB 545 AGNMTLVNTVNLNN--DSELAANLTLNVTKNYTLNDASKLSANKLNLVNDVTLNSK 603
QY 159 KRAAS-----VKDV-----LNAGNNIKGVKPGTASDNVDF---VRTY 193
DB 604 STLSAGELTFPKVKVKNVTLNNDSELAANLTLNASHNVTLNKSKLSAQKADIKAVNLTN 663
QY 194 DTVEFL--SADTKTTV-----NVESKDKGKTEYKIGAKTSVKEKDKLVG 240
DB 664 DTTELTAKNLDINSTIITNNGTIAIFANITTEKLNKKEKALILAEQNLNFTVNGSHYEN 723
QY 241 KGK-----GENGSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTGOADKFE 289
DB 724 KGDIVSKDKATVTFESKNSDFTSNGSKLVNAQN-----QLKVVNNFTISQDDIT 773
QY 290 ---TVTSTKVTFA-SGNGTTA-TVSKDDQGNITVKYDVNVGDALNV---NOLQNSG--- 338
DB 774 LIGNVTLNASGFTNSGNLTVKTLVDGIDIONFTNKGNTLVGEDLHIKSKTKIINDGKLI 833
QY 339 ---WNLDSKAVAGSGKVI-----SGN-----VSPSKGKMDET 369
DB 834 SIKNLNISSEADFINGTLLEGIEALKIATKGNFNKKEKAILASNLSDISVAEKG--KTF 891
QY 370 N---INAGNNIEITRNGK--NIDIATSMTPQSFSSVSLGAGADAPTLSDDEGALNVGSK- 423
DB 892 NNGTIESCKNLNITNTGAFLVNDATIR-----SFGVLNITSTGNVSNNGTLISNERL 944
QY 424 DANKPVRTITNVAPG-----VKEGDTNVAQLKGVAQ--NUNNRIDNVNGNARAGI 471
DB 945 NITSAANFTNESGTVMSNGLLNIIAKOGNITNKLIIASRQOLNLTAVADNITND--SNI 1002
QY 472 AQAATAGLVQAYLPKGSMAIGGTGLGEAGYAGYSSISAGGNWLIK----- 520
DB 1003 SNKTAVLHSL-----GNISLNSKDQVYNLGEIYAGNNISVKAHQHNDVKLM 1049
QY 521 -----GTAS-----GNSRGHFGASASVGY 539
DB 1050 GDITTKTKGQASYKLYQASNGHGFGNDGSSGY 1082

RESULT 15

A41477

190K surface antigen precursor - Rickettsia rickettsii

C:Species: Rickettsia rickettsii

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 08-Oct-1999

C:Accession: A41477

R:Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L.

Infect. Immun. 58, 2760-2769, 1990

A:Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated, ne

A:Reference number: A41477; MUID:90354033; PMID:2117568

A:Accession: A41477

A:Molecule type: DNA

A:Residues: 1-2249 <AND>

A:Cross-references: GB:M31227; NID:g152465; PIDN:AAA26380.1; PID:g152466

A:Note: the authors translated the codon GAT for residue 430 as Gly, and CAA for residue

C:Keywords: surface antigen; tandem repeat

F:1-20/Domain: signal sequence (uncleaved) #status predicted <SIGU>

Query Match 7.7%; Score 210; DB 2; Length 2249;

Best Local Similarity 23.8%; Pred. NO. 0.0092;

Matches 139; Conservative 68; Mismatches 255; Indels 122; Gaps 27;

QY 9 LESVQRSVVGSIQASMEGSEVELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKONTNEN 68
DB 114 LNIQTNTVVGSI--ITKGNL-----LPVTLNACKSLTLNGN---N 148
QY 69 TNASFTYSLKKD-LTGLINVEKESFGANG-----KKVNIIS--DTKGLNFAKE 116
DB 149 AVAAHGHGFDAPADNYTGLGNIALG---GANAALIIOASAPSKITLAGNIDGGGIIITVK 204
QY 117 TAGTNGDPTVHLNGIGSTLMLNTGATNTVNDV---TDDEKKRAASVKDVNLNAGWN 173
DB 205 DAAINGT-----IGNTNALATNVGAGTATLGGAIVKATTTKLTNAASVLTLTNANAV 257
QY 174 IKGVKPGTASDNVDFVRYDTVEFLSADTKTT---TVNVESKD---NG---KTEVKI 223
DB 258 LTGAIDNTTGGDNVGNLNGALSOVTDIGNTSLATISVGAGTATLGGAIVKATTTKL 317
QY 224 GAKTSVKEKDKLVG---KKGKENGSSSTDEGEGLVTAK-----EVIDAVNKGWRMKT 275
DB 318 TDAASAVKFTPVVVVTVGAIDNTGNANNGIVTFTGNSTVTVGNVTNALATVNVGAGLLO- 376
QY 276 TTANGQTGOADKFEVTVSGTKVTFPASNGTGTATVSKDDQGNIT---VKYDWN---VGDAL 329
DB 377 --VQGGVVVKANTINLTDNASAVTFT--NPVVVTVGAIDNTGNANNGIVTFTGNSTVTDIG 432
QY 330 NVNOLONGSNLDSKAVAGSSGKYLISGNVSPSKGKMDETIVNNA--GNNIETRNGKNID 387
DB 433 NTNALATVNVGAGTATLGGAIVKATTTKLTNAASVLTLT--NANAVLTGAIDNTTGGDNV 491
QY 388 IAT-----SMTPOFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRITNVA 435
DB 492 VLNLNGALSOVTVGNIGNTSLATISVGAG--TATLGGAIVKATTTKLTDAASAVKFTN-- 547
QY 436 PGVKEGDTNVAQLKGVAQNLRNIDNVNGNARA---GIAQAATAGLVQAYLPKGSMM 491
DB 548 PVVVTGAIDNTG-----NANNGIVTFTGNSTVTDIGNTSLATISV-----GAGTA 594
QY 492 AIGGG-----TYLGEAGYAGYSSISAGGNWLIKGTASGNSRG 529
DB 595 TLGGAVIKATTTKLTNAASVLTLTNANAVLTGAIDNTTGGDNV 638

Search completed: October 6, 2003, 09:33:32

Job time : 19.4863 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 8.35443 Seconds
(without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-34

Perfect score: 2735

Sequence: 1 TDEDEEELESVQSRVWGS1.....TASGNSRGHFGASVGYQW 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	210	7.7	OMPA_RICRI	P15921 rickettsia
2	206.5	7.6	OMPB_RICCN	Q9kka3 r outer mem
3	201	7.3	OMPB_RICRI	Q53047 r outer mem
4	198	7.2	YDBA_ECOLI	P33666 escherichia
5	197	7.2	HLVA_PROMI	P16466 proteus mir
6	189.5	6.9	OMPA_RICCN	Q52657 rickettsia
7	186	6.8	OMPB_RICJA	O06853 r outer mem
8	184.5	6.7	BIGA_SALTY	P25927 salmonella
9	180	6.6	SLAP_CAMFE	P35827 campylobact
10	179.5	6.6	ALYS_ENTFA	P37710 enterococcu
11	179	6.5	HLVA_SERMA	P15320 serratia ma
12	179	6.5	OMPB_RICTY	P96989 r outer mem
13	177	6.5	AG43_ECOLI	P39180 escherichia
14	175.5	6.4	YDEK_ECOLI	P32051 escherichia
15	173	6.3	ICEN_XANCT	P18127 xanthomonas
16	172	6.3	SLAP_CAUCR	P35828 caulobacter
17	172	6.3	120K_RICRI	P14914 rickettsia
18	170.5	6.2	PVDB_PLAKN	P50493 plasmodium
19	170	6.2	YEEI_ECO57	Q8x8v7 escherichia
20	168.5	6.2	1569	P52143 escherichia
21	166.5	6.1	OMPB_RICRP	Q53020 r outer mem
22	166.5	6.1	YEEJ_ECOLI	P76347 escherichia
23	166	6.1	FLIC_SHIFL	Q08860 shigella fl
24	165	6.0	APU_THETU	P38536 t anlyopull
25	164.5	6.0	YMBJ_CAEEL	P34487 caenorhabdi
26	163.5	6.0	Y869_CAEEL	Q09624 caenorhabdi
27	161.5	5.9	WAPA_BACSU	Q07833 bacillus su
28	160	5.9	Y456_CHLTR	O84462 chlamydia t
29	160	5.9	PMPC_CHLTR	O84419 chlamydia t
30	159.5	5.8	HP11_DEIRA	P56867 deinococcus
31	159	5.8	AIDA_ECOLI	Q03155 escherichia
32	159	5.8	IGA0_HAEIN	P44969 haemophilus
33	159	5.8	IGA2_HAEIN	P45384 haemophilus

RESULT 1

ID	OMPA_RICRI	STANDARD;	PRT;	2249 AA.
AC	P15921;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmpA).			
DE	antigen) (rOmpA) (rOmpA).			
GN	OMPA			
OS	Rickettsia rickettsii.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;			
OC	Rickettsiaceae; Rickettsiae; Rickettsia.			
OX	NCBI_TaxID=783;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=R;			
RX	MEDLINE=90354033; PubMed=2117568;			
RA	Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;			
RT	"A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";			
RL	Infect. Immun. 58:2760-2769(1990).			
CC	-!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.			
CC	-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.			
CC	-!- PTM: GLYCOSYLATED (PROBABLE).			
CC	-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
EMBL; M31227; AAA6380.1; -				
PIR; A41477; A41477.				
DR InterPro; IPR006315; Autotransport.				
DR InterPro; IPR005546; Autotransporter.				
DR Pfam; PF03757; Autotransporter; 1.				
DR TIGRPFAM; TIGR01414; autotrans_bar1; 3.				
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.				
FT SIGNAL 1 28 POTENTIAL.				
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.				
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.				
FT REPEAT 212 286 A (TYPE I).				
FT REPEAT 287 358 B (TYPE II).				
FT REPEAT 359 430 C (TYPE II).				
FT REPEAT 431 505 D (TYPE II).				
FT REPEAT 506 577 E (TYPE II).				
FT REPEAT 578 652 F (TYPE II).				
FT REPEAT 653 724 G (TYPE II).				
FT REPEAT 725 799 H (TYPE II).				
FT REPEAT 800 874 I (TYPE II).				
FT REPEAT 875 949 J (TYPE II).				

Q9pj6 chlamydia m
P49051 bacillus an
Q06969 salmonella
Q9rb65 chlamydia p
Q48253 helicobacte
Q9x38 helicobacte
P22251 campylobact
P45354 haemophilus
P45355 haemophilus
P03275 human adeno
Q92812 chlamydia p
Q01714 rattus norv

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FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match
Best Local Similarity 7.7%; Score 210; DB 1; Length 2249;
Matches 139; Conservative 68; Mismatches 255; Indels 122; Gaps 27;

Qy- 9 LESVORSVGSIOASMEGSVELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNEN 68
Db 114 LNIQTNTVVGSI--ITKGNL-----LPVTLNAGKSLTLNGN---N 148
Qy 69 TNASSFTYSLKGD-LTGILINIVETEKLSFGANG-----KKNVNIIS--DTKGLNFAKE 116
Db 149 AVAANGHGFADADNYTGLGNALG----GANAAIIIOAAPSKITLAGNIDGGIIVKT 204
Qy 117 TAGTNGDFTVHLNGISGTLTDLMLNTGATTNVNDNV---TDDEKKRAASVKDVLNAGWN 173
Db 205 DAAINGT-----IGNTNALATNVVGAGTATLGGAVIKATTTKLTNAASVLTLTNANAV 257
Qy 174 IKGVKPGFTASDNDVFRYDTVEFLSADTKTT---TVNVESKD---NG---KKEVKI 223
Db 258 LTGAIDNTTGGDNGVGLNGLALSOVTDIGNTSLATISVGAGTATLGGAVIKATTTKL 317
Qy 224 GAKTSVIKEKDKLVTG----KKGENGSSPDEGEGLVTAK-----EVIDAVNKAGWRMT 275
Db 318 TDAASAVKFTNPVVVTGAIDNTGNANGIVTFTGTSVTVGNVGNATLTVNVGAGLLQ- 376
Qy 276 TTANGQTQADKFFVTSGKVTFTASNGTATVSKDDQGNIT---VKYDVN---VGDAL 329
Db 377 --VOGVVVKANTINLTNDNASAVTFT--NPVVVTGAIDNTGNANGIVTFTGTSVTVGDIG 432
Qy 330 NVNOLQSGWNLDSKAVAGSGKVIISGNVSPSKGMBETVNINA--GNNIETRNKNID 387
Db 433 NTNALATNVVGAGTATLGGAVIKATTTKLTNAASVLTLTNANAVLTGADNTTGGDNVG 491
Qy 388 IAT-----SMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVA 435
Db 492 VLNLGALSQVVTGNTGNATSLATISVGAG--TATLGGAVIKATTTKLTDAASAVKFTN-- 547
Qy 436 PGVKEGDTVVAQLKGVAQNLNNRIDNVNGNARA----GTAQATATAGLVOAYLPKGSMM 491
Db 548 PVVVTGAIDNTG-----NANNINGIVTFTGTSVTVGDIGNTSLATISV-----GAGTA 594
Qy 492 AIGGG-----TYLGEAGYATGYSSISAGGNWILKGTASGNSRG 529
Db 595 TLGGAVIKATTTKLTNAASVLTLTNANAVLTGADNTTGGDNVG 638

RESULT 2
OMP_RICCN STANDARD; PRT; 1655 AA.
ID OMPB_RICCN
AC O9KKA3; Q9KX98; Q9XC45;
DF 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
DE OMPB OR R1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_taxid=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
```

```

Dd 335 VVSVD-----NGKVATIDGQVYAKDMVIOASNAVQVNFHRHVDVGT 376
Qy 134 TLDTMLNTGATNTVT--NDNV--TDDEKKRAASV-----KDVINAGWNKGVKPGTASDNV 187
Dd 377 DGTAFKTAASKVAITONSFGTDFGNLAQAIIIVPWTWLTNGNFTGDSNPGNTAG--- 433
Qy 188 DFVRYTD---TVEFLSADTKTTTVN-----VESKONG-----KKTEVKIGAKTSVKEK 233
Dd 434 --VITFDANGTLASASADANVAVTNNTITAIEASAGVGVQLSGTHAAELRLGNAGSVFKLA 491
Qy 234 DGKLVTCG-----CKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGQA 285
Dd 492 DGTGVINKVNOTALVGLAAGTITLDGSATIG-----DIGNAGG-----AAALQGITLAN 543
Qy 286 DKFETVY-----SGTKVTFASGNGTTATVSKDQGNITTVKYDV-----NVGDAL 329
Dd 544 DATKTLGLGANIIGANGTINQANGTIKLAS--TQNIVVDFDLAIATDQTGVVDAS 601
Qy 330 NVNQLQNGWNLSKAVAGSSGKVISQVNSPSKGM--DETIVNIN---AGNN--JEITRNG 383
Dd 602 SLTNAQPTLTINGKIGTGVGANNKTLGQFNIGSSKTVLSGDVAINELVIGNNGAVQFAHNT 661
Qy 384 KNIDTATSMTPQ-----FSSV-----SLGAGADAPTLSVDDEGALNVGSKDANKPVRITNV 434
Dd 662 YLITRTTNAAGQGGKIIFNPVNNNTTATGTGTLNLS--ATNPLAEINFGSKGAANVDTVLNV 720
Qy 435 APGVKEGDTVNVQALQKVAQNLRNIDNVNG--NARAGIAQAIAFAGLVQ-----AYLP 486
Dd 721 GKGVLN--YATNITTTDA---NVGSFIENAGTNIVSG-----TVGQOQNKFTVALDN 770
Qy 487 GKSMATGGTYTIGEAGYAGYSSISAGNWIKGTASGNSRG 529
Dd 771 GTTVKFLGNATFNNGNTTIAAN--STLQIGGNVTADEVASADGTG 812

RESULT 3
OMP_RICRI
ID OMPB_RICRI STANDARD; PRT; 1654 AA.
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 3:1579-1586(1989).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN-R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kDa surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.

```

```

CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL; X16353; CAA34403.1; -.
DR PIR; S18227; S18227.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 kDa SURFACE-EXPOSED PROTEIN.
FT CHAIN 1334 1654 32 kDa BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 7.38; Score 201; DB 1; Length 1654;
Best Local Similarity 22.88; Pred. No. 0.013;
Matches 136; Conservative 79; Mismatches 228; Indels 154; Gaps 32;

Qy 15 SVVSGISQASMEGSVELETISLSMTNDSKEFVDVPVIVVTLKAGDNLKIKONTNENTNASSF 74
Dd 287 NITGSLGNLKGVEFTNVAV---DQG-----LTANAGANAVIGTNGAGRAAGF 334
Qy 75 TYSLKDLTGLINVETEKLSFGANGKRVNIISDTKGLNFAKFAKTAGTGTDTTV--HLNGIGS 133
Dd 335 VVSVD-----NGKVATIDGQVYAKDMVIOASNAVQVNFHRHVDVGA 376
Qy 134 TLDTMLNTGATNTVTNDN--VTDDEKKRAASVK--DVLNAGWNKIG--VKPGTASDNV 187
Dd 377 DGTAFKTAASKVITITQDSNFGNTDFGNLAQAIIIVPWTWLTNGNFTGDSNPGNTAG--- 433
Qy 188 DFVRYTD---TVEFLSADTKTTTVN---VESKONG-----KKTEVKIGAKTSVKEK 233
Dd 434 --VITFDANGTLESASADANVAVTNNTITAIEASAGVGVQLSGTHAAELRLGNAGSVFKLA 491
Qy 234 DGKLVTCG-----CKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGQA 285
Dd 492 DGTGVINKVNOTALVGLAAGTITLDGSATIGD--IGNAGGAALQRIITLAN----- 543
Qy 286 DKFETVTSKTVTFASGNGT-----TATVSKDDQGNITTVKYDV-----NVG 326
Dd 544 DAKKTLTGGANIIGAGGGTIDLQANGTIKLTST-----QNNIVVDFDLAIATDQTGV 598
Qy 327 DALNVNQLQNGWN-----LDSKAVA---GSSGKVIS--GNVSPSKGKMDVTNINAG 374
Dd 599 DASSLTNAQPTLTINGKIGTIGANNKTLGQFNIGSSKTVLSNGNVA-----INELVIGNDG 653
Qy 375 -----NNIEITR-----NGKNI--DIATSMTPQFSVSLVAGADAPTLSVDDEGALNV 420
Dd 654 AVQFAHDTYLTITRTTNAAGQGGKIIFNPVNNNTTLAGTNLGS-----ATNPLAEINEF 706
Qy 421 GSKDANKPVRITNVAPGVKEGDTVNVQALQKVAQNLRNIDNVNG--NARAGIAQAIAFAG 479
Dd 707 GSKGVNVDY--VLNVGEGVNL--YATNITTTDA---NVGSFVFNAGTNIVSG-----TVG 755
Qy 480 LVQ-----AYLPKSMMAIGGGTYLGEAGYAGYSSISAGNWIKGTASGNSRG 529
Dd 756 GQOQNKFTVALENGTTTVKFLGNATFNNGNTTIAAN--STLQIGGNVTADEVASADGTG 811

RESULT 4
YDBA_ECOLI
ID YDBA_ECOLI STANDARD; PRT; 2003 AA.
AC P33666; P76087; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

```

208 KQVYHNGELVIT---GDNATV--NNNGKTTVDG-----KDTGCTEINGNCKVKVLDGD 250

93 LSFANGKVKVNIISPT-----KG-----INFAKETAGTNGDPTVH 127

257 LDVSGGGHGIDITGDSATVNDKGTMTVTDPESMGIQDGDKAIVNNEGESTINGCTGTQ 316

128 LNG-----IGSTLITDMLLTGATTNTVNDNVTDQ-----EKK 159

317 INGDDATANNNGKTTVDGKSDTGTETEINGNCKVLDGDLDVSGGGHGIDITGDSATVDNK 376

160 RAASVKDVLNAGWNKGVKPGTTSADNDVFRVTYVEFLSADTKTNTVNVESKDNGKK- 218

377 GMTVTDPEISIGIQVDG--DQAVVNEGESAINTNGCTGTQINGDDATANNNGKTTVDGKDS 435

219 --TEVKIGAKTSVIREKDGKL-VTGKRGK---ENGSTDEGEGLVTAKE-----VIDA- 265

436 TGTEI-AGNNGKVI--QDGDLDVSGGGHGIDITGDSATVDNKGTMTVTDPEISIGIQDGD 492

266 ---VNKAGWRMKTTFANGQTGOADKFEETVSGTKVTFASGNGTGTATVSKDD-----QGN 317

493 QAIVANNEG---ESTITNGTGT-----TQINGNDAT-ANNNGKTTVDGKSDTGTKIAGNI 542

318 TVKYDVNVGDALNV---NQLNSGWN--LDSK-----AVAGSSGKVISGNVSPSKGMD 366

543 GI-----VNLGDSLTVTGGAHVGENIDNGTVNNKGDIIVVSDTSGIVLINGEGATVSN 599

367 ETVNTNAGNIEITRGNKNDIATSM-TPOFSS-VSLGAGADAPTLSDVD-----EGA 417

600 VNVVS-NEATGFSITNNSKVSGLAGSMQVGFSTGVDLNGNNNSVTLAAKDLKVVGQKATG 658

418 LNVGSKDANKPVRIITNAPGVKEGDVNTVAQL-----KGVAQNLRNIDNVNGNARAGI--- 471

659 INV-SGDAN-TVNITGNVLVDKKTADNAAEVFPDPSVGINVYSGDNNVTLDGKLFVWSD 716

472 -----AQAIATAGLVQAYLPCKSMALGGTGYLGE-----AGYA 505

717 SEVTSRQSNLFDGSAEKTSGLV-VIGDGTVMNMGGLLIGEKKNALADGSQVTSRLRTGYS 775

506 I-----GYSSISAGGNWIKG 521

776 YTSVIWVSGESSVYINGDTTISG 798

RESULT 5

HLVA_PROMI

ID HLVA_PROMI STANDARD; PRT; 1577 AA.

AC P16466;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-NOV-1990 (Rel. 16, Last annotation update)

DE Hemolysin precursor.

DE GN

GN HPMA.

OS Proteus mirabilis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Proteus.

OC NCBI_TaxID=584;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.

RC STRAIN=Isolate 477-12;

RA MEDLINE=90170827; PubMed=2407716;

RX Uphoff T.S., Welch R.A.;

RT "Nucleotide sequencing of the proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";

RT J. Bacteriol. 172:1206-1216(1990).

RL -I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.

CC -I- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.

CC -I- SUBCELLULAR LOCATION: Outer membrane.

CC -I- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA

RESULT 6
OMPA_RICCN


```
QY 125 --TVHLNGIGSTLT-----DMLNTGAT-TNVTNDVNTDEKKRAASVKDVL 168
D 125 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 455 TGTSDISGAGTGTVIDGNARVNNDGDMTITDGTGTHGTDNVVID----- 502
QY 169 NAGHNKIKVKGTTASDNVDFRYDVEFLSADTKTTVNVEKDN-----GKKTEVK 222
D 169 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 503 NAG-----STTVS-----GAD--ATALYIEG-DNALVINEGNOT-IS 535
QY 223 IGAKTSVIKEDKG-----LVTGKG-----KGGSSSTDEGEGLVT--AKEVI--DA 265
D 223 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 536 GGAVGTRIDGDAHTTNTGDIADVGAGSAVILNDGSLTQAGDLLVTDGAMLIITYGT 595
QY 266 VNKAGWRMKTITANGQTQADKFEFTVTSKTFP-----ASNGTTATVSKDDQGNIT 318
D 266 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 596 GNEA-----KNTGNATVRDADSVGFVAGKTEKKNKGIDIDVSLNGTCAVLS-GDMSQVT 649
QY 319 VKYDVNVGDALNVQNLQNSGNLDSKAVAGSSGV-ISGNVSPS-----GKMDET 368
D 319 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 650 LDGDLNV--VSQDSEGVFSFATGVSFSGDSNADITGNVNIADYQDDLAAGAPLPT 706
QY 369 VNINAGNNIETRNGK-NI-----DIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKD 424
D 369 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 707 GVYVGGNGNTVTLGALNIDNDLSATGGQYLDVVGSLVTDGDDNDVEID--GGINI--TH 762
QY 425 ANKPVRTNVAPGKGVGDTNVVAOLKG---VAQNLNNRDN---VNGN---ARAGIAQAI 475
D 425 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 763 SEDPLDGT-----ADITGIS-VSGNSTVTLNGHSTIDNTVVGHHVVLARVYNGGSL 814
QY 476 -----ATAGLVQAYLP-----GKSMMAIGGTVLGEAG-----YAI-----GYSSISA 513
D 476 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 815 ILGDDSVVDVNVNVIPTGYTYTNALLMADGETSIENKNGDITSHGVYSVIRADNGSEVSN 874
QY 514 GGNWLIKGTASNGSRGHFGASASVG 538
D 514 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 875 SGDILVATSSNSEDRAAITRAGS 899

RESULT 9
SLAP_CAMFE STANDARD; PRT; 933 AA.
AC P35827;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE S-layer protein (Surface array protein) (SAP).
GN SAP.
OS Campylobacter fetus.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=196;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=84-32 / 23D;
RX MEDLINE=90354446; PubMed=2387868;
RA Blaser M.J., Gotschlich E.C.;
RT "Surface array protein of Campylobacter fetus. Cloning and gene
structure."
RN J. Biol. Chem. 265:14529-14535(1990).
RN [2]
RN ERRATUM.
RX MEDLINE=91035477; PubMed=2229082;
RA Blaser M.J., Gotschlich E.C.;
RN J. Biol. Chem. 265:19372-19372(1990).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CC CRITICAL FOR VIRULENCE.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; J05577; AAA23032.1; -.
KW Cell wall; S-layer.
SQ SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;

Query Match 6.6%; Score 180; DB 1; Length 933;
Best Local Similarity 22.8%; Pred. No. 0.071;
Matches 133; Conservative 69; Mismatches 231; Indels 150; Gaps 23;

QY 1 TDEEEELSVQSVSVGSIOASMEGSVELETISL-MTNDSEKFEVDPIYVTVLKAGDNL 59
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 310 TDASKSVNVEIT--GTITAFTAAGTKVDVVAGKISALTADSRISV-----NL 355
QY 60 KIKONTNENTNASSET-YSLK-----KDLTGLINVETEKLSFGANGKKVNIISDTKGLNFA 114
D 60 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 356 TATNDTITLTSANAATSVNLKORQAKDAT-----ITSAMOOKYNNRRNRRIATITSAT--A 408
QY 115 KETAGTNGDTTVHLNGIGSTLTMDLLNTGA-----TTNVTNDNVTDDEK----- 158
D 115 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 409 VENLTVKHATNVALNGGMDKLTATVLDNAALTAALDKSASTLNLINSVNGPKHLIYSSK 468
QY 159 -----KRAASVKQVLNAGWNKIKGVKPGTTASDNVDFVRYTDTVEFLSADTKTTTVNVES 212
D 159 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 469 RRYCKEKRAA-----KVKLNTTA-----ATDQTVTLKANA 499
QY 213 KDNKKTEVKIGAKTSVIKEDKGLVYCKGKENGSSSTDEGEGLVTAKEVIDAVNKAGWR 272
D 213 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 500 TDNSLEFDSATAKTTSVTASGSKTLVTKA-----EVEITLVN-----IDTTAFN 544
QY 273 MKTTTANGOTGOADKE--ETVTSCTKVTFFASNGTGTATVSK--DDOGNITVKYDVNVGDA 328
D 273 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 545 ALQSVSPFGKTGGGKFSVKTGTDGDKIEFV---GTTLTGEGVIDAPGNDTIAMKSAALTS 601
QY 329 LNVNQLQNSGNLDSKAVAG---SSGKVISGNVSPSKGMDETVNIAGNNIETRNGKN 385
D 329 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 602 ANFTMKIENVAISDAVATADLSSAFKNSVIITKEAADTLTINKQVI-----N 654
QY 386 IDIATSMTPQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVRTNVAPGKGVGDTN 445
D 386 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 655 FTAADAGSVKLITVTKLN---DVTALMIWVKIIVLDAADK-----TNIALGTAADKAL 704
QY 446 VAQLKGVAQNLNNRDNVNGNARAGIAQATATAGLVQAYLPKGSMAITGG----- 495
D 446 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 705 V-----IDTGIELNITSLVKATSPETTATVNAKLTDVTSIIDGMQITLGHAGT 755
QY 496 -GTYLG-----EAGYAIGYSSISAGGNWIKGTASGNS 527
D 496 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 756 AGTDYSKVSMDASALKAGLTFDASAITLGANATIKGSGADS 798

RESULT 10
ALYS_ENTFA STANDARD; PRT; 737 AA.
ID ALYS_ENTFA
AC P37710;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Autolysin precursor (EC 3.2.1.-) (Peptidoglycan hydrolase)
DE (Beta-glycosidase).
GN EF0799;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91358349; PubMed=1679432;
RA Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;
RT "Cloning, sequencing, and expression in Escherichia coli of a
Streptococcus faecalis autolysin.";
```



```
QY 218 KT-----EVKIGAKTSVIKEDGKLVTKGKGNGS--STDEG-----EGLVTAK 260
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 366 VTEHLVDVLGKGTN-FKTADSKVII-----TENASFGSTDFGNLAVQIVPVNKKILTGN 420
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 261 EVIDAVNK--AGWRMKTTTANGC--TGQADKEETVTS-----GKVTTFASG----- 302
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 421 FIGDANKNGTAG--VITFANGTLVSGNDPNIIVVTNIKAIEVGAGIVQLSGIHAEL 478
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 303 -NGTATVSKDDGNTIVKVDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPS 361
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 479 RLNAGSIFKLADGTV-INGPVNQNPVNNALAAAGSIQLDGSAII--TGDI--GNGAVN 533
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 362 KGRMDET-----VNINAGNNIEITRGNKI-----DIAT 390
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 534 AALQDITLANDASKILTLGSAITIGANAGGAIHFQANGGTIQLTSTQNILVDFDLDT 593
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 391 SMTPOFSSVL-----GAGADAPTLSVDDEGALNVGSK----- 423
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 594 DQGVVDASSLTNNQITINGSITIGANTKTL-----GRFNVGSSKTIILNAGDVAINEL 648
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 424 --DANKPVRT-IVAPGVKRGEDVTNVAQLKGVAQNLRNIDVNGNARAGIAQAIATAGL 480
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 649 VMENDGSVHLTHYTLTKTINAANQCKIIIVADPINTDTALADGTNLGSAESPLSIHF 708
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 481 VQAYLPKSKMAWGGTYLGEAGYA-----IGYSSISAGNNWIKGTASG 525
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DQ 709 ATRAAANGDSLHLHGKGVNL----YANNITTTDANVSLHFRSGTISVSGTVGG 758
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 13
AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT; 1039 AA.
AC P39180; P761614; P76360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubdaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map."
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RX Henderson I.R., Owen P.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
```

```
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli." J. Bacteriol. 171:3634-3640(1989).
RL [5]
RN SEQUENCE OF 53-63.
RP STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12."
RL Electrophoresis 18:1259-1313(1997).
RN [6]
RN GENE NAME.
RX MEDLINE=97257509; PubMed=9103983;
RA Henderson I.R., Meehan M., Owen P.;
RT "Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
K-12."
RL FEMS Microbiol. Lett. 149:115-120(1997).
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
FUNCTION AS AN ADHESIN.
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
CHAIN).
CC -1- SUBCELLULAR LOCATION: Outer membrane-associated.
CC -1- SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETTELLA PERTACTIN.
CC
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CC EMBL; AE000291; AAC75061.1; ALT_INIT.
CC EMBL; D90838; BAA15825.1; ALT_INIT.
CC EMBL; D90839; BAA15832.1; ALT_INIT.
CC EMBL; U24429; AAB47869.1; -.
CC HSP; P07505; ISRD.
CC EcoGene; EG12686; flu.
CC InterPro; IPR006315; Autotransport.
CC InterPro; IPR005546; Autotransporter.
CC InterPro; IPR004899; Pertactin.
CC Pfam; PF03797; Autotransporter; 1.
CC Pfam; PF03212; Pertactin; 1.
CC TIGRFAMs; TIGR01414; autotrans_bar1; 1.
CC Outer membrane; Signal; Complete proteome.
CC SIGNAL 1 52
CC CHAIN 53 551 ANTIGEN 43 ALPHA CHAIN.
CC CHAIN 552 1039 ANTIGEN 43 BETA CHAIN.
CC VARIANT 2 2 K -> N (IN STRAIN ML 308-225).
CC VARIANT 41 42 SL -> FF (IN STRAIN ML 308-225).
CC VARIANT 46 46 T -> K (IN STRAIN ML 308-225).
CC VARIANT 157 157 W -> L (IN STRAIN ML 308-225).
CC VARIANT 177 177 V -> F (IN STRAIN ML 308-225).
CC VARIANT 188 188 V -> L (IN STRAIN ML 308-225).
CC VARIANT 303 305 ATN -> STI (IN STRAIN ML 308-225).
CC VARIANT 320 320 A -> T (IN STRAIN ML 308-225).
CC VARIANT 372 372 N -> Q (IN STRAIN ML 308-225).
CC VARIANT 493 493 E -> V (IN STRAIN ML 308-225).
CC VARIANT 497 497 S -> N (IN STRAIN ML 308-225).
CC VARIANT 585 585 H -> Y (IN STRAIN ML 308-225).
CC VARIANT 709 709 E -> K (IN STRAIN ML 308-225).
CC VARIANT 721 721 M -> T (IN STRAIN ML 308-225).
CC VARIANT 751 753 GHL -> SHF (IN STRAIN ML 308-225).
CC VARIANT 803 803 S -> P (IN STRAIN ML 308-225).
CC VARIANT 815 815 A -> V (IN STRAIN ML 308-225).
CC VARIANT 824 824 C -> S (IN STRAIN ML 308-225).
CC VARIANT 829 835 LNLVHTS -> MNLIYNA (IN STRAIN ML 308-
```


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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 ; Search time 39.7345 Seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-34
Perfect score: 2735
Sequence: 1 TDEDEEELESVQSVVSGI.....TASGSRGHFGASAVGYQW 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2735	100.0	592	2	Q93QY2	Q93QY2 neisseria m
2	2690	98.4	592	2	Q9JPS9	Q9JPS9 neisseria m
3	2527	92.4	592	16	Q9JQW4	Q9JQW4 neisseria m
4	2464.5	90.1	594	2	Q9JPI3	Q9JPI3 neisseria m
5	2464.5	90.1	594	2	Q9JPS2	Q9JPS2 neisseria m
6	2447.5	89.5	599	2	Q9JPR8	Q9JPR8 neisseria m
7	2426.5	88.7	598	2	Q9JPS0	Q9JPS0 neisseria m
8	2426.5	88.7	598	2	Q93QY5	Q93QY5 neisseria m
9	2426.5	88.7	598	2	Q9JPT0	Q9JPT0 neisseria m
10	2423.5	88.6	594	2	Q9JPH7	Q9JPH7 neisseria m
11	2412.5	88.2	598	2	Q9JPR9	Q9JPR9 neisseria m
12	2404.5	87.9	594	2	Q93QY4	Q93QY4 neisseria m
13	2401	87.8	590	2	Q9JPS3	Q9JPS3 neisseria m
14	2397	87.6	600	2	Q9JPS6	Q9JPS6 neisseria m
15	2363.5	86.4	526	2	Q9JPS4	Q9JPS4 neisseria m
16	2361.5	86.3	530	2	Q9JPS1	Q9JPS1 neisseria m

17	2338	85.5	600	2	Q9JPS5	Q9JPS5 neisseria m
18	2330.5	85.2	591	2	Q9JPS7	Q9JPS7 neisseria m
19	2330.5	85.2	591	16	Q9JRI8	Q9JRI8 neisseria m
20	2323.5	85.0	591	2	Q93QY3	Q93QY3 neisseria m
21	2315.5	84.7	592	2	Q9AQF0	Q9AQF0 neisseria m
22	2297.5	84.0	599	2	Q9JPS8	Q9JPS8 neisseria m
23	2296.5	84.0	595	2	Q9JPH0	Q9JPH0 neisseria m
24	2294.5	83.9	598	2	Q9JPR7	Q9JPR7 neisseria m
25	2256.5	82.5	599	2	Q93QY1	Q93QY1 neisseria m
26	2244.5	82.1	589	2	Q9JPI0	Q9JPI0 neisseria m
27	946	34.6	2353	2	P71401	P71401 haemophilus
28	883	32.3	1204	2	Q8GM76	Q8GM76 haemophilus
29	870.5	31.8	1096	2	Q8GM79	Q8GM79 haemophilus
30	869.5	31.8	1098	2	Q48152	Q48152 haemophilus
31	869.5	31.8	1210	2	Q8GM74	Q8GM74 haemophilus
32	866.5	31.7	1210	2	Q8GM75	Q8GM75 haemophilus
33	588	21.5	1002	2	Q8GM78	Q8GM78 haemophilus
34	585.5	21.4	1004	2	Q8GM77	Q8GM77 haemophilus
35	415	15.2	1299	16	Q9FX36	Q9FX36 pasteurella
36	392.5	14.4	2059	16	Q9PD50	Q9PD50 xylella fas
37	378.5	13.8	2314	2	Q8QW8	Q8QW8 moraxella c
38	377	13.8	1588	16	Q8XDG4	Q8XDG4 escherichia
39	368.5	13.5	1190	16	Q9PC04	Q9PC04 xylella fas
40	368	13.5	1964	2	Q8QW9	Q8QW9 moraxella c
41	367	13.4	1461	16	Q8ZL64	Q8ZL64 salmonella
42	363	13.3	1107	16	Q9F2D8	Q9F2D8 salmonella
43	361	13.2	1778	16	Q8FCB2	Q8FCB2 escherichia
44	345	12.6	2712	16	Q9FX35	Q9FX35 pasteurella
45	337.5	12.3	688	2	Q8RQ60	Q8RQ60 actinobacil

ALIGNMENTS

RESULT 1

Q93QY2	ID	Q93QY2	PRELIMINARY;	PRT;	592 AA.
AC	Q93QY2;				
DT	01-DEC-2001	(Tremblrel. 19, Created)			
DT	01-DEC-2001	(Tremblrel. 19, Last sequence update)			
DT	01-OCT-2002	(Tremblrel. 22, Last annotation update)			
DE	NhaA outer membrane protein.				
GN	NHA.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
OC	Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=H41;				
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;				
RT	Identification and characterization of a gene encoding a novel outer				
RT	membrane protein of Neisseria meningitidis."				
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF157609; AAK68870.1; -				
DR	InterPro; IPR005594; Yada.				
DR	Pfam; PF03895; Yada; 1.				
SQ	SEQUENCE 592 AA; 61869 MW; F9403A0B4A18EEA7 CRC64;				

Query Match		100.0%;	Score 2735;	DB 2;	Length 592;
Best Local Similarity		100.0%;	Pred. No. 4.4e-106;		
Matches 541;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TDEDEEELESVQSVVSGI	QASMEGSVELETISLSMTNDSKFEVDPIYVVTLKAGDNLK	60	
Db	52	TDEDEEELESVQSVVSGI	QASMEGSVELETISLSMTNDSKFEVDPIYVVTLKAGDNLK	111	
Qy	61	IKONTNENTNASSFTYSLKKDLTGLIN	VEKISFGANGKKVNIISTKTGINFAKETAGT	120	
Db	112	IKONTNENTNASSFTYSLKKDLTGLIN	VEKISFGANGKKVNIISTKTGINFAKETAGT	171	
Qy	121	NGDTTVHLNGIGSTLTDM	LNTGATTNVTNDVTDDEKKRAASVQKVLNAGWITKGVKPG	180	

Db 172 NGDTTVHLNGIGSTLTMLNTGATNTVNDVNDDEKKRAASVKDVLNAGNNIKGVKPG 231
QY 181 TTASDNVDFVRTYDVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVKEKDGKLVG 240
Db 232 TTASDNVDFVRTYDVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVKEKDGKLVG 291
QY 241 KKGKGENGSTDRGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFTETVSGTKVTFA 300
Db 292 KKGKGENSGSTDRGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFTETVSGTKVTFA 351
QY 301 SGNGTATATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 360
Db 352 SGNGTATATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 411
QY 361 SKGKMDETVNIAGNNIEITRNGKNDIATSMPTQFSSVSLGAGADAPTLSVDDDEGALNV 420
Db 412 SKGKMDETVNIAGNNIEITRNGKNDIATSMPTQFSSVSLGAGADAPTLSVDDDEGALNV 471
QY 421 GSKDANKPVRTINVPAGVKEGDTVNVQALKGVAQNLRNDRIDNVNGNARAGIAQAATATAGL 480
Db 472 GSKDANKPVRTINVPAGVKEGDTVNVQALKGVAQNLRNDRIDNVNGNARAGIAQAATATAGL 531
QY 481 VQAYLPKGSMAAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQ 540
Db 532 VQAYLPKGSMAAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQ 591
QY 541 W 541
Db 592 W 592

RESULT 2

Q9JPS9 ID Q9JPS9 PRELIMINARY; PRT; 592 AA.
AC Q9JPS9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=860800;
RA PIZZA M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada, 1.
SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;

Query Match
Best Local Similarity 98.4%; Score 2690; DB 2; Length 592;
Matches 533; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 TDEDEEELSVQSVGSQASMEGSGVELETISLSMTNDSKEFVDPYIVVTLKAGDNLK 60
Db 52 TDEDEEELSVQSVGSQASMEGSGVELETISLSMTNDSKEFVDPYIVVTLKAGDNLK 111
QY 61 IKONTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKNIIISDTKGLNFAKETAGT 120
|||||

Db 112 IKONTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKNIIISDTKGLNFAKETAGT 171
QY 121 NGDTTVHLNGIGSTLTMLNTGATNTVNDVNDDEKKRAASVKDVLNAGNNIKGVKPG 180
Db 172 NGDTTVHLNGIGSTLTMLNTGATNTVNDVNDDEKKRAASVKDVLNAGNNIKGVKPG 231
QY 181 TTASDNVDFVRTYDVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVKEKDGKLVG 240
Db 232 TTASDNVDFVRTYDVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVKEKDGKLVG 291
QY 241 KKGKGENSGSTDRGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFTETVSGTKVTFA 300
Db 292 KKGKGENSGSTDRGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFTETVSGTKVTFA 351
QY 301 SGNGTATATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 360
Db 352 SGNGTATATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 411
QY 361 SKGKMDETVNIAGNNIEITRNGKNDIATSMPTQFSSVSLGAGADAPTLSVDDDEGALNV 420
Db 412 SKGKMDETVNIAGNNIEITRNGKNDIATSMPTQFSSVSLGAGADAPTLSVDDDEGALNV 471
QY 421 GSKDANKPVRTINVPAGVKEGDTVNVQALKGVAQNLRNDRIDNVNGNARAGIAQAATATAGL 480
Db 472 GSKDANKPVRTINVPAGVKEGDTVNVQALKGVAQNLRNDRIDNVNGNARAGIAQAATATAGL 531
QY 481 VQAYLPKGSMAAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQ 540
Db 532 VQAYLPKGSMAAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQ 591
QY 541 W 541
Db 592 W 592

RESULT 3

Q9JQW4 ID Q9JQW4 PRELIMINARY; PRT; 592 AA.
AC Q9JQW4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Putative surface fibril protein (outer membrane protein GNA992).
GN NMA1200 OR GNA992.
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=63699, 487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=22491 / Serogroup A / Serotype 4A;
RC MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Rajals K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajadream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491.";
RL Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=205900, B2133, F6124, AND Z2491;
RX MEDLINE=20175756; PubMed=10710308;
RA PIZZA M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;

RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing."
DR EMBL: AL162755; CAB84461.1; -
DR EMBL: AF226357; AAF42506.1; -
DR EMBL: AF226365; AAF42514.1; -
DR EMBL: AF226373; AAF42522.1; -
DR EMBL: AF226386; AAF42535.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
KW Complete proteome.
SQ SEQUENCE 592 AA; 61745 MW; AD22E2F5EEF8F754 CRC64;

Query Match 92.4%; Score 2527; DB 16; Length 592;
Best Local Similarity 93.4%; Pred. No. 1.8e-97;
Matches 507; Conservative 9; Mismatches 23; Indels 4; Gaps 2;
QY 1 TDEDEEELESVQSVVGSIQASMEGSVELETISLMTNDSKEFVDPYIVVTLKAGDNLK 60
Db 52 TDEDEEELESVQSVVGSIQASMEGSVELETISLMTNDSKEFVDPYIVVTLKAGDNLK 111
QY 61 IKONTNENTWASFTYSLKADLTGLINVEFKLSFGANGKKVNIISDTKGLNFAKETAGT 120
Db 112 IKONTNENTWASFTYSLKADLTGLINVEFKLSFGANGKKVNIISDTKGLNFAKETAGT 171
QY 121 NGDTTVHLNGIGSTLDTMLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWIKGYKPG 180
Db 172 NGDTTVHLNGIGSTLDTMLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWIKGYKPG 229
QY 181 TTA--SDNVDFVRYTDFEFLSADTKTTTVNVESKDKNGKKTVEKIGAKTSVIEKDGKLV 238
Db 230 STTGQSENVDVRYTDFEFLSADTKTTTVNVESKDKNGKKTVEKIGAKTSVIEKDGKLV 289
QY 239 TGKKGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEVTSQPKVT 298
Db 290 TGKKGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEVTSQPKVT 349
QY 299 FASGNGTATVSKDDQGNITVKYDVNVGDALNVQLNSGNWLDLSKAVAGSSGKVISGNV 358
Db 350 FASGNGTATVSKDDQGNITVKYDVNVGDALNVQLNSGNWLDLSKAVAGSSGKVISGNV 409
QY 359 SPKGRKDEVTNINAGNIEITRNGKNIDITATMTPOFSSVSLGAGADAPTLVSDDEGAL 418
Db 410 SPKGRKDEVTNINAGNIEITRNGKNIDITATMTPOFSSVSLGAGADAPTLVSDDEGAL 469
QY 419 NVGSKDANKPVRITNVAPVKEGDVTVNVAOLKGVQNLNNDVNVGNARAGIAQAATA 478
Db 470 NVGSKDANKPVRITNVAPVKEGDVTVNVAOLKGVQNLNNDVNVGNARAGIAQAATA 529
QY 479 GLVQAYLPGKSMMAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGHFGASASVG 538
Db 530 GLVQAYLPGKSMMAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGHFGASASVG 589
QY 539 YQW 541
Db 590 YQW 592

RESULT 4
Q9JPI3 ID Q9JPI3 PRELIMINARY; PRT; 594 AA.
AC Q9JPI3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=NG3/88, and B2322;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -
DR EMBL: AF226369; AAF42518.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;
Query Match 90.1%; Score 2464.5; DB 2; Length 594;
Best Local Similarity 90.7%; Pred. No. 7.2e-95;
Matches 498; Conservative 11; Mismatches 27; Indels 13; Gaps 3;
QY 1 TDEDEEELESVQSVVGSIQASMEGSVELETISLMTNDS-----KEFVDPYIVVT 52
Db 51 TDDDDLLLEPVQRTAPVLSFHADSEGTGEK-----VTEDSNMGVYFDKKGVLTAAGTIT 105
QY 53 LKAGDNLKIKONTNENTWASFTYSLKADLTGLINVEFKLSFGANGKKVNIISDTKGLN 112
Db 106 LKAGDNLKIKONTNENTWASFTYSLKADLTGLINVEFKLSFGANGKKVNIISDTKGLN 165
QY 113 FAKETAGTNGDTTVHLNGIGSTLDTMLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGW 172
Db 166 FAKETAGTNGDTTVHLNGIGSTLDTMLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGW 225
QY 173 NIKGVKPGTTASDNVDFVRYTDFEFLSADTKTTTVNVESKDKNGKKTVEKIGAKTSVIE 232
Db 226 NIKGVKPGTTASDNVDFVRYTDFEFLSADTKTTTVNVESKDKNGKKTVEKIGAKTSVIE 285
QY 233 KDGKLVTKGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEVTS 292
Db 286 KDGKLVTKGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEVTS 345
QY 293 SGTKVTFASGNGTATVSKDDQGNITVKYDVNVGDALNVQLNSGNWLDLSKAVAGSSGK 352
Db 346 SGTKVTFASGNGTATVSKDDQGNITVKYDVNVGDALNVQLNSGNWLDLSKAVAGSSGK 405
QY 353 VISGNVSPSKGKDEVTNINAGNIEITRNGKNIDITATMTPOFSSVSLGAGADAPTLV 412
Db 406 VISGNVSPSKGKDEVTNINAGNIEITRNGKNIDITATMTPOFSSVSLGAGADAPTLV 465
QY 413 DDEGALNVGSKDANKPVRITNVAPVKEGDVTVNVAOLKGVQNLNNDVNVGNARAGIA 472
Db 466 DDEGALNVGSKDANKPVRITNVAPVKEGDVTVNVAOLKGVQNLNNDVNVGNARAGIA 525
QY 473 QAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGHFG 532
Db 526 QAIATAGLVQAYLPGKSMMAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGHFG 585
QY 533 ASASVGQW 541
Db 586 ASASVGQW 594
RESULT 5
Q9JPS2 ID Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.


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Qy 533 ASASVGQW 541
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Db 591 ASASVGQW 599

RESULT 7
ID Q9JPS0 PRELIMINARY; PRT; 598 AA.
AC Q9JPS0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarcelli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RA "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H15;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226381; AAF42530.1; -.
DR EMBL; AF157607; AAK68868.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0B8A63CB CRC64;

Query Match 88.7%; Score 2426.5; DB 2; Length 598;
Best Local Similarity 89.2%; Pred. No. 2.7e-93;
Matches 493; Conservative 11; Mismatches 28; Indels 21; Gaps 5;

Qy 3 EDEEELESVQR-SVVGSIQASMEGSVELETISLMTNDSKEFVDPII-----VVT 52
:|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 DDDLLLEPVQRTAVVLSFRSDKGTGEGE-----TEDSNWV--YFDEKRVLKAGAIT 105

Qy 53 LKAGDNLIKIKONTNNTNA-----SSFTYSLKKDLTLGLINVTETKLSFGANGKKVNIISDT 108
|||||
Db 106 LKAGDNLIKIKONTNNTNNTNDSSTYSLKKDLTLGLINVTETKLSFGANGKKVNIISDT 165

Qy 109 KGLNFAKETAGTNGDTTVHLNGIGSTLTDMLLNTGATTNVTNDVTDDEKRAASVKDVL 168
|||||
Db 166 KGLNFAKETAGTNGDPTVHLNGIGSTLTDMLLNTGATTNVTNDVTDDEKRAASVKDVL 225

Qy 169 NAGNNIKGVKPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTS 228
|||||
Db 226 NAGNNIKGVKPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTS 285

Qy 229 VIKEDGKLVTKGKKGNGSSSTDEEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKF 288
|||||
Db 226 NAGNNIKGVKPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTS 285

Qy 288 VIKEDGKLVTKGKKGNGSSSTDEEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKF 345
|||||
Db 286 VIKEDGKLVTKGKKGNGSSSTDEEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKF 345

Qy 289 ETVTSGTKVTFASNGTATTATVSKDDQGNITVKYDYNVGDALNVNQLNSGNLDSKAVAG 348
|||||
Db 346 ETVTSGTKVTFASNGTATTATVSKDDQGNITVKYDYNVGDALNVNQLNSGNLDSKAVAG 405

Qy 349 SSGKVISGNVSPSKGKMDETVNIAGNNIETRNKKNIDIAITSMPTQFSSVSLGAGADAP 408
|||||
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Db 406 SSGKVISGNVSPSKGMDETVNIAGNNIEITRNKGNIDIAISMTPTQFSSVSLGAGADAP 465
QY 409 TLSVDDEGALNVGSKDANKPVRITNVAPGVKEDVTNVAQLKGVAQNLRNIDNVNGNAR 468
Db 466 TLSVDDEGALNVGSKDANKPVRITNVAPGVKEDVTNVAQLKGVAQNLRNIDNVNGNAR 525
QY 469 AGIAQAIATAGLVAQYLPCKSMMAIGGGTYLGEAGYATIGYSSISAGGNNIIGKTASGNSR 528
Db 526 AGIAQAIATAGLVAQYLPCKSMMAIGGGTYRGEAGYATIGYSSISDTGNNVIRKGTASGNSR 585
QY 529 GHFGASASVGYOW 541
Db 586 GHFGTSASVGYOW 598

RESULT 9
QJUP70 PRELIMINARY; PRT; 598 AA.
AC QJUP70;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
DR EMBL; AF226359; AAF42508.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 88.7%; Score 2426.5; DB 2; Length 598;
Best Local Similarity 89.0%; Pred. No. 2.7e-93;
Matches 492; Conservative 12; Mismatches 28; Indels 21; Gaps 5;

QY 3 EDEEELESVQR-SVVGSIQASMEGSVELETISLSMTNDSKRFVDPYI-----VVT 52
Db 53 DDDDLLEPVQRTAVVLSFRSDEKGTGEGE-----TEDSNWAV--YFDEKRVLKAGAIT 105
QY 53 LKAGNLKIKONTNENTNA-----SFTYSLKKDLTGLINVEFKLSFGANGKKNVNIISDT 108
Db 106 LKAGNLKIKONTNENTNENTNDSSTYSLSKDLTDLTSVETKLSFGANGKKNVNIISDT 165
QY 109 KGLNFAKETAGTNGDTTVHLNGIGSTLTDLMLNTGATTNVTNDVDEKRAASVKDVL 168
Db 166 KGLNFAKETAGTNGDPTVHLNGIGSTLTDLMLNTGATTNVTNDVDEKRAASVKDVL 225
QY 169 NAGNWKIKVGPCTTASDNVDFVRYTDFEVSADTKTTTVNVESKDNKGKTEVKGAKTS 228
Db 226 NAGNWKIKVGPCTTASDNVDFVRYTDFEVSADTKTTTVNVESKDNKGKTEVKGAKTS 285
QY 229 VIKEDKGLVTKGKGNGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKF 288
Db 286 VIKEDKGLVTKGKGNGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKF 345
QY 289 ETVTSGTKVTASNGTGTATYSKDDGNTVYKYDYNVDALNVQNLQNSGNWLDKAVAG 348
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Db 346 ETVTSGTKVTASNGTGTATYSKDDGNTVYKYDYNVDALNVQNLQNSGNWLDKAVAG 405
QY 349 SSGKVISGNVSPSKGMDETVNIAGNNIEITRNKGNIDIAISMTPTQFSSVSLGAGADAP 408
Db 406 SSGKVISGNVSPSKGMDETVNIAGNNIEITRNKGNIDIAISMTPTQFSSVSLGAGADAP 465
QY 409 TLSVDDEGALNVGSKDANKPVRITNVAPGVKEDVTNVAQLKGVAQNLRNIDNVNGNAR 468
Db 466 TLSVDDEGALNVGSKDANKPVRITNVAPGVKEDVTNVAQLKGVAQNLRNIDNVNGNAR 525
QY 469 AGIAQAIATAGLVAQYLPCKSMMAIGGGTYLGEAGYATIGYSSISAGGNNIIGKTASGNSR 528
Db 526 AGIAQAIATAGLVAQYLPCKSMMAIGGGTYRGEAGYATIGYSSISDTGNNVIRKGTASGNSR 585
QY 529 GHFGASASVGYOW 541
Db 586 GHFGTSASVGYOW 598

RESULT 10
QJUP7 PRELIMINARY; PRT; 594 AA.
AC QJUP7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BZ198, and 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
DR EMBL; AF226358; AAF42507.1; -.
DR EMBL; AF157604; AAK68865.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62361 MW; 436BDDDED68263C5C CRC64;

Query Match 88.6%; Score 2423.5; DB 2; Length 594;
Best Local Similarity 89.4%; Pred. No. 3.6e-93;
Matches 491; Conservative 10; Mismatches 31; Indels 17; Gaps 4;

QY 3 EDEEELESVQR-SVVGSIQASMEGSVELETISLSMTNDSKRFVDPYI-----VVT 52
Db 53 DDDDLLEPVQRTAVVLSFRSDEKGTGEGE-----TEDSNWAV--YFDEKRVLKAGAIT 105
QY 53 LKAGNLKIKONTNENTNASSFTYSLKKDLTGLINVEFKLSFGANGKKNVNIISDTKGLN 112
Db 106 LKAGNLKIKONTNENTNDSSTYSLSKDLTDLTSVETKLSFGANGKKNVNIISDTKGLN 165
QY 113 FAKETAGTNGDTTVHLNGIGSTLTDLMLNTGATTNVTNDVDEKRAASVKDVLNAGW 172
```



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Db 166 FAKETAGTNGDPTVHLNGIGSTLDTLINTGATTNVTNDNVTDDKKRAASVKDVLNAGW 225
Qy 173 NIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVLIKE 232
Db 226 NIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVLIKE 285
Qy 233 KDGKLVTKGKGGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQOAKDFEVT 292
Db 286 KDGKLVTKGKGGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQOAKDFEVT 345
Qy 293 SGTKVTTFASNGTATTATVSKDDQGNITVKYDNNVGDALNVNQLQSGNWLDSKAVAGSSGK 352
Db 346 SGTNVTTFASNGTATTATVSKDDQGNITVKYDNNVGDALNVNQLQSGNWLDSKAVAGSSGK 405
Qy 353 VISGNVSPSKGKMDETVNNAGNIEITRNKNIDTATSMPTQPFSSVSLGAGADPTLSV 412
Db 406 VISGNVSPSKGKMDETVNNAGNIEITRNKNIDTATSMAPQFSSVSLGAGADPTLSV 465
Qy 413 DDEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNNGNARAGIA 472
Db 466 DDEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNNGNARAGIA 525
Qy 473 QAIATAGLVQAYLPCKSMMAIGGTYLGEAGYATGYSSISAGGNWIIKGTASGNSRGHFG 532
Db 526 QAIATAGLVQAYLPCKSMMAIGGTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGHFG 585
Qy 533 ASASVGYQW 541
Db 586 ASASVGYQW 594

RESULT 11
Q9JPR9 PRELIMINARY; PRT; 598 AA.
ID Q9JPR9
AC Q9JPR9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226382; AAF42531.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 88.2%; Score 2412.5; DB 2; Length 598;
Best Local Similarity 88.8%; Pred. No. 1e-92;
Matches 491; Conservative 10; Mismatches 31; Indels 21; Gaps 5;

Qy 3 EDEEEELVESVQR--SVVGSIOASMEGSVELETISLSMTNDSKEFVDPIYI-----VVT 52
Db 53 DDDLLYLEPQVORTAVVLSFRSDKEGTGEK-----TEDSNVAV--YFDERKVLKAGAIT 105
Qy 53 LKAGDNLKIKONTNENTNA-----SFTYSLKDLTGLTNVETEKLSFGANGKKNVITSDT 108
```

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Db 106 LKAGDNLKIKONTNENTNDSFTYSLKDLTGLTDSVETEKLSFGANGKKNVITSDT 165
Qy 109 KGLNFAKETAGTNGDPTVHLNGIGSTLDTLINTGATTNVTNDNVTDDKKRAASVKDVL 168
Db 166 KGLNFAKETAGTNGDPTVHLNGIGSTLDTLINTGATTNVTNDNVTDDKKRAASVKDVL 225
Qy 169 NAGNIIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTS 228
Db 226 NAGNIIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTS 285
Qy 229 VIKEDGKLVTKGKGGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQOAKDF 288
Db 286 VIKEDGKLVTKGKGGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGQTQOAKDF 345
Qy 289 ETVTSGTKVTTFASNGTATTATVSKDDQGNITVKYDNNVGDALNVNQLQSGNWLDSKAVAG 348
Db 346 ETVTSGTNTVTTFASNGTATTATVSKDDQGNITVKYDNNVGDALNVNQLQSGNWLDSKAVAG 405
Qy 349 SSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDTATSMPTQPFSSVSLGAGADAP 408
Db 406 SSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDTATSMAPQFSSVSLGAGADAP 465
Qy 409 TLSVDDEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNNGNAR 468
Db 466 TLSVDDEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNNGNAR 525
Qy 469 AGIAQATATAGLVQAYLPCKSMMAIGGTYLGEAGYATGYSSISAGGNWIIKGTASGNSR 528
Db 526 AGIAQATATAGLVQAYLPCKSMMAIGGTYRGEAGYATGYSSISDGGNWIIGKTASGNSR 585
Qy 529 GHFGASASVGYQW 541
Db 586 GHFGASASVGYQW 598

RESULT 12
Q93QY4 PRELIMINARY; PRT; 594 AA.
ID Q93QY4
AC Q93QY4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Outer membrane protein.
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srikanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B0483A8EA2 CRC64;

Query Match 87.9%; Score 2404.5; DB 2; Length 594;
Best Local Similarity 88.7%; Pred. No. 2.2e-92;
Matches 487; Conservative 15; Mismatches 34; Indels 13; Gaps 3;

Qy 1 TDEEEELVESVQR--SVVGSIOASMEGSVELETISLSMTNDS-----KEFVDPIYIVVT 52
Db 51 TTDDLLYLEPQVORTAVVLSFRSDKEGTGEK-----VTEDSNMGVYFDKKGVLTAAGTIT 105
Qy 53 LKAGDNLKIKONTNENTNASSFTYSLKDLTGLTNVETEKLSFGANGKKNVITSDTKGLN 112
Db 106 LKAGDNLKIKONTNENTNASSFTYSLKDLTGLTSGVTEKLSFGANSKKNVITSDTKGLN 165
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QY 113 FAKETAGTNGDPTVHLNGIGSTFLTDMLLNTGATTNTVNDVNDDEKKRAASVKDVLNAGW 172
DB 166 FAKKTAETNGDPTVHLNGIGSTFLTDMLLNTGATTNTVNDVNDDEKKRAASVKDVLNAGW 225
QY 173 NIKGVKPGTTASDNVDVFRVYDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKE 232
DB 226 NIKGVKPGTTASDNVDVFRVYDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKE 285
QY 233 KDKGLVTKGKGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFEFTV 292
DB 286 KDKGLVTKGKGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFEFTV 345
QY 293 SGTKTVPASGNTTATVSKDDGNTTVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGK 352
DB 346 SGTNTVPASGNTTATVSKDDGNTTVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGK 405
QY 353 VLSGNVSPSKGMDETVNLNAGNNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSV 412
DB 406 VLSGNVSPSKGMDETVNLNAGNNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSV 465
QY 413 DDEGALNVGSKDANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLRNIDNVNGNARAGIA 472
DB 466 DDEGALNVGSKDANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLRNIDNVNGNARAGIA 525
QY 473 QAIATAGLVQAYLPCKSMMAIGGGTYLGEAGYAICYSSISAGGNWIIKGTASGNSRGRHFG 532
DB 526 QAIATAGLVQAYLPCKSMMAIGGGTYLGEAGYAICYSSISAGGNWIIKGTASGNSRGRHFG 585
QY 533 ASASVGYOW 541
DB 586 ASASVGYOW 594
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RESULT 13

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Q9JPS3
ID Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG828;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226378; AAF42527.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;
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Query Match 87.8%; Score 2401; DB 2; Length 590;
Best Local Similarity 88.5%; Pred. No. 3.1e-92;
Matches 483; Conservative 21; Mismatches 30; Indels 12; Gaps 4;
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QY 1 TDEDEEEESVQSV-VGSIQASMEGSVELETISLMTNDSKEFVDPYIV---VTLKA 55
DB 52 TDEDEEDLPQRTVAVLIVNSDKEGTGEKEVE-ENSDWAVYFNEKGLTAGTITLKA 110
```

```
QY 56 GDNLIKQNTNENTNASSFTYSLKKDLTGLINVEKELSGFANGKXVNIISDTKGLNPAK 115
DB 111 GDNLIKQ-----NGTFTYSLKKDLTGLINVEKELSGFANGKXVNIISDTKGLNPAK 164
QY 116 ETAGNNGDPTVHLNGIGSTFLTDMLLNTGATTNTVNDVNDDEKKRAASVKDVLNAGWNK 175
DB 165 ETAGNNGDPTVHLNGIGSTFLTDMLLNTGATTNTVNDVNDDEKKRAASVKDVLNAGWNK 224
QY 176 GVKPGTTASDNVDVFRVYDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKD 235
DB 225 GVKPGTTASDNVDVFRVYDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKD 284
QY 236 KLVTKGKGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFEFTVSGT 295
DB 285 KLVTKGKGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFEFTVSGT 344
QY 296 KVPFASGNTTATVSKDDGNTTVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIS 355
DB 345 KVPFASGNTTATVSKDDGNTTVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIS 404
QY 356 GNVSPSKGMDETVNLNAGNNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSVDE 415
DB 405 GNVSPSKGMDETVNLNAGNNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSVDE 464
QY 416 GALNVGSKDANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLRNIDNVNGNARAGIAQAI 475
DB 465 GALNVGSKDANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLRNIDNVNGNARAGIAQAI 524
QY 476 ATAGLVQAYLPCKSMMAIGGGTYLGEAGYAICYSSISAGGNWIIKGTASGNSRGRHFGASA 535
DB 525 ATAGLVQAYLPCKSMMAIGGGTYLGEAGYAICYSSISAGGNWIIKGTASGNSRGRHFGASA 584
QY 536 SVGYOW 541
DB 585 SVGYOW 590
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RESULT 14

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Q9JPS6
ID Q9JPS6 PRELIMINARY; PRT; 600 AA.
AC Q9JPS6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42520.1; -.
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 600 AA; 36256963E0598CD1 CRC64;
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Query Match 87.6%; Score 2397; DB 2; Length 600;
Best Local Similarity 89.4%; Pred. No. 4.6e-92;
Matches 487; Conservative 12; Mismatches 38; Indels 8; Gaps 4;
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Qy	2	DEDEEELESVQSV-VGSIQASMEGSGVELETISLMTNDSKEVPDIYIV----	VTUKAG 56
Db	59	DNEEEYLEPVRTPAPVLSFYSDAEDTGEKEV--TENTNGIYDFKNGVKAAGTITLTKAG 116	
Qy	57	DNLIKIKONTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNPAKE 116	
Db	117	DNLIKIKONTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNPAKE 176	
Qy	117	TAGTNGDTTVHLNGIGSTLTDMLINTGATTNVTNDVNTDDEKKRAASVKDVLNAGWNIKG 176	
Db	177	TAGTNGDTTVHLNGIGSTLTDMLINTGATTNVTNDVNTDDEKKRAASVKDVLNAGWNIKG 236	
Qy	177	VKPGTTASDNVDFVRYTDTVEFLSADPKTTTNNVESKDNKKTEVKIGAKTSVIKEDGK 236	
Db	237	VKPGTTASDNVDFVRYTDTVEFLSADPKTTTNNVESKDNKKTEVKIGAKTSVIKEDGK 296	
Qy	237	LVTKGKGENGSSDDEGGLVTAKEVIDAVNKAGWRMKTTTANGQKQADKFEVTSGTK 296	
Db	297	LVTKGKGENGSSDDEGGLVTAKEVIDAVNKAGWRMKTTTANGQKQADKFEVTSGTK 356	
Qy	297	VTFASGKGTATVSKDDQGNITVYKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISG 356	
Db	357	VTFASGKGTATVSKDDQGNITVYKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISG 416	
Qy	357	NVSPSKGMDETVNNAGNIEITRNKNIDIAISMTPPQFSSVSLGAGADAPTLSVDDEG 416	
Db	417	NVSPSKGMDETVNNAGNIEITRNKNIDIAISMTPPQFSSVSLGAGADAPTLSVDGD- 475	
Qy	417	ALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRIDNVNGHARAGIAQIA 476	
Db	476	ALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRIDNVNGHARAGIAQIA 535	
Qy	477	TAGLVQVAYLPCKSMMAIGGGTYLGEAGYAIYSGYSSISAGGNWIKGTASGNSRHFAGAS 536	
Db	536	TAGLVQVAYLPCKSMMAIGGGTYLGEAGYAIYSGYSSISAGGNWIKGTASGNSRHFAGAS 595	
Qy	537	VGQW 541	
Db	596	VGQW 600	

RESULT 15

Q9JPS4	ID	Q9JPS4	PRELIMINARY;	PRT;	526 AA.
AC	Q9JPS4;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DE	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)				
GN	Outer membrane protein GNA992.				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
OC	Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=NG6/88;				
RX	MEDLINE=20175756; PubMed=10710308;				
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,				
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,				
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,				
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,				
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,				
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,				
RA	Moxon E.R., Grandi G., Rappuoli R.;				
RT	*Identification of Vaccine Candidates Against Serogroup B				
RT	Meningococcus by Whole-Genome Sequencing.*;				
RL	Science 287:1816-1820(2000).				
DR	EMBL: AF226377; AAF42526.1; -.				
DR	InterPro: IPR005594; Yada.				
DR	Pfam: PF03895; Yada; 1.				
SQ	SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;				

		Query Match	86.4%;	Score 2363.5;	DB 2;	Length 526;
		Best Local Similarity	95.2%;	Pred. No. 9.6e-91;		
		Matches 471;	Conservative 5;	Mismatches 14;	Indels 5;	Gaps 2;
Qy	51	VTUKAGNLKIKQ----	NTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKVNIIS 106			
Db	33	VTUKAGNLKIKONTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKVNIIS 92				
Qy	107	DTKGLNFAKKTAGTNGDTTVHLNGIGSTLTDMLINTGATTNVTNDVNTDDEKKRAASVKD 166				
Db	93	DTKGLNFAKKTAGTNGDTTVHLNGIGSTLTDMLINTGATTNVTNDVNTDDEKKRAASVKD 152				
Qy	167	VLNAGWNIKGVKPGTTASDNVDFVRYTDTVEFLSADPKTTTNNVESKDNKKTEVKIGAK 226				
Db	153	VLNAGWNIKGVKPGTTASDNVDFVRYTDTVEFLSADPKTTTNNVESKDNKKTEVKIGAK 212				
Qy	227	TSVIKEDGKLVTKGKGENGSSDDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGOAD 286				
Db	213	TSVIKEDGKLVTKGKGENGSSDDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGOAD 272				
Qy	287	KFETVTSGTKVTFAASNGTATTATVSKDDQGNITVYKYDVNVGDALNVNQLNSGWNLDKAV 346				
Db	273	KFETVTSGTNVTFAASNGTATTATVSKDDQGNITVYKYDVNVGDALNVNQLNSGWNLDKAV 332				
Qy	347	AGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKNIDIAISMTPPQFSSVSLGAGAD 406				
Db	333	AGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKNIDIAISMTPPQFSSVSLGAGAD 392				
Qy	407	APTLSDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRIDNVNGN 466				
Db	393	APTLSDVGD-ALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRIDNVNGN 451				
Qy	467	ARAGIAQAIATAGLVQAYLPCKSMMAIGGGTYLGEAGYAIYSGYSSISAGGNWIKGTASGN 526				
Db	452	ARAGIAQAIATAGLVQAYLPCKSMMAIGGGTYLGEAGYAIYSGYSSISAGGNWIKGTASGN 511				
Qy	527	SRGHFGASASVGQW 541				
Db	512	SRGHFGASASVGQW 526				

Search completed: October 6, 2003, 09:30:48
Job time : 40.7345 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 ; Search time 39.6746 Seconds
(without alignments)
1848.329 Million cell updates/sec

Title: US-09-771-382-36

Perfect score: 2350

Sequence: 1 TDETGLINYTEKLSFGANG.....TASGSRGHFGASVGYQW 462

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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- 10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
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- 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2350	100.0	513	22 AAU06183	N. meningitidis H4
2	2337	99.4	592	20 AAY23744	A surface protein
3	2337	99.4	592	22 AAU06172	N. meningitidis H4
4	2261	96.2	598	20 AAY23738	A surface protein
5	2261	96.2	598	20 AAY23742	A surface protein
6	2261	96.2	598	22 AAU06177	N. meningitidis H1
7	2261	96.2	598	22 AAU06178	N. meningitidis B2
8	2260	96.2	599	20 AAY23743	A surface protein
9	2260	96.2	599	22 AAU06176	N. meningitidis H3

10	2247	95.6	594	20 AAY23739	A surface protein
11	2247	95.6	594	22 AAU06179	N. meningitidis B2
12	2213.5	94.2	512	22 AAU06182	N. meningitidis PM
13	2213	94.2	594	20 AAY23740	A surface protein
14	2213	94.2	594	21 AAY57044	BAS029 amino acid
15	2213	94.2	594	22 AAU06174	N. meningitidis EG
16	2210.5	94.1	591	20 AAY27202	Amino acid sequenc
17	2210.5	94.1	591	20 AAY23741	A surface protein
18	2210.5	94.1	591	20 AAY23746	A surface protein
19	2210.5	94.1	591	22 AAU06171	N. meningitidis PM
20	2210.5	94.1	591	22 AAU06175	N. meningitidis EG
21	2207.5	93.9	591	21 AAY57045	BAS029 amino acid
22	2206.5	93.9	592	20 AAY23737	A surface protein
23	2136	90.9	592	22 AAU06180	N. meningitidis Z2
24	2116	90.0	589	20 AAY23745	A surface protein
25	2116	90.0	589	22 AAU06173	N. meningitidis P2
26	2113	89.9	592	20 AAY27203	Amino acid sequenc
27	2032	86.5	502	22 AAU06186	N. meningitidis PM
28	1953	83.1	604	22 AAU06181	N. meningitidis su
29	1861.5	79.2	433	22 AAU06185	N. meningitidis PM
30	1740.5	74.1	407	22 AAU06184	N. meningitidis PM
31	876	37.3	2353	17 AAR99393	Haemophilus adhesi
32	876	37.3	2411	21 AAB23860	Haemophilus influe
33	865	36.8	1094	21 AAB23858	Haemophilus influe
34	849.5	36.1	1098	17 AAR99392	Haemophilus adhesi
35	727	30.9	245	20 AAY27201	Amino acid sequenc
36	613	26.1	679	17 AAR99394	Haemophilus adhesi
37	613	26.1	679	21 AAB23855	Haemophilus influe
38	580	24.7	116	21 AAB37832	Neisserial conserv
39	571.5	24.3	1002	21 AAB23854	Haemophilus influe
40	551.5	23.5	1004	21 AAB23857	Haemophilus influe
41	511	21.7	1104	21 AAB23856	Haemophilus influe
42	511	21.7	1104	21 AAB23859	Haemophilus influe
43	390.5	16.6	298	24 AAB30477	Haemophilus influe
44	371.5	15.8	2139	24 ABP71294	M. catarrhalis sur
45	371	15.8	2314	22 AAB69136	M. catarrhalis les

ALIGNMENTS

RESULT 1	
AAU06183	
ID	AAU06183 standard; Protein; 513 AA.
XX	
AC	AAU06183;
DT	24-OCT-2001 (first entry)
XX	
DE	N. meningitidis H41 Nhha deletion mutant.
XX	
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW	mutant; muteln.
XX	
OS	Neisseria meningitidis strain H41.
OS	Synthetic.
XX	
PH	Location/Qualifiers
FT	Key
FT	Peptide
FT	1..51
FT	/label= Signal_peptide
FT	52..513
FT	/label= Mature_Nhha_deletion_mutant
FT	/note= "Predicted mature protein, specifically
FT	claimed in claim 12"
XX	
PN	WO200155182-A1.
XX	
XX	
PD	02-AUG-2001.
XX	
PF	25-JAN-2001; 2001WO-AU000069.
XX	
XX	
PR	25-JAN-2000; 2000US-0177917.
XX	

PA (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
DR N-PSDB; AAS09173.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 6; 9lpp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain H41 surface
CC antigen Nhha deletion mutant.
XX
SQ Sequence 513 AA;

Query Match 100.0%; Score 2350; DB 22; Length 513;
Best Local Similarity 100.0%; Pred. No. 1e-139;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TDEGLINVEEKLKSGANGKKNVLIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLMDL 60
DB 52 TDEGLINVEEKLKSGANGKKNVLIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLMDL 111
QY 61 LNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKTTASDNVDFVRYDTVEFL 120
DB 112 LNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKTTASDNVDFVRYDTVEFL 171
QY 121 SADTKTTVNVESKDNKGKTEVKIGAKTSVIEKDKGLVTGKKGNGSSDDEGEGLVTA 180
DB 172 SADTKTTVNVESKDNKGKTEVKIGAKTSVIEKDKGLVTGKKGNGSSDDEGEGLVTA 231
QY 181 KEVIDAVNKAQWRMKTITANGOTQADKFETVTSCTKVTFAAGNGTTATVSKDDQGNITV 240
DB 232 KEVIDAVNKAQWRMKTITANGOTQADKFETVTSCTKVTFAAGNGTTATVSKDDQGNITV 291
QY 241 KYDYNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNIEI 300
DB 292 KYDYNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNIEI 351
QY 301 TRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVK 360
DB 352 TRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVK 411
QY 361 EGDVTNVAQLKGVQNLNRRIDNVNGNARAGIAQAIATAGLVQAYLPKGSMAIGGGTYL 420
DB 412 EGDVTNVAQLKGVQNLNRRIDNVNGNARAGIAQAIATAGLVQAYLPKGSMAIGGGTYL 471
QY 421 GEAGYATGYSSISAGGNWIKGTASGNSRGHFGASASVGYQW 462
DB 472 GEAGYATGYSSISAGGNWIKGTASGNSRGHFGASASVGYQW 513

RESULT 2
RAY23744
ID AAY23744 standard; Protein; 592 AA.
XX
AC AAY23744;
XX
DT 08-SEP-1999 (first entry)
XX

DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
FF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
FI WPI; 1999-418754/35.
DR N-PSDB; AAX85796.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 118-120; 132pp; English.
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 592 AA;

Query Match 99.4%; Score 2337; DB 20; Length 592;
Best Local Similarity 99.8%; Pred. No. 8.1e-139;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 DETGLINVEEKLKSGANGKKNVLIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLMDL 61
DB 132 DETGLINVEEKLKSGANGKKNVLIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLMDL 191
QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKTTASDNVDFVRYDTVEFLS 121
DB 192 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVPKTTASDNVDFVRYDTVEFLS 251
QY 122 ADTKTTVNVESKDNKGKTEVKIGAKTSVIEKDKGLVTGKKGNGSSDDEGEGLVTA 181
DB 252 ADTKTTVNVESKDNKGKTEVKIGAKTSVIEKDKGLVTGKKGNGSSDDEGEGLVTA 311
QY 182 EVIDAVNKAQWRMKTITANGOTQADKFETVTSCTKVTFAAGNGTTATVSKDDQGNITV 241
DB 312 EVIDAVNKAQWRMKTITANGOTQADKFETVTSCTKVTFAAGNGTTATVSKDDQGNITV 371
QY 242 YDYNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNIEI 301
DB 372 YDYNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNIEI 431
QY 302 RNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVK 361
DB 432 RNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVK 491
QY 362 GDTVNTVAQLKGVQNLNRRIDNVNGNARAGIAQAIATAGLVQAYLPKGSMAIGGGTYL 421
DB 492 GDTVNTVAQLKGVQNLNRRIDNVNGNARAGIAQAIATAGLVQAYLPKGSMAIGGGTYL 551
QY 422 EAGYATGYSSISAGGNWIKGTASGNSRGHFGASASVGYQW 462

Db 552 EAGYAIQYSSISAGGNWIKGTASGNSRGHFGASASVGYQW 592

RESULT 3

AAU06172 ID AAU06172 standard; Protein; 592 AA.

XX AC AAU06172;

XX 24-OCT-2001 (first entry)

XX N. meningitidis H41 surface antigen NhhA polypeptide sequence.

XX Surface antigen NhhA; meningococcal disease; meningitis vaccine.

XX Neisseria meningitidis strain H41.

XX Key Location/Qualifiers

FT Peptide 1..51

FT Region /label= Signal_peptide

FT /label= C1

FT /note= "Conserved region 1"

FT 51..102

FT /label= V1

FT /note= "Variable region 1"

FT 52..592

FT /label= Mature_NhhA

FT /note= "Predicted mature protein, specifically

FT claimed in claim 12"

FT 103..114

FT /label= C2

FT /note= "Conserved region 2"

FT 115..124

FT /label= V2

FT /note= "Variable region 2"

FT 125..188

FT /label= C3

FT /note= "Conserved region 3"

FT 189..210

FT /label= V3

FT /note= "Variable region 3"

FT 211..229

FT /label= C4

FT /note= "Conserved region 4"

FT 230..236

FT /label= V4

FT /note= "Variable region 4"

FT 237..592

FT /label= C5

FT /note= "Conserved region 5"

XX WO200155182-A1.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

XX (UYQU) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;

XX WPI; 2001-488774/53.

XX N-PSDB; AAS09162.

XX New NhhA surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.

XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen NhhA
CC (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen NhhA
CC from N. meningitidis strain H41 is 1 of 10 NhhA polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 592 AA;

Query Match 99.4%; Score 2337; DB 22; Length 592;
Best Local Similarity 99.8%; Pred. No. 8.1e-139;
Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DETGLINVEKELSGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNIGISTLTDMLL 61
DB 132 DLTGLINVEKELSGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNIGISTLTDMLL 191
QY 62 NTGATTNTVNDNVTDDKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYDTVEFLS 121
DB 192 NTGATTNTVNDNVTDDKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYDTVEFLS 251
QY 122 ADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGKGNGSSSTDEGEGLVTAK 181
DB 252 ADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDGKLVTKGKGNGSSSTDEGEGLVTAK 311
QY 182 EVIDAVNKAGWRMKTTTANGQTQADKFFETVTSCTKVTTFASGNGTTATVSKDDQGNITVK 241
DB 312 EVIDAVNKAGWRMKTTTANGQTQADKFFETVTSCTKVTTFASGNGTTATVSKDDQGNITVK 371
QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEIT 301
DB 372 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEIT 431
QY 302 RNGKNIDIAISMTPTQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVKITNVAPGVKE 361
DB 432 RNGKNIDIAISMTPTQFSSVSLGAGADAPTLSDDEGALNVGSKDANKPVKITNVAPGVKE 491
QY 362 GDVTNTVAQLKGVAQNLNNDVNGNARAGIAQAIATAGLVQAYLPCKSMMAIGGGTYLG 421
DB 492 GDVTNTVAQLKGVAQNLNNDVNGNARAGIAQAIATAGLVQAYLPCKSMMAIGGGTYLG 551
QY 422 EAGYAIQYSSISAGGNWIKGTASGNSRGHFGASASVGYQW 462
DB 552 EAGYAIQYSSISAGGNWIKGTASGNSRGHFGASASVGYQW 592

RESULT 4

AAV23738

ID AAV23738 standard; Protein; 598 AA.

XX AC AAV23738;

XX 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

XX Surface protein; surface glycoprotein; infection; vaccine;

XX immunoreactive peptide.

XX Neisseria meningitidis.

XX WO99311132-A1.

XX 24-JUN-1999.

```
XX 14-DEC-1998; 98WO-AU01031.
PF
XX
PR 12-DEC-1997; 97GB-0026398.
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYOU ) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI; 1999-418754/35.
DR N-PSDB; AAX85790.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1; Page 91-93; 132pp; English.
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 598 AA;

Query Match 96.2%; Score 2261; DB 20; Length 598;
Best Local Similarity 96.5%; Pred. No. 4.9e-134;
Matches 445; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 DETGLINVEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDLML 61
DB 138 DLTDLSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDL 197

QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGCTTASDNVDFVRTYDTVEFLS 121
DB 198 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGCTTASDNVDFVRTYDTVEFLS 257

QY 122 ADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKGKGENSGSTDEGEGLVTAK 181
DB 258 ADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKGKGENSGSTDEGEGLVTAK 317

QY 182 EVIDAVNKAGWRKMTTANGQTQADKFEVTSCTKVTASGNGTATVSKDDQGNITVK 241
DB 318 EVIDAVNKAGWRKMTTANGQTQADKFEVTSCTKVTASGNGTATVSKDDQGNITVK 377

QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVINAGNNIEIT 301
DB 378 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVINAGNNIEIT 437

QY 302 RNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
DB 438 RNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 497

QY 362 GDVTNVAQLKGVAQNLRNDRDNGNARAGIAQAIAATAGLVQAYLPCKSMAIGGGTYLG 421
DB 498 GDVTNVAQLKGVAQNLRNDRDNGNARAGIAQAIAATAGLVQAYLPCKSMAIGGGTYRG 557

QY 422 EAGYAGYSSISAGGNNWIKGTASGNSRHFHGASASVGYQW 462
DB 558 EAGYAGYSSISDTGNWIKGTASGNSRHFHGTSASVGYQW 598

RESULT 5
AAY23742
ID AAY23742 standard; Protein; 598 AA.
XX
AC AAY23742;
XX
```

```
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
XX 24-JUN-1999.
XX
XX 14-DEC-1998; 98WO-AU01031.
XX
XX 12-DEC-1997; 97GB-0026398.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX (UYOU ) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI; 1999-418754/35.
XX N-PSDB; AAX85794.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections
XX
XX Claim 1; Page 108-110; 132pp; English.
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 598 AA;

Query Match 96.2%; Score 2261; DB 20; Length 598;
Best Local Similarity 96.7%; Pred. No. 4.9e-134;
Matches 446; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 2 DETGLINVEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDLML 61
DB 138 DLTDLSVTEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDL 197

QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGCTTASDNVDFVRTYDTVEFLS 121
DB 198 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGCTTASDNVDFVRTYDTVEFLS 257

QY 122 ADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKGKGENSGSTDEGEGLVTAK 181
DB 258 ADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKGKGENSGSTDEGEGLVTAK 317

QY 182 EVIDAVNKAGWRKMTTANGQTQADKFEVTSCTKVTASGNGTATVSKDDQGNITVK 241
DB 318 EVIDAVNKAGWRKMTTANGQTQADKFEVTSCTKVTASGNGTATVSKDDQGNITVK 377

QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVINAGNNIEIT 301
DB 378 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVINAGNNIEIT 437

QY 302 RNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
DB 438 RNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 497

QY 362 GDVTNVAQLKGVAQNLRNDRDNGNARAGIAQAIAATAGLVQAYLPCKSMAIGGGTYLG 421
DB 498 GDVTNVAQLKGVAQNLRNDRDNGNARAGIAQAIAATAGLVQAYLPCKSMAIGGGTYRG 557
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FT /label= C2
FT /note= "Conserved region 2"
FT 117..130
FT /label= V2
FT /note= "Variable region 2"
FT 131..194
FT /label= C3
FT /note= "Conserved region 3"
FT 195..216
FT /label= V3
FT /note= "Variable region 3"
FT 217..235
FT /label= C4
FT /note= "Conserved region 4"
FT 236..242
FT /label= V4
FT /note= "Variable region 4"
FT 243..598
FT /label= C5
FT /note= "Conserved region 5"
PN WO200155182-A1.
PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
XX N-PSDB; AAS09168.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 9lpp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain B210 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
XX Sequence 598 AA;
XX
XX Query Match 96.2%; Score 2261; DB 22; Length 598;
XX Best Local Similarity 96.5%; Pred. No. 4.9e-134;
XX Matches 445; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
QY 2 DETGLINVEYEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSLTDMLL 61
DB 138 DLTDLTSTVEYEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSLTDTLL 197
QY 62 NTGATTNVTNDVTDDEKKRAASVKVDVLNAGWNIKGVKPGFTASDNVDFVRTYDVEFLS 121
DB 198 NTGATTNVTNDVTDDEKKRAASVKVDVLNAGWNIKGVKPGFTASDNVDFVRTYDVEFLS 257
QY 122 ADTKTTTVNVEKDKNGKKEVVKIGAKTSVKEKDKGLVTGKGENSGSSDDEGGLVTAK 181
|||||

Db 258 ADTKTTTVNVEKDKNGKKEVVKIGAKTSVKEKDKGLVTGKGENSGSSDDEGGLVTAK 317
QY 182 EVIDAVNKAGWRMKTITTTANGOTGOADKFETVTSKTKVTFASGNGTTFATVSKDDOGNITVK 241
|||||
Db 318 EVIDAVNKAGWRMKTITTTANGOTGOADKFETVTSKTKVTFASGNGTTFATVSKDDOGNITVK 377
|||||
QY 242 YDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDFTVNTNAGNIEIT 301
|||||
Db 378 YDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDFTVNTNAGNIEIT 437
|||||
QY 302 RNKNNDIATSMTPQFSVSLGACADAPTLSDVDDDEGALNVGSKDANKPVRTNVPAGVKE 361
|||||
Db 438 RNKNNDIATSMTPQFSVSLGACADAPTLSDVDDDEGALNVGSKDANKPVRTNVPAGVKE 497
|||||
QY 362 GDVTNVAQLKGVAGQNLNRRIDNVNGNARAGIAQAIAATAGLQVAYLPKGSMAIGGTYLG 421
|||||
Db 498 GDVTNVAQLKGVAGQNLNRRIDNVNGNARAGIAQAIAATAGLQVAYLPKGSMAIGGTYLG 557
|||||
QY 422 EAGYAIQYSSISAGNWIIRKGTASGNSRGHFGASASVGYOW 462
|||||
Db 558 EAGYAIQYSSISDGTGNWIKGTASGNSRGHFGTSASVGYOW 598
|||||
RESULT 8
AAAY23743
ID AAAY23743 standard; Protein; 599 AA.
XX
XX AC AAAY23743;
XX
XX DT 08-SEP-1999 (first entry)
XX
XX DE A surface protein of Neisseria meningitidis.
XX
XX KW Surface protein; surface glycoprotein; infection; vaccine;
XX KW immunoreactive peptide.
XX
XX OS Neisseria meningitidis.
XX
XX PN WO9931132-A1.
XX
XX PD 24-JUN-1999.
XX
XX PF 14-DEC-1998; 98WO-AU01031.
XX
XX PR 12-DEC-1997; 97GB-0026398.
XX
XX PA (ISIS-) ISIS INNOVATION LTD.
XX (UYQU) UNIV QUEENSLAND.
XX
XX PI Jennings MP, Moxon ER, Peak IRA;
XX WPI: 1999-418754/35.
XX N-PSDB; AAX85795.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections
XX
XX PS Claim 1; Page 114-115; 132pp; English.
XX
XX CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX SQ Sequence 599 AA;
XX
XX Query Match 96.2%; Score 2260; DB 20; Length 599;
XX Best Local Similarity 96.5%; Pred. No. 5.6e-134;
XX

Db 499 GDVTNVAQLKGVQNLNRRIDNVGNARAGIAQAIAATAGLVQAYLPKGSMAIGGGTYRG 558

Qy 422 EAGYAIYSSISAGSNWIIKGTASGSRGHRFGASVGYQW 462

Db 559 EAGYAIYSSISDGSNWIIGKTASGSRGHRFGASVGYQW 599

RESULT 10

AAU06179

ID AAY23739 standard; Protein; 594 AA.

XX AAY23739;

AC AAY23739;

DT 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

DE Surface protein; surface glycoprotein; infection; vaccine;

KW immunoreactive peptide.

XX Neisseria meningitidis.

XX WO9931132-A1.

PN 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

PA (UYQU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

PI WPI; 1999-418754/35.

DR N-PSDB; AAX85791.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

XX Claim 1; Page 95-97; 132pp; English.

XX The present sequence represents a surface protein of Neisseria

CC meningitidis which is approximately 62 kDa. The N. meningitidis

CC surface glycoproteins, nucleic acids, the primers and optionally

CC a thermostable polymerase, or antibodies are useful in a kit for

CC the detection or diagnosis of N. meningitidis infection in humans.

CC The N. meningitidis surface glycoproteins can also be used to

CC prevent or treat N. meningitidis infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also

CC be used to identify immunoreactive peptides.

XX Sequence 594 AA;

SQ

Query Match 95.6%; Score 2247; DB 20; Length 594;

Best Local Similarity 96.3%; Pred. No. 3.6e-133;

Matches 444; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 2 DETGLINVEVEKLSFGANGKVVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSLTDLML 61

Db 134 DLTLDTSVETKLSFGANGKVVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSLTDL 193

Qy 62 NTGATTNVTNDVTDDEKRAASKVDVNLNAGWNIKGVKPGTASDNVDVFTYDTVEFLS 121

Db 194 NTGATTNVTNDVTDDEKRAASKVDVNLNAGWNIKGVKPGTASDNVDVFTYDTVEFLS 253

Qy 122 ADTKTTTVNVESKDKGKTEVKIGAKTSVIKEKDKLVTKGKGSGSSTDEGEGLVTAK 181

Db 254 ADTKTTTVNVESKDKGKTEVKIGAKTSVIKEKDKLVTKGKGSGSSTDEGEGLVTAK 313

Qy 182 EVIDAVNKAGWRMKTITTTANGOTGQADKFEITVTSCTNTVTFASGKTTTATVSKDDOGNITVK 241

Db 314 EVIDAVNKAGWRMKTITTTANGOTGQADKFEITVTSCTNTVTFASGKTTTATVSKDDOGNITVK 373

Qy 242 YDNNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEIT 301

Db 374 YDNNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEIT 433

Qy 302 RNGKNIDIATSWTPQSFSSVSLGACADAPTLLSVDDGALNVGSKDANKPVRITNYPGVKE 361

Db 434 RNGKNIDIATSWTPQSFSSVSLGACADAPTLLSVDDGALNVGSKDANKPVRITNYPGVKE 493

Qy 362 GDVTNVAQLKGVQNLNRRIDNVGNARAGIAQAIAATAGLVQAYLPKGSMAIGGGTYLG 421

Db 494 GDVTNVAQLKGVQNLNRRIDNVGNARAGIAQAIAATAGLVQAYLPKGSMAIGGGTYRG 553

Qy 422 EAGYAIYSSISAGSNWIIKGTASGSRGHRFGASVGYQW 462

Db 554 EAGYAIYSSISDGSNWIIGKTASGSRGHRFGASVGYQW 594

RESULT 11

AAU06179

ID AAU06179 standard; Protein; 594 AA.

XX AAU06179;

AC AAU06179;

DT 24-OCT-2001 (first entry)

XX N. meningitidis BZ198 surface antigen Nhha polypeptide sequence.

DE Surface antigen Nhha; meningococcal disease; meningitis vaccine.

KW Neisseria meningitidis strain BZ198.

XX Key Location/Qualifiers

FT 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT 51..104

FT /label= V1

FT /note= "Variable region 1"

FT 105..116

FT /label= C2

FT /note= "Conserved region 2"

FT 117..126

FT /label= V2

FT /note= "Variable region 2"

FT 127..190

FT /label= C3

FT /note= "Conserved region 3"

FT 191..212

FT /label= V3

FT /note= "Variable region 3"

FT 213..231

FT /label= C4

FT /note= "Conserved region 4"

FT 232..238

FT /label= V4

FT /note= "Variable region 4"

FT 239..594

FT /label= C5

FT /note= "Conserved region 5"

XX WO200155182-A1.

PN 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

XX (UYQU) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;

PI

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XX DR WPI: 2001-488774/53.
XX DR N-PSDB; AAS09169.
XX PT New Nhha surface antigen polypeptides and polynucleotides from
XX PT Neisseria meningitidis, useful in producing vaccines for treating or
XX PT preventing broad spectrum of Neisseria meningitidis -
XX PS Claim 9; Fig 1; 91pp; English.
XX CC The present invention relates to the isolation of novel Neisseria
XX CC meningitidis mutant polypeptides of the surface antigen Nhha
XX CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX CC characterised by deletions of non-conserved amino acids, particularly
XX CC the deletion of variable regions. The deletion mutants are useful in
XX CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX CC spectrum of N. meningitidis, and in designing and/or screening of
XX CC medicaments. The mutant proteins when used as a vaccine can effectively
XX CC immunise against a broader spectrum of N. meningitidis strains than
XX CC would be expected from a corresponding wild-type surface antigen.
XX CC The present sequence representing the wild type surface antigen Nhha
XX CC from N. meningitidis strain B2198 is 1 of 10 Nhha polypeptide sequences
XX CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX CC the present invention.
XX PS Sequence 594 AA;
XX CC
XX CC Query Match 95.6%; Score 2247; DB 22; Length 594;
XX CC Best Local Similarity 96.3%; Pred. No. 3.6e-133;
XX CC Matches 444; Conservative 2; Mismatches 15; Indels 0; Gaps 0;
XX CC
XX CC QY 2 DETGLINVEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSTLDMLL 61
XX CC Db 134 DLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLDTLL 193
XX CC
XX CC QY 62 NTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRYDTVEFLS 121
XX CC Db 194 NTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRYDTVEFLS 253
XX CC
XX CC QY 122 ADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTGKGGKNGSSTDEGEGLVTAK 181
XX CC Db 254 ADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTGKGGKNGSSTDEGEGLVTAK 313
XX CC
XX CC QY 182 EVIDAVNKAGWRMKTITANGQTQADKFFETVTSKTVTFASNGGTTATVSKDQGNITVK 241
XX CC Db 314 EVIDAVNKAGWRMKTITANGQTQADKFFETVTSKTVTFASNGGTTATVSKDQGNITVK 373
XX CC
XX CC QY 242 YDYNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIEIT 301
XX CC Db 374 YDYNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIEIT 433
XX CC
XX CC QY 302 RNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
XX CC Db 434 RNGKNIDTATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 493*
XX CC
XX CC QY 362 GDVTNVAQLKGVAQNLNNRIDNVNAGNAGIAQAIATAGLVQAYLPKGSMAIGGTYLG 421
XX CC Db 494 GDVTNVAQLKGVAQNLNNRIDNVNAGNAGIAQAIATAGLVQAYLPKGSMAIGGTYRG 553
XX CC
XX CC QY 422 EAGYAIYGSSISAGGWIILKGTASGNSRGHFGASASVGYQW 462
XX CC Db 554 EAGYAIYGSSISDGGWIIKGTASGNSRGHFGASASVGYQW 594
XX CC
XX CC RESULT 12
XX CC AAU06182
XX ID AAU06182 standard; Protein; 512 AA.
XX AC AAU06182;
XX AC
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis PMC21 Nhha deletion mutant #1.
```

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XX Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutein.
XX OS Neisseria meningitidis strain PMC21.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 1..51
FT Protein 52..512
FT /label= Signal_peptide
FT /label= Mature_Nhha_deletion_mutant_#1
FT /note= "Predicted mature protein, specifically
XX claimed in claim 12"
XX PN WO200155182-A1.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-AU00069.
XX PR 25-JAN-2000; 2000US-0177917.
XX PA (UYQU ) UNIV QUEENSLAND.
XX PI Peak IRA, Jennings MP;
XX DR WPI: 2001-488774/53.
XX DR N-PSDB; AAS09172.
XX PT New Nhha surface antigen polypeptides and polynucleotides from
XX PT Neisseria meningitidis, useful in producing vaccines for treating or
XX PT preventing broad spectrum of Neisseria meningitidis -
XX PS Claim 12; Fig 5; 91pp; English.
XX CC The present invention relates to the isolation of novel Neisseria
XX CC meningitidis mutant polypeptides of the surface antigen Nhha
XX CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX CC characterised by deletions of non-conserved amino acids, particularly
XX CC the deletion of variable regions. The deletion mutants are useful in
XX CC diagnostics, therapeutic and prophylactic vaccines against a broader
XX CC spectrum of N. meningitidis, and in designing and/or screening of
XX CC medicaments. The mutant proteins when used as a vaccine can effectively
XX CC immunise against a broader spectrum of N. meningitidis strains than
XX CC would be expected from a corresponding wild-type surface antigen.
XX CC The present sequence represents N. meningitidis strain PMC21 surface
XX CC antigen Nhha deletion mutant #1.
XX PS Sequence 512 AA;
XX CC
XX CC Query Match 94.2%; Score 2213.5; DB 22; Length 512;
XX CC Best Local Similarity 95.4%; Pred. No. 3.9e-131;
XX CC Matches 440; Conservative 4; Mismatches 16; Indels 1; Gaps 1;
XX CC
XX CC QY 2 DETGLINVEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSTLDMLL 61
XX CC Db 53 NETDLTSVGTGKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLDTLL 112
XX CC
XX CC QY 62 NTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRYDTVEFLS 121
XX CC Db 113 NTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRYDTVEFLS 172
XX CC
XX CC QY 122 ADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTGKGGKNGSSTDEGEGLVTAK 181
XX CC Db 173 ADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTGKGGKNGSSTDEGEGLVTAK 232
XX CC
XX CC QY 182 EVIDAVNKAGWRMKTITANGQTQADKFFETVTSKTVTFASNGGTTATVSKDQGNITVK 241
XX CC Db 233 EVIDAVNKAGWRMKTITANGQTQADKFFETVTSKTVTFASNGGTTATVSKDQGNITVK 292
XX CC
XX CC QY 242 YDYNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIEIT 301
XX CC Db 301 YDYNVGDALNVNQLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIEIT 301
```

Db	293	YDVNVGDDALNVNQNLQNSGWNILDSKAVAGSSGKVISGHNVSFSGKMGKMDETVNNAGNNIEIT	355
QY	302	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKE	361
Db	353	RNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKDKNKPVRIITNVAPGVKE	411
QY	362	GDVTWVAQLKGVQAQNLNRIDNVNGNARAGIAQAIAATAGLVQAYLPGKSNMAIGGGTYLG	421
Db	412	GDVTWVAQLKGVQAQNLNRIDNVGDNARAGIAQAIAATAGLVQAYLPGKSNMAIGGGTYRG	471
QY	422	EAGYAIGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW	462
Db	472	EAGYAIGYSSISDGGNWIIRGTASGNSRGHFGASASVGYQW	512
RESULT 13			
AAY23740			
ID	AAY23740 standard; Protein; 594 AA.		
AC	AAY23740;		
XX			
DT	08-SEP-1999 (first entry)		
DE	A surface protein of Neisseria meningitidis.		
XX			
KW	Surface protein; surface glycoprotein; infection; vaccine;		
KW	Immunoreactive peptide.		
XX			
OS	Neisseria meningitidis.		
XX			
PN	W09931132-A1.		
XX			
PD	24-JUN-1999.		
XX			
PF	14-DEC-1998; 98WO-AU01031.		
XX			
PR	12-DEC-1997; 97GB-0026398.		
XX			
PA	{ISIS-} ISIS INNOVATION LTD.		
PA	{UYQU } UNIV QUEENSLAND.		
XX			
PI	Jennings MP, Moxon ER, Peak IRA;		
XX			
DR	WPI; 1999-418754/35.		
XX	N-PSDB; AAX85792.		
XX			
PT	Neisseria meningitidis surface proteins useful for treating N.		
PT	meningitidis infections		
XX			
PS	Claim 1; Page 100-101; 132pp; English.		
XX			
CC	The present sequence represents a surface protein of Neisseria		
CC	meningitidis which is approximately 62 kDa. The N. meningitidis		
CC	surface glycoproteins, nucleic acids, the primers and optionally		
CC	a thermostable polymerase, or antibodies are useful in a kit for		
CC	the detection or diagnosis of N. meningitidis infection in humans.		
CC	The N. meningitidis surface glycoproteins can also be used to		
CC	prevent or treat N. meningitidis infection in humans, especially		
CC	in the form of vaccines. The proteins and antibodies can also		
CC	be used to identify immunoreactive peptides.		
XX			
SQ	Sequence 594 AA;		
Query Match 94.2%; Score 2213; DB 20; Length 594;			
Best Local Similarity 95.0%; Pred. No. 5e-131;			
Matches 438; Conservative 5; Mismatches 18; Indels 0; Gaps 0			
QY	2	DEFTGLINVEKELSFANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSLTDMEL	61
Db	134	DLTDLTSLVGTKEKLSFANSKNVITSDTKGLNFAKKTAEETNGDTTVHLNGIGSLTDLTL	193
QY	62	NTGATTNTVNDVDDDEKKRAASKVDVLNAGWIKGVKPGTITASDNVDFVRYDYVFEFLS	121

Db	194	NTGATTTNTDNDVDEKKRAASVKDVLNAGWNIKGVKPGCTTASDNVDFVRTYDVTVEFLS	255
Qy	122	ADTKTTTNNVESKDKGKTEVKIGAKTSVIKEKDGKLVTKGKGKENGSGSTDEGEGLVTAK	181
Db	254	ADTKTTTNNVESKDKGKTEVKIGAKTSVIKEKDGKLVTKGKGKENGSGSTDEGEGLVTAK	313
Qy	182	EVIDAVNKAGWRMKTITANGQTGQADKPEFVTSTGKVTTFASGNGTTATVSKDDQGNITVK	241
Db	314	EVIDAVNKAGWRMKTITANGQTGQADKPEFVTSTGKVTTFASGNGTTATVSKDDQGNITVK	373
Qy	242	YDVNVGDALNVLNQNSGNWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIINAGNNIEIT	301
Db	374	YDVNVGDALNVLNQNSGNWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIINAGNNIEIT	433
Qy	302	RNGKNIDIATSWTPOFSSVSLGAGADAPTLVSVDDEGALNVGSKDANKPVRITNVPVKVE	361
Db	434	RNGKNIDIATSWTPOFSSVSLGAGADAPTLVSVDDEGALNVGSKDANKPVRITNVPVKVE	493
Qy	362	GDVTNVAQLKGVQNLNHRIDNVNGNARAGIAQAATATAGLVQAYLPGKSMMAIGGGTYIG	421
Db	494	GDVTNVAQLKGVQNLNHRIDNVNGNARAGIAQAATATAGLVQAYLPGKSMMAIGGGTYIG	553
Qy	422	EAGYAGYSSISAGGNWIIKGTASGNSRGHFGASASVGYQW	462
Db	554	EAGYAGYSSISDGGNWIIRKGTASGNSRGHFGASASVGYQW	594
RESULT 14			
AAV57044			
ID	AAV57044 standard; Protein; 594 AA.		
XX			
AC	AAV57044;		
XX			
DT	21-FEB-2000 (first entry)		
XX			
DE	BASB029 amino acid sequence from N. meningitidis strain ATCC13090.		
XX			
KW	BASB029; <i>Neisseria meningitidis</i> ; surface fibril protein; HSF; diagnosis;		
KW	treatment; prevent; antibacterial drug.		
XX			
OS	<i>Neisseria meningitidis</i> .		
XX			
Key	Location/Qualifiers		
FT	Misc-difference 104		
FT	/note= "Encoded by AATC"		
XX			
PN	W09958683-A2.		
XX			
PD	18-NOV-1999.		
XX			
PF	07-MAY-1999; 99WO-EP03255.		
XX			
PR	13-MAY-1998; 98GB-0010276.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.		
XX			
PI	Ruelle J;		
XX			
DR	WPI; 2000-053103/04.		
DR	N-PSDB; AAZ39864.		
XX			
PT	New polypeptide from <i>Neisseria meningitidis</i> useful for diagnosis,		
PT	treatment or prevention of bacterial infections in mammal		
XX			
PS	Claim 4; Fig 2; 74pp; English.		
XX			
CC	This is the <i>Neisseria meningitidis</i> BASB029 amino acid sequence from		
CC	serogroup B strain ATCC13090. The BASB029 protein is homologous to the		
CC	<i>Haemophilus influenzae</i> surface fibril (HSF) protein. The invention		
CC	relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and		
CC	polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.		
CC	BASB029 polypeptides are useful in a method of diagnosing a <i>Neisseria</i>		
CC	<i>meningitidis</i> infection in a mammal. Compositions containing BASB029		

CC polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BAS029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BAS029, polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism receiving the protein.

XX Sequence 594 AA;

Query Match 94.2%; Score 2213; DB 21; Length 594;
Best Local Similarity 95.0%; Pred. No. 5e-131;
Matches 438; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 DETGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLDMLL 61
DB 134 DLTDLTSVGTCKLSFSANSKNVNIISDTKGLNFAKTAETNGDTTVHLNGIGSTLDTLL 193
QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKPGCTTASDNVDFVRYDTVEFLS 121
DB 194 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKPGCTTASDNVDFVRYDTVEFLS 253
QY 122 ADTKTTTNNVESKDNCKKTEVKIGAKTSVIKEDGKLVTKGKGSGSSTDDEGLVTAK 181
DB 254 ADTKTTTNNVESKDNCKKTEVKIGAKTSVIKEDGKLVTKGKGSGSSTDDEGLVTAK 313
QY 182 EVIDAVNKGAGRMKTTTANGOTGQADKFEETVTSKTFTASGNGTTATVSKDQGNITVK 241
DB 314 EVIDAVNKGAGRMKTTTANGOTGQADKFEETVTSKTFTASGNGTTATVSKDQGNITVK 373
QY 242 YDNNVDALNNQNLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIEIT 301
DB 374 YDNNVDALNNQNLQNSGNLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIEIT 433
QY 302 RKGKNTDIATSMTPQPSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRIITNVPQVKE 361
DB 434 RKGKNTDIATSMTPQPSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRIITNVPQVKE 493
QY 362 GDVTNVAQLKGVQNLNNRINDVNGNARAGIAQAIATAGLVQAYLPCKSMMAIGGTYLG 421
DB 494 GDVTNVAQLKGVQNLNNRINDVNGNARAGIAQAIATAGLVQAYLPCKSMMAIGGTYRG 553
QY 422 EAGYATGYSSISAGGNIKGTASGNSRGHFGASASVGQW 462
DB 554 EAGYATGYSSISDGGNIIKGTASGNSRGHFGASASVGQW 594

RESULT 15

AAU06174
ID AAU06174 standard; Protein: 594 AA.

XX AC AAU06174;

XX DT 24-OCT-2001 (first entry)

XX DE N. meningitidis EG327 surface antigen NhhA polypeptide sequence.

XX KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain EG327.

XX FH key Location/Qualifiers

FT Region 1..50

FT FT /label= C1

FT FT /note= "Conserved region 1"

FT FT 51..104

FT FT /label= V1

FT Region /note= "Variable region 1"
FT 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT 117..126
FT /label= V2
FT /note= "Variable region 2"
FT 127..190
FT /label= C3
FT /note= "Conserved region 3"
FT 191..212
FT /label= V3
FT /note= "Variable region 3"
FT 213..231
FT /label= C4
FT /note= "Conserved region 4"
FT 232..238
FT /label= V4
FT /note= "Variable region 4"
FT 239..594
FT /label= C5
FT /note= "Conserved region 5"

WO200155182-A1.

02-AUG-2001.

25-JAN-2001; 2001WO-AU000069.

25-JAN-2000; 2000US-0177917.

(UYQU) UNIV QUEENSLAND.

Peak IRA, Jennings MP;

WPI; 2001-488774/53.

N-PSDB; AAS09164.

New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -

Claim 9; Fig 1; 91pp; English.

The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain EG327 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention.

XX SQ Sequence 594 AA;

Query Match 94.2%; Score 2213; DB 22; Length 594;

Best Local Similarity 95.0%; Pred. No. 5e-131;

Matches 438; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 DETGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLDMLL 61

DB 134 DLTDLTSVGTCKLSFSANSKNVNIISDTKGLNFAKTAETNGDTTVHLNGIGSTLDTLL 193

QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKPGCTTASDNVDFVRYDTVEFLS 121

DB 194 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKPGCTTASDNVDFVRYDTVEFLS 253

Qy	122	ADTKTTTVNVESKDNKGKTEVKIGAKTSV	IKEDGKLV	TKGKGKNGSS	TDEGGLVTAK	181			
Db	254	ADTKTTTVNVESKDNKGRTTEVKIGAKTSV	IKEDGKLV	TKGKGKNGSS	TDKGEGLVTAK	313			
Qy	182	EVIDAVNKAGWRMKT	TTTANGQT	GOADKFET	VTSGTKVTF	FASGNGCTTATVSKDDOGNITVK	241		
Db	314	EVIDAVNKAGWRMKT	TTTANGQT	GOADKFET	VTSGTNVTF	FASGKGT	TATVSKDDOGNITVM	373	
Qy	242	YDVNVGDALNVNQLQNSGWNLD	SKAVAGSSGK	VISGNVSP	SKGKMD	ETVNVINAGNNTIEIT	301		
Db	374	YDVNVGDALNVNQLQNSGWNLD	SKAVAGSSGK	VISGNVSP	SKGKMD	ETVNVINAGNNTIEIT	433		
Qy	302	RNGKNIDIAT	SMT	PQFS	SVSLGAGADAPT	LSVDD	EGALNVGSKDANKPVRIT	361	
Db	434	RNGKNIDIAT	SMT	PQFS	SVSLGAGADAPT	LSVDD	EGALNVGSKDANKPVRIT	493	
Qy	362	GDVTNVAQLKGV	AOQLN	NRIDNV	NGNARAG	IAQAIATAG	LVAQLPGKSMMA	IGGGTYLG	421
Db	494	GDVTNVAQLKGV	AOQLN	NRIDNV	NGNARAG	IAQAIATAG	LVAQLPGKSMMA	IGGGTYRG	553
Qy	422	EAGYAIGYSSIS	AGGNWII	IKGTASG	NSRGHFGAS	ASVGYQW	462		
Db	554	EAGYAIGYSSIS	DGNNWII	IKGTASG	NSRGHFGAS	ASVGYQW	594		

Search completed: October 6, 2003, 09:22:42
Job time : 40.6746 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2337	99.4	592	3	US-09-377-155-17	Sequence 17, Appl	
2	2337	99.4	592	4	US-09-669-974-17	Sequence 17, Appl	
3	2261	96.2	598	3	US-09-377-155-5	Sequence 5, Appl	
4	2281	96.2	598	3	US-09-377-155-13	Sequence 13, Appl	
5	2281	96.2	598	4	US-09-669-974-5	Sequence 5, Appl	
6	2261	96.2	598	4	US-09-669-974-13	Sequence 13, Appl	
7	2260	96.2	599	3	US-09-377-155-15	Sequence 15, Appl	
8	2260	96.2	599	4	US-09-669-974-15	Sequence 15, Appl	
9	2247	95.6	594	3	US-09-377-155-7	Sequence 7, Appl	
10	2247	95.6	594	4	US-09-669-974-7	Sequence 7, Appl	
11	2213	94.2	594	3	US-09-377-155-9	Sequence 9, Appl	
12	2213	94.2	594	4	US-09-669-974-9	Sequence 9, Appl	
13	2210.5	94.1	591	3	US-09-377-155-11	Sequence 11, Appl	
14	2210.5	94.1	591	3	US-09-377-155-21	Sequence 21, Appl	
15	2210.5	94.1	591	4	US-09-669-974-11	Sequence 11, Appl	
16	2210.5	94.1	591	4	US-09-669-974-21	Sequence 21, Appl	
17	2206.5	93.9	592	3	US-09-377-155-2	Sequence 2, Appl	
18	2206.5	93.9	592	4	US-09-669-974-2	Sequence 2, Appl	
19	2116	90.0	589	3	US-09-377-155-19	Sequence 19, Appl	
20	2116	90.0	589	4	US-09-669-974-19	Sequence 19, Appl	
21	876	37.3	2353	3	US-09-377-155-33	Sequence 33, Appl	
22	876	37.3	2353	3	US-08-913-942-4	Sequence 4, Appl	
23	876	37.3	2353	4	US-09-669-974-33	Sequence 33, Appl	
24	876	37.3	2351	4	US-09-268-347-36	Sequence 36, Appl	
25	869.5	37.0	2414	4	US-09-268-347-47	Sequence 47, Appl	
26	865	36.8	1094	4	US-09-268-347-32	Sequence 32, Appl	
27	855	36.4	1912	1	US-08-409-995-4	Sequence 4, Appl	

Db 432 RRGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 491
Qy 362 GDTNVNVAQLKGVQAOQLNNRNDNVNGNARAGIAQAIAATAGLVQAYLPKSKMAIGGGTYLG 421
Db 492 GDTNVNVAQLKGVQAOQLNNRNDNVNGNARAGIAQAIAATAGLVQAYLPKSKMAIGGGTYLG 551
Qy 422 EAGYAIGYSSISAGGNWIKGTASGNSRGHFGASASVGYOW 462
Db 552 EAGYAIGYSSISAGGNWIKGTASGNSRGHFGASASVGYOW 592

RESULT 2

US-09-669-974-17

; Sequence 17, Application US/09669974

; Patent No. 6333173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; PRIOR FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 17

; LENGTH: 592

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-669-974-17

Query Match

Best Local Similarity 99.4%; Score 2337; DB 4; Length 592;

Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DETGLINVEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 61
Db 132 DLGLLINVEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 191
Qy 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDVFTYDTVEFLS 121
Db 192 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDVFTYDTVEFLS 251
Qy 122 ADTKTTTVNYESKDNGKTEVKIGAKTSVIKEDGKLVTKGKGENSGSTDEGEGLVTAK 181
Db 252 ADTKTTTVNYESKDNGKTEVKIGAKTSVIKEDGKLVTKGKGENSGSTDEGEGLVTAK 311
Qy 182 EVIDAVNKAQWRKMTTANGOTQADKFETVTSKTKVTFASGNGTTATVSKDDQGNITVK 241
Db 312 EVIDAVNKAQWRKMTTANGOTQADKFETVTSKTKVTFASGNGTTATVSKDDQGNITVK 371

Qy 242 YDENVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEIT 301
Db 372 YDENVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEIT 431
Qy 302 RRGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
Db 432 RRGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 491
Qy 362 GDTNVNVAQLKGVQAOQLNNRNDNVNGNARAGIAQAIAATAGLVQAYLPKSKMAIGGGTYLG 421
Db 492 GDTNVNVAQLKGVQAOQLNNRNDNVNGNARAGIAQAIAATAGLVQAYLPKSKMAIGGGTYLG 551
Qy 422 EAGYAIGYSSISAGGNWIKGTASGNSRGHFGASASVGYOW 462
Db 552 EAGYAIGYSSISAGGNWIKGTASGNSRGHFGASASVGYOW 592

RESULT 3

US-09-377-155-5

; Sequence 5, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; CURRENT FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 598

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-377-155-5

Query Match 96.2%; Score 2261; DB 3; Length 598;
Best Local Similarity 96.5%; Pred. No. 3.1e-172;
Matches 445; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
Qy 2 DETGLINVEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 61
Db 138 DLGLTSVETEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 197
Qy 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDVFTYDTVEFLS 121
Db 198 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDVFTYDTVEFLS 257
Qy 122 ADTKTTTVNYESKDNGKTEVKIGAKTSVIKEDGKLVTKGKGENSGSTDEGEGLVTAK 181
Db 258 ADTKTTTVNYESKDNGKTEVKIGAKTSVIKEDGKLVTKGKGENSGSTDEGEGLVTAK 317
Qy 182 EVIDAVNKAQWRKMTTANGOTQADKFETVTSKTKVTFASGNGTTATVSKDDQGNITVK 241
Db 318 EVIDAVNKAQWRKMTTANGOTQADKFETVTSKTKVTFASGNGTTATVSKDDQGNITVK 377
Qy 242 YDENVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEIT 301
Db 378 YDENVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEIT 437
Qy 302 RRGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
Db 438 RRGKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 497
Qy 362 GDTNVNVAQLKGVQAOQLNNRNDNVNGNARAGIAQAIAATAGLVQAYLPKSKMAIGGGTYLG 421
Db 498 GDTNVNVAQLKGVQAOQLNNRNDNVNGNARAGIAQAIAATAGLVQAYLPKSKMAIGGGTYLG 557
Qy 422 EAGYAIGYSSISAGGNWIKGTASGNSRGHFGASASVGYOW 462
Db 558 EAGYAIGYSSISDTGNWIKGTASGNSRGHFGISASVGYOW 598

RESULT 4

US-09-377-155-13

; Sequence 13, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PR1
; ORGANISM: Neisseria meningitidis
; US-09-377-155-13

Query Match 96.2%; Score 2261; DB 3; Length 598;
Best Local Similarity 96.7%; Pred. No. 3.1e-172;
Matches 446; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
QY 2 DETGLINVEETKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDMLL 61
DB 138 DLTDLTSVETKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDMLL 197
QY 62 NTGATTNVNDNVTDDDEKRAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLS 121
DB 198 NTGATTNVNDNVTDDDEKRAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLS 257
QY 122 ADTKTTTVNVESKDNCKKTEVKIGAKTSVKEKDKGLVTCGKKGENGSSSTDEGEGLVTAK 181
DB 258 ADTKTTTVNVESKDNCKKTEVKIGAKTSVKEKDKGLVTCGKKGENGSSSTDEGEGLVTAK 317
QY 182 EVIDAVNAGWRMKTITANGQTQADKFETVTSCTKVTTFASNGTGTATVSKDQGNITVK 241
DB 318 EVIDAVNAGWRMKTITANGQTQADKFETVTSCTKVTTFASNGTGTATVSKDQGNITVK 377
QY 242 YDNNVGDALNVNOLQNSGNWNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNIEIT 301
DB 378 YDNNVGDALNVNOLQNSGNWNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNIEIT 437
QY 302 RGNKNIDIAISMTPOQSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
DB 438 RGNKNIDIAISMTPOQSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 497
QY 362 GDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYLG 421
DB 498 GDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRG 557
QY 422 EAGYATGYSSISAGGNIWIKGTASGNSRGHFGASASVGYQW 462
DB 558 EAGYATGYSSISDTGNWVINGTASGNSRGHFGASASVGYQW 598

RESULT 5
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PR1

; ORGANISM: Neisseria meningitidis
; US-09-669-974-5
Query Match 96.2%; Score 2261; DB 4; Length 598;
Best Local Similarity 96.5%; Pred. No. 3.1e-172;
Matches 445; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
QY 2 DETGLINVEETKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDMLL 61
DB 138 DLTDLTSVETKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDMLL 197
QY 62 NTGATTNVNDNVTDDDEKRAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLS 121
DB 198 NTGATTNVNDNVTDDDEKRAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLS 257
QY 122 ADTKTTTVNVESKDNCKKTEVKIGAKTSVKEKDKGLVTCGKKGENGSSSTDEGEGLVTAK 181
DB 258 ADTKTTTVNVESKDNCKKTEVKIGAKTSVKEKDKGLVTCGKKGENGSSSTDEGEGLVTAK 317
QY 182 EVIDAVNAGWRMKTITANGQTQADKFETVTSCTKVTTFASNGTGTATVSKDQGNITVK 241
DB 318 EVIDAVNAGWRMKTITANGQTQADKFETVTSCTKVTTFASNGTGTATVSKDQGNITVK 377
QY 242 YDNNVGDALNVNOLQNSGNWNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNIEIT 301
DB 378 YDNNVGDALNVNOLQNSGNWNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNIEIT 437
QY 302 RGNKNIDIAISMTPOQSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
DB 438 RGNKNIDIAISMTPOQSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 497
QY 362 GDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYLG 421
DB 498 GDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRG 557
QY 422 EAGYATGYSSISAGGNIWIKGTASGNSRGHFGASASVGYQW 462
DB 558 EAGYATGYSSISDTGNWVINGTASGNSRGHFGASASVGYQW 598

RESULT 6
US-09-669-974-13
; Sequence 13, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PR1
; ORGANISM: Neisseria meningitidis
; US-09-669-974-13

Query Match 96.2%; Score 2261; DB 4; Length 598;
Best Local Similarity 96.7%; Pred. No. 3.1e-172;
Matches 446; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
QY 2 DETGLINVEETKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDMLL 61
DB 138 DLTDLTSVETKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDMLL 197

QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGNWKGVKPGTTASDNVDVFTYDTVEFLS 121
DB 198 NTGATTNVTNDVTDDEKKRAASVKDVLNAGNWKGVKPGTTASDNVDVFTYDTVEFLS 257
QY 122 ADTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDKGLVTGKGKGENSSDDEGGLVTAK 181
DB 258 ADTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDKGLVTGKGKGENSSDDEGGLVTAK 317
QY 182 EVIDAVNKAGWRMKTTFANGOTGQADKFETVTSCTKVTFFASGNGTTFATVSKDDOGNITVK 241
DB 318 EVIDAVNKAGWRMKTTFANGOTGQADKFETVTSCTKVTFFASGNGTTFATVSKDDOGNITVK 377
QY 242 YDNNVGDALNNQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 301
DB 378 YDNNVGDALNNQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 437
QY 302 RGNKNIDIASMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRTTNVAPGVKE 361
DB 438 RGNKNIDIASMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRTTNVAPGVKE 497
QY 362 GDTVNTVAQLKGVAQNLRNDNVNGNARAGIAQAIAATAGLVAQYLPKGSMAIGGGTYLG 421
DB 498 GDTVNTVAQLKGVAQNLRNDNVNGNARAGIAQAIAATAGLVAQYLPKGSMAIGGGTYRG 557
QY 422 EAGYAIGYSSISAGSNWIIKGTASGNSRGHFGASASVGYOW 462
DB 558 EAGYAIGYSSISDTGNVIRKGTASGNSRGHFGASASVGYOW 598

RESULT 7

US-09-377-155-15

; Sequence 15, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; CURRENT FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 599

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-377-155-15

Query Match

Best Local Similarity 96.2%; Score 2260; DB 3; Length 599;

Matches 445; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 DETGLINVEVEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 61

DB 139 DLDTLTSVETEKLVSFGANGKKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLL 198

QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGNWKGVKPGTTASDNVDVFTYDTVEFLS 121

DB 199 NTGATTNVTNDVTDDEKKRAASVKDVLNAGNWKGVKPGTTASDNVDVFTYDTVEFLS 258

QY 122 ADTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDKGLVTGKGKGENSSDDEGGLVTAK 181

DB 259 ADTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDKGLVTGKGKGENSSDDEGGLVTAK 318

QY 182 EVIDAVNKAGWRMKTTFANGOTGQADKFETVTSCTKVTFFASGNGTTFATVSKDDOGNITVK 241

DB 319 EVIDAVNKAGWRMKTTFANGOTGQADKFETVTSCTKVTFFASGNGTTFATVSKDDOGNITVK 378

QY 242 YDNNVGDALNNQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 301
DB 379 YDNNVGDALNNQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 438
QY 302 RGNKNIDIASMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRTTNVAPGVKE 361
DB 439 RGNKNIDIASMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRTTNVAPGVKE 498
QY 362 GDTVNTVAQLKGVAQNLRNDNVNGNARAGIAQAIAATAGLVAQYLPKGSMAIGGGTYLG 421
DB 499 GDTVNTVAQLKGVAQNLRNDNVNGNARAGIAQAIAATAGLVAQYLPKGSMAIGGGTYRG 558
QY 422 EAGYAIGYSSISAGSNWIIKGTASGNSRGHFGASASVGYOW 462
DB 559 EAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 599

RESULT 8

US-09-669-974-15

; Sequence 15, Application US/09669974

; Patent No. 6333173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; CURRENT FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 599

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-669-974-15

Query Match

Best Local Similarity 96.2%; Score 2260; DB 4; Length 599;

Matches 445; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 DETGLINVEVEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 61

DB 139 DLDTLTSVETEKLVSFGANGKKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLL 198

QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGNWKGVKPGTTASDNVDVFTYDTVEFLS 121

DB 199 NTGATTNVTNDVTDDEKKRAASVKDVLNAGNWKGVKPGTTASDNVDVFTYDTVEFLS 258

QY 122 ADTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDKGLVTGKGKGENSSDDEGGLVTAK 181

DB 259 ADTKTTTVNYESKDNKGKTEVKIGAKTSVKEKDKGLVTGKGKGENSSDDEGGLVTAK 318

QY 182 EVIDAVNKAGWRMKTTFANGOTGQADKFETVTSCTKVTFFASGNGTTFATVSKDDOGNITVK 241

DB 319 EVIDAVNKAGWRMKTTFANGOTGQADKFETVTSCTKVTFFASGNGTTFATVSKDDOGNITVK 378

QY 242 YDNNVGDALNNQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 301

DB 379 YDNNVGDALNNQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNNAGNNEIT 438

QY 302 RGNKNIDIASMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRTTNVAPGVKE 361

DB 439 RGNKNIDIASMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPVRTTNVAPGVKE 498

QY 362 GDTVNTVAQLKGVAQNLRNDNVNGNARAGIAQAIAATAGLVAQYLPKGSMAIGGGTYLG 421

Db 499 G D V T N V A Q L K G V A Q N L N N R I D N V D G N A R A G I A Q A I A T A G L V Q A Y L P G K S M A I G G T Y R G 558
Qy 422 E A G Y A I G Y S S I S A G G N W I K G T A S G N S R G H F G A S A S V G Y Q W 462
Db 559 E A G Y A I G Y S S I S D G G N W I K G T A S G N S R G H F G A S A S V G Y Q W 599

RESULT 9
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR FILING DATE: 1997-12-12
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match 95.6%; Score 2247; DB 3; Length 594;
Best Local Similarity 96.3%; Pred. No. 4.1e-171;
Matches 444; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 2 DETGLINVETEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDPTTVHLNGIGSTLTDMLL 61
Db 134 L D L D L S V E T E K L S F G A N G K N V I T S D T K G L N F A K E T A G T N G D P T T V H L N G I G S T L D T L L 193

Qy 62 N T G A T T N V T N D N V T D D E K K R A A S V K D V L N A G W N I K G V K P G T T A S D N V D F V R T Y D T V E F L S 121
Db 194 N T G A T T N V T N D N V T D D E K K R A A S V K D V L N A G W N I K G V K P G T T A S D N V D F V R T Y D T V E F L S 253

Qy 122 A D T K T T V N V E S K D N G K K T E V K I G A K T S V I K E K D G K L V T G K G K G E N G S S T D E G E G L V T A K 181
Db 254 A D T K T T V N V E S K D N G K K T E V K I G A K T S V I K E K D G K L V T G K G K G E N G S S T D E G E G L V T A K 313

Qy 182 E V I D A V N K A G W R K M T T A N G O T Q O A D K F E T V T S G T K V T F A S G N G T T A T V S K D D Q G N I T V K 241
Db 314 E V I D A V N K A G W R K M T T A N G O T Q O A D K F E T V T S G T K V T F A S G N G T T A T V S K D D Q G N I T V K 373

Qy 242 Y D V N V G D A L N V N Q L S G W N L S K A V A G S S G K V I S G N V S P S K G M D E T V N I N A G N N I E I T 301
Db 374 Y D V N V G D A L N V N Q L S G W N L S K A V A G S S G K V I S G N V S P S K G M D E T V N I N A G N N I E I T 433

Qy 302 R N G K N I D I A T S M T P Q F S S V S L G A D A P T L S V D D E G A L N V G S K D A N K P V R I T N V A P G V K E 361
Db 434 R N G K N I D I A T S M A P Q F S S V S L G A D A P T L S V D D E G A L N V G S K D T N K P V R I T N V A P G V K E 493

Qy 362 G D V T N V A Q L K G V A Q N L N N R I D N V N G N A R A G I A Q A I A T A G L V Q A Y L P G K S M A I G G T Y R G 421
Db 494 G D V T N V A Q L K G V A Q N L N N R I D N V D G N A R A G I A Q A I A T A G L V Q A Y L P G K S M A I G G T Y R G 553

Qy 422 E A G Y A I G Y S S I S A G G N W I K G T A S G N S R G H F G A S A S V G Y Q W 462
Db 554 E A G Y A I G Y S S I S D G G N W I K G T A S G N S R G H F G A S A S V G Y Q W 594

RESULT 10
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173

; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match 95.6%; Score 2247; DB 4; Length 594;
Best Local Similarity 96.3%; Pred. No. 4.1e-171;
Matches 444; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 2 DETGLINVETEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDPTTVHLNGIGSTLTDMLL 61
Db 134 L D L D L S V E T E K L S F G A N G K N V I T S D T K G L N F A K E T A G T N G D P T T V H L N G I G S T L D T L L 193

Qy 62 N T G A T T N V T N D N V T D D E K K R A A S V K D V L N A G W N I K G V K P G T T A S D N V D F V R T Y D T V E F L S 121
Db 194 N T G A T T N V T N D N V T D D E K K R A A S V K D V L N A G W N I K G V K P G T T A S D N V D F V R T Y D T V E F L S 253

Qy 122 A D T K T T V N V E S K D N G K K T E V K I G A K T S V I K E K D G K L V T G K G K G E N G S S T D E G E G L V T A K 181
Db 254 A D T K T T V N V E S K D N G K K T E V K I G A K T S V I K E K D G K L V T G K G K G E N G S S T D E G E G L V T A K 313

Qy 182 E V I D A V N K A G W R K M T T A N G O T Q O A D K F E T V T S G T K V T F A S G N G T T A T V S K D D Q G N I T V K 241
Db 314 E V I D A V N K A G W R K M T T A N G O T Q O A D K F E T V T S G T K V T F A S G N G T T A T V S K D D Q G N I T V K 373

Qy 242 Y D V N V G D A L N V N Q L S G W N L S K A V A G S S G K V I S G N V S P S K G M D E T V N I N A G N N I E I T 301
Db 374 Y D V N V G D A L N V N Q L S G W N L S K A V A G S S G K V I S G N V S P S K G M D E T V N I N A G N N I E I T 433

Qy 302 R N G K N I D I A T S M T P Q F S S V S L G A D A P T L S V D D E G A L N V G S K D A N K P V R I T N V A P G V K E 361
Db 434 R N G K N I D I A T S M A P Q F S S V S L G A D A P T L S V D D E G A L N V G S K D T N K P V R I T N V A P G V K E 493

Qy 362 G D V T N V A Q L K G V A Q N L N N R I D N V N G N A R A G I A Q A I A T A G L V Q A Y L P G K S M A I G G T Y R G 421
Db 494 G D V T N V A Q L K G V A Q N L N N R I D N V D G N A R A G I A Q A I A T A G L V Q A Y L P G K S M A I G G T Y R G 553

Qy 422 E A G Y A I G Y S S I S A G G N W I K G T A S G N S R G H F G A S A S V G Y Q W 462
Db 554 E A G Y A I G Y S S I S D G G N W I K G T A S G N S R G H F G A S A S V G Y Q W 594

RESULT 11
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 94.2%; Score 2213; DB 3; Length 594;
Best Local Similarity 95.0%; Pred. No. 2.1e-168;
Matches 438; Conservative 5; Mismatches 18; Indels 0; Gaps 0;
QY 2 DETGLINIVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 61
DB 134 DLTLDSVGTGTEKLSFSANSKNVNIISDTKGLNFAKTAETNGDTTVHLNGIGSTLTDLL 193
QY 62 NTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDTVEFLS 121
DB 194 NTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDTVEFLS 253
QY 122 ADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGKGENSSSTDEGGLVTAK 181
DB 254 ADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGKGENSSSTDEGGLVTAK 313
QY 182 EVIDAVNKAGWRMKTITANGOTGOADKFEFVTSKTVTFASGNGTTATVSKDQGNITVK 241
DB 314 EVIDAVNKAGWRMKTITANGOTGOADKFEFVTSKTVTFASGNGTTATVSKDQGNITVK 373
QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVINAGNNIEIT 301
DB 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVINAGNNIEIT 433
QY 302 RGNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
DB 434 RGNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 493
QY 362 GDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPCKSMMAIGGGTYLG 421
DB 494 GDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPCKSMMAIGGGTYRG 553
QY 422 EAGYAIGYSSISAGGNNIIKGTASGNSRGRHFGASASVGYOW 462
DB 554 EAGYAIGYSSISDGGNNIIKGTASGNSRGRHFGASASVGYOW 594

RESULT 12
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 94.2%; Score 2213; DB 4; Length 594;
Best Local Similarity 95.0%; Pred. No. 2.1e-168;
Matches 438; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
QY 2 DETGLINIVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 61
DB 134 DLTLDSVGTGTEKLSFSANSKNVNIISDTKGLNFAKTAETNGDTTVHLNGIGSTLTDLL 193
QY 62 NTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDTVEFLS 121
DB 194 NTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDTVEFLS 253
QY 122 ADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGKGENSSSTDEGGLVTAK 181
DB 254 ADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGKGENSSSTDEGGLVTAK 313
QY 182 EVIDAVNKAGWRMKTITANGOTGOADKFEFVTSKTVTFASGNGTTATVSKDQGNITVK 241
DB 314 EVIDAVNKAGWRMKTITANGOTGOADKFEFVTSKTVTFASGNGTTATVSKDQGNITVK 373
QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVINAGNNIEIT 301
DB 374 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETVINAGNNIEIT 433
QY 302 RGNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
DB 434 RGNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 493
QY 362 GDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPCKSMMAIGGGTYLG 421
DB 494 GDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPCKSMMAIGGGTYRG 553
QY 422 EAGYAIGYSSISAGGNNIIKGTASGNSRGRHFGASASVGYOW 462
DB 554 EAGYAIGYSSISDGGNNIIKGTASGNSRGRHFGASASVGYOW 594

RESULT 13
US-09-377-155-11
; Sequence 11, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11
Query Match 94.1%; Score 2210.5; DB 3; Length 591;
Best Local Similarity 95.4%; Pred. No. 3.3e-168;
Matches 440; Conservative 3; Mismatches 17; Indels 1; Gaps 1;
QY 2 DETGLINIVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 61
DB 132 DLTLDSVGTGTEKLSFSANSKNVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLL 191
QY 62 NTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDTVEFLS 121
DB 192 NTGATTNVTNDNVTDDDEKKRAASVKDVLNAGWNIKGVPKGTASDNVDFVRTYDTVEFLS 251

QY 122 ADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGKKGNGSSTDEGEGLVTAK 181
Db 252 ADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGKKGNGSSTDEGEGLVTAK 311
QY 182 EVIDAVNKGWRMKTITANGQTQADKPFETVSGTKVTFASNGTATTATVSKDDQGNITVK 241
Db 312 EVIDAVNKGWRMKTITANGQTQADKPFETVSGTKVTFASNGTATTATVSKDDQGNITVK 371
QY 242 YDENVGDLNVLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVNIINAGNNIET 301
Db 372 YDENVGDLNVLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVNIINAGNNIET 431
QY 302 RGNKNDIATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDANKPVRIITNVAPGVKE 361
Db 432 RGNKNDIATSMTPQFSSVSLGAGADAPTLSDVDDG-ALNVGSKDANKPVRIITNVAPGVKE 490
QY 362 GDTVNVQALKGVAQNINNRIDNVNGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYLG 421
Db 491 GDTVNVQALKGVAQNINNRIDNVNGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYRG 550
QY 422 EAGYAIYSSISAGGNWIIKGTASNSRGHFGASASGVQW 462
Db 551 EAGYAIYSSISDGGNWIIGKGTASNSRGHFGASASGVQW 591

RESULT 14

US-09-377-155-21

; Sequence 21, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn ver. 2.0

; SEQ ID NO 21

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-377-155-21

Query Match 94.1%; Score 2210.5; DB 3; Length 591;

Best Local Similarity 95.4%; Pred. No. 3.3e-168;

Matches 440; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

QY 2 DETGLINVETKLSFGANGKKNIIISDTKGLNFAKETAGTNGDVTVHLNGIGSTLTDMLL 61
Db 132 DLTDLTSVGTKLSFSANGKNVITSDTKGLNFAKETAGTNGDVTVHLNGIGSTLTDMLL 191
QY 62 NFGATTNTVNDVTDDEKKRAASVKDVLNAGNIIKGVKPGTASDNVDFVRYDTVFEFLS 121
Db 192 NFGATTNTVNDVTDDEKKRAASVKDVLNAGNIIKGVKPGTASDNVDFVRYDTVFEFLS 251
QY 122 ADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGKKGNGSSTDEGEGLVTAK 181
Db 252 ADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGKKGNGSSTDEGEGLVTAK 311
QY 182 EVIDAVNKGWRMKTITANGQTQADKPFETVSGTKVTFASNGTATTATVSKDDQGNITVK 241
Db 312 EVIDAVNKGWRMKTITANGQTQADKPFETVSGTKVTFASNGTATTATVSKDDQGNITVK 371
QY 242 YDENVGDLNVLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVNIINAGNNIET 301
Db 372 YDENVGDLNVLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVNIINAGNNIET 431

QY 302 RGNKNDIATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDANKPVRIITNVAPGVKE 361
Db 432 RGNKNDIATSMTPQFSSVSLGAGADAPTLSDVDDG-ALNVGSKDANKPVRIITNVAPGVKE 490
QY 362 GDTVNVQALKGVAQNINNRIDNVNGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYLG 421
Db 491 GDTVNVQALKGVAQNINNRIDNVNGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYRG 550
QY 422 EAGYAIYSSISAGGNWIIKGTASNSRGHFGASASGVQW 462
Db 551 EAGYAIYSSISDGGNWIIGKGTASNSRGHFGASASGVQW 591

RESULT 15

US-09-669-974-11

; Sequence 11, Application US/09669974

; Patent No. 6333173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; PRIOR FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-669-974-11

Query Match 94.1%; Score 2210.5; DB 4; Length 591;

Best Local Similarity 95.4%; Pred. No. 3.3e-168;

Matches 440; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

QY 2 DETGLINVETKLSFGANGKKNIIISDTKGLNFAKETAGTNGDVTVHLNGIGSTLTDMLL 61
Db 132 DLTDLTSVGTKLSFSANGKNVITSDTKGLNFAKETAGTNGDVTVHLNGIGSTLTDMLL 191
QY 62 NFGATTNTVNDVTDDEKKRAASVKDVLNAGNIIKGVKPGTASDNVDFVRYDTVFEFLS 121
Db 192 NFGATTNTVNDVTDDEKKRAASVKDVLNAGNIIKGVKPGTASDNVDFVRYDTVFEFLS 251
QY 122 ADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGKKGNGSSTDEGEGLVTAK 181
Db 252 ADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKGLVTGKKGNGSSTDEGEGLVTAK 311
QY 182 EVIDAVNKGWRMKTITANGQTQADKPFETVSGTKVTFASNGTATTATVSKDDQGNITVK 241
Db 312 EVIDAVNKGWRMKTITANGQTQADKPFETVSGTKVTFASNGTATTATVSKDDQGNITVK 371
QY 242 YDENVGDLNVLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVNIINAGNNIET 301
Db 372 YDENVGDLNVLQNSGNLDSKAVAGSSGKVIISGNVSPSKGKMDETVNIINAGNNIET 431
QY 302 RGNKNDIATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDANKPVRIITNVAPGVKE 361
Db 432 RGNKNDIATSMTPQFSSVSLGAGADAPTLSDVDDG-ALNVGSKDANKPVRIITNVAPGVKE 490
QY 362 GDTVNVQALKGVAQNINNRIDNVNGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYLG 421
Db 491 GDTVNVQALKGVAQNINNRIDNVNGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYRG 550
QY 422 EAGYAIYSSISAGGNWIIKGTASNSRGHFGASASGVQW 462
Db 551 EAGYAIYSSISDGGNWIIGKGTASNSRGHFGASASGVQW 591

Db 551 EAGYAGYSSISDGGNWI1KGTASGNSRGHFGASASVGYOW 591

Search completed: October 6, 2003, 09:35:58
Job time : 14.3548 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 13.2249 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-36

Perfect score: 2350
Sequence: 1 TDETGLINVETKLSFGANG.....TASGSRGHFGASVGVQW 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2210.5	94.1	591	2 G81133	adhesin NMB0992 (i
2	2136	90.9	592	2 A81888	probable surface f
3	390.5	16.6	298	2 I64138	adhesin homolog HI
4	360	15.3	1588	2 A86036	probable adhesin z
5	360	15.3	1588	2 H91188	probable adhesin E
6	359.5	15.3	2059	2 D82671	surface protein XF
7	357	15.2	1190	2 A82615	surface protein XF
8	348.5	14.8	1107	2 AC0976	probable autotrans
9	317	13.5	658	2 AH0110	probable surface p
10	212.5	9.0	1004	2 C82672	surface-exposed ou
11	207	8.8	3705	2 AD0123	probable autotrans
12	200.5	8.5	1910	2 AF0394	probable adhesin h
13	195	8.3	1536	2 A43855	high-molecular-wei
14	190	8.1	4919	2 T31105	hypothetical prote
15	188.5	8.0	936	2 I40711	sapB protein - Cam
16	187.5	8.0	365	2 AB3486	cell surface prote
17	187.5	8.0	2249	2 A14477	190K surface antig
18	186	8.0	2020	2 C48399	ABC-type transport
19	186	7.9	1651	2 JC1340	outer membrane pro
20	184.5	7.9	5188	2 B85547	probable RTX famli
21	183.5	7.8	5291	2 F90696	hypothetical prote
22	181	7.7	1109	2 A56143	surface-array prot
23	181	7.7	2551	2 B98047	hypothetical prote
24	180.5	7.7	1477	2 B43855	high-molecular-wei
25	180.5	7.7	1655	2 E97835	hypothetical prote
26	180	7.7	1361	2 T03415	S-layer protein -
27	179.5	7.6	364	2 A81019	adhesin/invasin, p
28	178.5	7.6	3029	2 S76109	hypothetical prote
29	178	7.6	4152	2 T31102	filamentous hemagg

30	177	7.5	1091	2 G64964	hypothetical prote
31	177	7.5	2468	2 A83412	hypothetical prote
32	176.5	7.5	893	2 A37284	surface-array prot
33	175.5	7.5	1275	2 T33369	hypothetical prote
34	174	7.4	585	2 F83809	hypothetical prote
35	173.5	7.4	1577	2 A35140	hemolysin A precur
36	173	7.4	1567	2 S11672	ice nucleation pro
37	172.5	7.3	1035	2 AD3203	autotransporter pr
38	172	7.3	585	2 F90961	flagellin (importe
39	171.5	7.3	1268	2 B99789	hemagglutinin/hemo
40	171.5	7.3	1270	2 E85649	hypothetical prote
41	171.5	7.3	1300	2 S07575	outer membrane pro
42	171.5	7.3	1430	2 AF0351	probable autotrans
43	171	7.3	978	2 D81411	probable lipoprote
44	171	7.3	3013	2 AB0480	probable invasin y
45	170	7.2	1052	2 AF2959	conserved hypotet

ALIGNMENTS

RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: G81133

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: G81133

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <FET>

A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match 94.1%; Score 2210.5; DB 2; Length 591;

Best Local Similarity 95.4%; Pred. No. 9.3e-110;

Matches 440; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

QY 2 DETGLINVETKLSFGANGKKVNIISDTKGLNPAKETAGTNGDPTTVHLNGIGSTLTDMLL 61

Db 132 DLTDLT SVGTEKLSFSANGKNVITSDTKGLNPAKETAGTNGDPTTVHLNGIGSTLTDTLL 191

QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKIGVKPGTTSADNDVFRVTDVTEFLS 121

Db 192 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKIGVKPGTTSADNDVFRVTDVTEFLS 251

QY 122 ADTKTTTVNVESKDNGKKEVKIGAKTSVTKEDGKLVTKGKGENGSSTDEGEGLVTAK 181

Db 252 ADTKTTTVNVESKDNGKKEVKIGAKTSVTKEDGKLVTKGKGENGSSTDEGEGLVTAK 311

QY 182 EVIDAVNKAQWRMKTITANGQTQADKFEFVTSCTKVTTFASNGTGTATVSKDQGNITVK 241

Db 312 EVIDAVNKAQWRMKTITANGQTQADKFEFVTSCTKVTTFASNGTGTATVSKDQGNITVK 371

QY 242 YDYNVGDALNVQLQNSGNLDSKAVAGSGKVISGNVSPSKKMDETVNNAGNIEIT 301

Db 372 YDYNVGDALNVQLQNSGNLDSKAVAGSGKVISGNVSPSKKMDETVNNAGNIEIT 431

QY 302 RGNKNTDIATSMTPQPFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITWVAPGVKE 361

Db 432 RGNKNTDIATSMTPQPFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITWVAPGVKE 490

QY 362 GDVTNVAQLKGVAGNQLNNRIDNVNGNARAGIAQAIATAGLVQAYLPCKSMMAIGGTYLG 421

Db 491 GDVTNVAQLKGVQALNNRINDVGNARAGIAQIAIATAGLVQAVLPKGSMAIGGGTYRG 550

Qy 422 EAGYAIGYSSISAGNNIIRKGTASNGRHFHGASASVGYQW 462

Db 551 EAGYAIGYSSISDGGNIIKGTASNGRHFHGASASVGYQW 591

RESULT 2

A81888

probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249)

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: A81888

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:2022556; PMID:10761919

A:Accession: A81888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-592 <PAR>

A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA1200

Query Match 90.9%; Score 2136; DB 2; Length 592;

Best Local Similarity 92.2%; Pred. No. 8.1e-106;

Matches 427; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

Qy 2 DETGLINVERTEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGISGTLTDLML 61

Db 132 DLTGILINVERTEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGISGTLTDLA 191

Qy 62 NTGATTTVNDVTDDEKKRAASKVQVNLNAGWNKGVKPGTTA--SDNVDFVRYTDFEF 119

Db 192 GSSASHVDAGNQST--HYTAASTKIDVNLNAGWNKGVKGTSTTGQSENVDVRYTDFEF 249

Qy 120 LSADTKTTTVNVEKDKNGKTEVKIGAKTSVIREKDKLVTKGKGKNGSGSTDEGELVT 179

Db 250 LSADTKTTTVNVEKDKNGKTEVKIGAKTSVIREKDKLVTKGKGKNGSGSTDEGELVT 309

Qy 180 AKEVIDAVNKGWRMKTNTTANGTGQADKPEFVTSFGKVTTFASGNGTTATVSKDDQGNIT 239

Db 310 AKEVIDAVNKGWRMKTNTTANGTGQADKPEFVTSFGKVTTFASGNGTTATVSKDDQGNIT 369

Qy 240 VKYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIE 299

Db 370 VMYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIE 429

Qy 300 ITRNGKNIDITATMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDANKPVRITNVAPGV 359

Db 430 ISRNGKNIDITATMTPQFSSVSLGAGADAPTLSDVDDGALNVGSKDANKPVRITNVAPGV 489

Qy 360 KEGDVTNVAQLKGVQALNNRINDVGNARAGIAQIAIATAGLVQAVLPKGSMAIGGGTY 419

Db 490 KEGDVTNVAQLKGVQALNNRINDVGNARAGIAQIAIATAGLVQAVLPKGSMAIGGGTY 549

Qy 420 LGEGYAIGYSSISAGNNIIRKGTASNGRHFHGASASVGYQW 462

Db 550 RGEAGYAIGYSSISDGGNIIKGTASNGRHFHGASASVGYQW 592

RESULT 3

I64138

adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997

C:Accession: I64138

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: I64138

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-298 <TIGR>

A:Cross-references: GB:U32846; GB:L42023; NID:gi574588; PID:gi574589; TIGR:HI1732

Query Match 16.6%; Score 390.5; DB 2; Length 298;

Best Local Similarity 48.9%; Pred. No. 6.9e-14;

Matches 91; Conservative 24; Mismatches 48; Indels 23; Gaps 5;

Qy 7 INVETEKLSDTTLTGNTTGAAGGATPKVTSITADGLKLAK---GTNGDTAVHLNGLAST 55

Db 114 LDVKTAKVSDTLTIGGNTTGAAGGATPKVTSITADGLKLAK---GTNGDTAVHLNGLAST 170

Qy 56 LTDMMLTGTATTVNDVTDDEKKRAASKVQVNLNAGWNKGVKPGTTASDNVDVRYTDF 115

Db 171 LPDVTNTGASTSVT-FSPSDIEKTRAATKIDVNLNAGWNKGVKAVAGGNTENVDLVAGYD 229

Qy 116 TVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIREKDKLVTKG-----GKGENG 168

Db 230 NVEFITGDKNTLDVLTAKENGKTEVKFTPKTSVIKDNNGKLLTKQLKADANTGTATNA 289

Qy 169 S-STDE 173

Db 290 TEDTDE 295

RESULT 4

A86036

probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: A86036

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: A86036

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1588 <STO>

A:Cross-references: GB:AE005174; NID:gi2518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP: A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z5029

Query Match 15.3%; Score 360; DB 2; Length 1588;

Best Local Similarity 24.9%; Pred. No. 2.2e-11;

Matches 141; Conservative 73; Mismatches 236; Indels 116; Gaps 18;

Qy 4 TGLINV---ETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGI----- 52

Db 1032 TQIINLAGNTDATYIQENGAGINVYRTNDDGLAFNDASAGQVGATAGTGVNVAKGDSV 1091

Qy 53 -----GSTLTDMMLNTGA-TTNTVNDNV-----TDDKKRAASKVQD- 87

Db 1092 AICQGSYSYDVTGTALGSSSVSRVIAKSRDTSITENGVIYGYDTTDDGELLGALSIGDD 1151

Qy 88 -----VNLNAGWNKGVKPGTTASDNVDVRYTDFVLSADTKTTTVNVEKDKNGK----- 138

Db 1152 GKYRQIIN-----VADGSEAHDAVT-VRQLQNAIGAVATTPPKYFHANSTEEDSLAVG 1203

Qy 139 KTEVKIGAKTSVIREK-----DCKLVTGKGRGE-----NGSSTDEGE 175

Db 1204 TDSLAMGAKITVNGDKIGIGYGAYVDANALNGIAIGSNAQVITHVNSIAIGNGSTTTTGA 1263

Qy 176 GLVTAKEVIDAVNKGWRMKTNTTANGQ-----TGQADKPEFVTSFGKVTTFASGNGTTA 228

[illegible][illegible][illegible]

Db 1719 HINGAISGGE--ING-HSDNSHGVE 1740

RESULT 13

A43855

high-molecular-weight surface-exposed protein HMW1 - Haemophilus influenzae

C:Species: Haemophilus influenzae

C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999

C:Accession: A43855

R:Barenkamp, S.J.; Leininger, E.

Infect. Immun. 60, 1302-1313, 1992

A:Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Haemophilus pertussis.

A:Reference number: A43855; MUID: 92192797; PMID: 1548058

A:Accession: A43855

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1536 <R>

A:Cross-references: GB:008876; GB:M84616; NID:9475770; PIDN:AAA20527.1; PID:9475771

A>Note: sequence inconsistent with the nucleotide translation

A>Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBIPI:89239)

Query Match 8.38; Score 195; DB 2; Length 1536;

Best Local Similarity 24.48; Pred. No. 0.011;

Matches 119; Conservative 68; Mismatches 191; Indels 110; Gaps 26;

Qy 8 NVTEKLSFGANGKVNIIISDTKGLNFAKETAGTN-----GDTTVHLNGIGSTLTQMLN 62

Db 858 NVTLIGSDFDNHQKPLTIKKDVI-INSGLTAGSNIVNAGNLTVESNANFKAITNFTFN 916

Qy 63 TGAT-TNVTNDNVTDDKBRASVKDVLNAGWMIKGVKPGTTASDNVDFVRYTDTVEFLS 121

Db 917 VGGFLDNKNGSNIS--IAKGGARFKDIDNS---KNLSITTNSS-----TYRTIISGN 964

Qy 122 ADTKTTTVNVESKDNKKTEVKIGAKTSVIKEDKGLVTKGK-----GEN 167

Db 965 ITNKNGLDNLITNE--GSDTEMQIGDVS---QKEGNLTISSDKINITKQITIKAGVDGEN 1019

Qy 168 GSSTDECEGLVTAK---EVIDAVNKGARMKTTTAN-----GOTGQADKFETVTSQT 216

Db 1020 SDSDATNNANLTIKTRELKLTQDLNITSGFNKAEITAKDGSDLITIGNTSADG---TNAK 1075

Qy 217 KVTF-----ASNGTGTATYSKDDQGNITVKYDVNVGDALNVNQLQNSGNLDSKAV 267

Db 1076 KVTFNQVKDKSIDAGHKVTLHSEKVTSGS-----NNNTEDSSD---NNAGLTIDAKNV 1126

Qy 268 AGSGKVIKSNVSPSKCKMDETVNIAGNIEITRNGKNIDIAF---SMTPTQSFSSVSLGA 324

Db 1127 -----TVNNNITSK-----AVSISATSGEITTKTGTINATTVGNVEITAQGSILGGI 1175

Qy 325 GADAPTLTSD-DEGALNVGSKDANKPVRIITNAPVKEGVDVTVNA--QLKGV-AQNLNLR 380

Db 1176 ESSSGSVTLTATGALAVNISGN-----TVTVTANSGALTYLAGSTIKGTSVTTSSQ 1229

Qy 381 IDNVNGNARAGIAQAATAGLVAQYLPGKSMMAIGGTYLGEAGYAGYSSISAGGNWII 440

Db 1230 SGDIGGTISGTTVEVKATESLITV-----QSNISKATV--GEANVT-----SATGT-I 1274

Qy 441 KGATASGNS 448

Db 1275 GGTISGNT 1282

RESULT 14

T31105

hypothetical protein 2 - Haemophilus ducreyi

C:Species: Haemophilus ducreyi

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T31105

R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.

J. Bacteriol. 180, 6013-6022, 1998

A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.

A:Reference number: Z20984; MUID: 99030326; PMID: 9811662

[illegible]

A:Gene: sapB

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Query Match      8.0%; Score 188.5; DB 2; Length 936;
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 119; Conservative 71; Mismatches 225; Indels 109; Gaps 25;

Qy 1 TDEGLINVEK--LSFGANGK-KVNII-----SDTKGLNFAKET---ACTNG 43
Db 310 TDASKSVNVEVTGTTAAGTGKVDVAGKITALTADTSATSVNLTATNDTITLTSANA 369
Qy 44 DTTVHLNGIGSTLFDMLLTGATTNTND-----NVTDDKKRAASVKDLNAGWNIGV 98
Db 370 ATSVNLKTGAASATITSANAANIITIDATGVAAVTSATAVENLTVKHATNVTLAGNMD 429
Qy 99 KPQTASDNDVF-----VRTYDVEFLSADTKTTTVNVESKD-----NGKKTEVKIGA-- 146
Db 430 KLATVTLDNAALTAADIKSASTLNLNSSVNGHNISTAAKDVTVHLSGSAKVKLNTTA 489
Qy 147 ---KTSVIKEK--DGKLVTKGKGSGSSTDEGEG---LVTAKEVIDAVNKAQWRMKT 198
Db 490 ATDQTVTLKANATDNSLEFDSGTAKTTSVTASGSGKTLVIKGAETLVN-----IDTTA 544
Qy 199 AN-----GOTGOADKF--ETVTSGTKVTFASNGGTTATVSK--DDQGNITVKYDVNVG 247
Db 545 FNGAADVSFGKDAQSGKFSVKTGTGDDKIEFV---GTTLTEGVSIDGAGNDTIAMKSAAL 601
Qy 248 DALNVNQLONGWNL---DSKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITR-- 302
Db 602 TSANFTWIKNIE-NVAISDAVATADLSSSAFKNIIITTKAADTTLTKDQVINFATAAD 660
Qy 303 -----NGKN--IDTATSMTPQFSSVSLGAGADAPTLSVDDE--GALNVGS-K 344
Db 661 RGSVKLITVKLNDVTGANDVVKIVLDAAAKDAISALGTEATDKALVIDTGIETLINITSLV 720
Qy 345 DANKPVRITNVAPGVKEGVDVTNVAQLKGVAQNLNRRIDNVNGNARAGIAQAIATAGLVQA 404
Db 721 KATSPENTANTV-NAKLTDTVTSII-----IDGDAKITLGHA-GTAGTDYS 763
Qy 405 YLPKSMMAIGGGTYLGEAGYAGYSSISAGGNWIKGTASGNS 448
Db 764 KVSMDARAL-----KAGLTEDASAITLGNATIKGGSGADS 800
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Search completed: October 6, 2003, 09:33:37
Job time : 16.2249 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 7.13446 Seconds
(without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-36

Perfect score: 2350

Sequence: 1 TDEGLINVEYKLSFGANG.....TASGNSRGHFGASASVGYQW 462

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	187.5	8.0	2249 1	OMPA_RICRI
2	187	8.0	2003 1	YDBA_ECOLI
3	180.5	7.7	1655 1	OMPBB_RICCN
4	180	7.7	1654 1	OMPBB_RICRI
5	179.5	7.6	737 1	ALYS_ENTFA
6	178	7.6	1953 1	BIGA_SALTY
7	177	7.5	1039 1	AG43_ECOLI
8	177	7.5	1656 1	OMPBB_RICJA
9	173.5	7.4	1577 1	HLVA_PROMI
10	173	7.4	1567 1	ICEN_XANCT
11	172.5	7.3	933 1	SLAP_CAMFE
12	170	7.2	1300 1	120K_RICRI
13	168	7.1	2021 1	OMPA_RICCN
14	166	7.1	1645 1	OMPBB_RICRY
15	165	7.0	1325 1	YDEK_ECOLI
16	164	7.0	1025 1	SLAP_CAUCR
17	163	6.9	1569 1	YFJA_ECOLI
18	161	6.9	1608 1	HLVA_SERMA
19	159	6.8	1286 1	AIDA_ECOLI
20	156.5	6.7	1007 1	Y741_CHLMU
21	156	6.6	1861 1	APU_THETU
22	155	6.6	948 1	HP11_DEIRA
23	154.5	6.6	1005 1	Y456_CHLTR
24	152.5	6.5	918 1	YVJB_CAEEL
25	152	6.5	1694 1	IGA0_HAEIN
26	152	6.5	1702 1	IGN2_HAEIN
27	151	6.4	550 1	FLIC_SHIEL
28	151	6.4	1643 1	OMPBB_RICPR
29	150.5	6.4	2660 1	YEEJ_ECO57
30	150	6.4	1148 1	ICEK_PSESX
31	150	6.4	1210 1	ICEN_PSEFL
32	149.5	6.4	484 1	P60_LISMO
33	149.5	6.4	2358 1	YEEJ_ECOLI

RESULT 1				
OMPA_RICRI				
ID	OMPA_RICRI	STANDARD;	PRT;	2249 AA.
AC	P15921;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).			
GN	OMPA.			
OS	Rickettsia rickettsii.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;			
OC	Rickettsiaceae; Rickettsiella; Rickettsia.			
OX	NCBI_TaxID=783;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=R:			
RX	MEDLINE=90354033; PubMed=2117568;			
RA	Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;			
RT	"A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";			
RL	Infect. Immun. 58:2760-2769(1990).			
CC	- - FUNCTION: ELICITS PROTECTIVE IMMUNITY.			
CC	- - SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.			
CC	- - PTM: GLYCOSYLATED (PROBABLE).			
CC	- - SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.			
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CC	EMBL; M31227; AAA26380.1; -.			
DR	PIR; A41477; A41477.			
DR	InterPro; IPR006315; Autotransport.			
DR	InterPro; IPR005546; Autotransporter.			
DR	Pfam; PF03797; Autotransporter; 1.			
DR	TIGRfams; TIGR01414; autotrans_bar1; 3.			
KW	Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.			
FT	SIGNAL	.1	28	POTENTIAL.
FT	CHAIN	29	2249	OUTER MEMBRANE PROTEIN A.
FT	DOMAIN	212	1180	13 X APPROXIMATE TANDEM REPEATS.
FT	REPEAT	212	286	A (TYPE I).
FT	REPEAT	287	358	B (TYPE II).
FT	REPEAT	359	430	C (TYPE II).
FT	REPEAT	431	505	D (TYPE I).
FT	REPEAT	506	577	E (TYPE II).
FT	REPEAT	578	652	F (TYPE I).
FT	REPEAT	653	724	G (TYPE II).
FT	REPEAT	725	799	H (TYPE I).
FT	REPEAT	800	874	I (TYPE I).
FT	REPEAT	875	949	J (TYPE I).

Db 556 GAHGVENIGDNTVANKGDIVVSDRTSGVINGEGATVSNVNTGDNVNS-NEATGFSITN 614
QY 304 GKNIDIAISM-TPOFSS-VSLGAGADAPTLSDVDD-----EGALNVGSKDANKPVRITN 354
Db 615 SGKVSLAGSMQVGFSTGVDLNNNSVTLAAKDLKVVQKATGINV-SGDAN-TVNITG 672
QY 355 VAPGVKEGDTNVAQL-----KGVAQNLNRIDNVGNARAGI-----AQAI 396
Db 673 NVLVDKDKTADNAAEYFFDPVSGVINGVSDNNVTLDGKLTIVVSDSEVTSRQSNLFDGSAE 732
QY 397 ATAGLVQVAYLPGCKSMMAITGGTGLGE-----AGYAI-----GYSSISAG 435
Db 733 KTSGLV-VIGDNTVMNMGGLELGEKNALADGSOVTSRLRTGTSYTSVIVVSGESSVYLN 791
QY 436 GNWIIKG 442
Db 792 GDTTISG 798
RESULT 3
ID OMPB_RICCN STANDARD; PRT; 1655 AA.
AC O9KKA3: O9KK98; Q9XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOMPb)
DE (OMP B) (Contains: 120 kDa surface-exposed protein (Surface protein
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
gene coding the outer-membrane protein rOMPb (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ-databases.
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
SIMILARITY).
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
(BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPb FAMILY.
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CC -----
DR EMBL; AE008659; AAL03623.1; -;
DR EMBL; AF123721; AAF34124.1; -;
DR EMBL; AF123726; AAF34129.1; -;
DR EMBL; AF149110; AAD39533.1; -;
DR PIR; E97835; E97835.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.
FT CHAIN 1335 1655 32 kDa BETA PEPTIDE.
FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).
FT CONFLICT 353 354 KD -> GH (IN REF. 3).
FT CONFLICT 776 776 F -> S (IN REF. 3).
FT CONFLICT 1159 1159 E -> D (IN REF. 3).
FT CONFLICT 1177 1177 G -> S (IN REF. 3).
FT CONFLICT 1492 1492 H -> R (IN REF. 3).
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D3FCE37 CRC64;
Query Match 7.7%; Score 180.5; DB 1; Length 1655;
Best Local Similarity 24.2%; Pred. No. 0.054;
Matches 121; Conservative 59; Mismatches 225; Indels 95; Gaps 26;
QY 19 NGKVNIIISDTKGLNPAKETAGTNGDTTV-HLNGTSGSTLTLMLLTGATNTVT-NDNV-T 75
Db 340 NGKVATIDGQVYAKDMVIGSANAVGQVNFHRHVDVGTGTTAFKTAASVAITQNSNFGT 399
QY 76 DDEKKRAASV---KDVLNAGNINIKVKGPGTTASDNVDFVRYD---TVVEFLSADPKTTT 128
Db 400 TDFGNLAQIIVPNTMTLNGNFTGDASNPGTAG-----VITFDANGLTASASADANVAV 454
QY 129 VN-----VESKNG-----KKEVKGIAKTSVIREKDGKLVTKG-----GKGENG 169
Db 455 TNNITAIERASGAGVQVLSGTHAAELRLGNAGSVFKLADGTGVINGKVNQTALVGGALAGT 514
QY 170 STDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVT-----SGTKVTF 220
Db 515 ITLDGSATITG---DIGNAGG---AAALOGITTLANDATKTLTLGGANIIGANGGTINF 566
QY 221 ASNGTGTATVSKDDOGNITVKYDV-----NVGDALNVNQLQNSGNWLDKRAVAGSSGK 273
Db 567 QANGGTIKLTS---TQNNIVVDFDLAIATDQTGVVDASSLTNAQTTLTKINGIGTVGANNKT 624
QY 274 VISGNVSPSKGKM-DETVNIN---AGNN---IETTRGNKIDIAITSTPQ-----FSSV--- 320
Db 625 LQGFNIGSSKTVLSDGDVAINELVIGNGAVQFAHTYLTITRTNAAGOGKIIFNPVNN 684
QY 321 --SLGAGADAPILSDVDEGALNVGSKDANKPVRITNVAPGVKEGDTNVAQLKGVQNLN 378
Db 685 NTTLATGTNLGS-ATNPLAEINFGSKGAANVDVTLNVGKGNL-YATNITTTDA---NVG 739
QY 379 NEDVNVG-NARAGIAQAATATAGLVQ-----AYLPKSMMAIGGTVLGEAGYAGYS 430
Db 740 SIFNAGGTNIVSG-----TVGGQGNKFNFTVALDNGTTVKFLGNATNGNTTAAAN-S 792
QY 431 SISAGNWTIKGTASGNSRG 450
Db 793 TLQIGGNYTADFVASADGTG 812
RESULT 4

455 TNNITAIEASGAGVWVSGTHAAELRLGNAGSIFKILADGTVINQKVNQIALVGGALAAAGT 514

170 STDEGEGLVTAKEVIDAVNKGAGRMKMTTANGOTQOADKFETVTSGETKVTFFASNGNT --- 226

515 IITLDGSATITGD--IGNAGGAALQRITLAN-----DAKKTLITLGGANIIGAGGTIDL 566

227 -----TATVSKDDQGNITVKYDV-----NVGDALNVNOLQNSGWN-----LD 263

567 QANGGRIKLTST-----QNNIVVDFDLAIATDQTGVVDASSLTNAQTTLTINGKIGTIGAN 621

264 SKAVA---GSSGKVLS-GNVSPSKGMDETVINAG-----NNIEITR-----NGKN 306

622 NKTLOGFNIGSSKTVILNSGVA-----INELVTGNDGAVQFAHDTYLTITRTNNAOGGKI 676

307 I--DIATSMTPQSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDV 364

677 IFNPVVNNGTTLAAGTNLGS-----ATNPLAEINFGSKGVNVDI-VLNVGEGVNL-YA 727

365 TNVAQLKGVANQNNRINDNVNG-NARAGIAQAIAATAGLVQ-----AYLPKGSMAIIGG 416

728 TNIITTTDA---NVGSFVNAGGTNIVSG-----TVGGQGGNKFNVTVALENGTTVKFLGN 778

417 GYVLGAGAGYAIGYSSISAGGNWIIKGTASGNSRG 450

779 ATPNGNTTIAAN-STLIQIGGNYTADCVASADGTG 811

RESULT 5

ALYS_ENTFA

ID	ALYS_ENTFA	STANDARD;	PRT;	737 AA.
AC	P37710;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	15-SEP-2003 (Rel. 42, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Autolysin precursor (EC 3.2.1.-) (Peptidoglycan hydrolase)			
GN	(Beta-glycosidase).			
OS	Enterococcus faecalis (Streptococcus faecalis).			
OC	Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.			
OX	NCBI_TaxID=1351;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91358349; PubMed=1679432;			
RA	Beliveau C., Potvin C., Trudel J., Asselin A., Bellemare G.;			
RA	"Cloning, sequencing, and expression in <i>Escherichia coli</i> of a			
RT	<i>Streptococcus faecalis</i> autolysin.";			
RL	J. Bacteriol. 173:5619-5623(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=V583 / ATCC 700802;			
RC	MEDLINE=22550857; PubMed=12663927;			
RA	Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,			
RA	Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,			
RA	Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,			
RA	Dougherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,			
RA	Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,			
RA	Ufferbach T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;			
RT	"Role of mobile DNA in the evolution of vancomycin-resistant			
RT	<i>Enterococcus faecalis</i> .";			
RL	Science 299:2071-2074(2003).			
CC	-I- FUNCTION: Hydrolyzes the cell wall of <i>E.faecalis</i> and			
CC	<i>M.lysodeikticus</i> . May play an important role in cell wall growth			
CC	and 'cell separation.			
CC	-I- SUBCELLULAR LOCATION: Secreted (Probable).			
CC	-I- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOLYCAN			
CC	BINDING.			
CC	-I- SIMILARITY: BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.			
CC	-----			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			

TIGRFAMS; TIGR01414; autotrans_bar1; 1.
KW Outer membrane; Signal; Complete proteome.
FT SIGNAL 1 52
FT CHAIN 53 551 ANTIGEN 43 ALPHA CHAIN.
FT CHAIN 552 1039 ANTIGEN 43 BETA CHAIN.
FT VARIANT 2 2 K -> N (IN STRAIN ML 308-225).
FT VARIANT 41 42 SL -> FF (IN STRAIN ML 308-225).
FT VARIANT 46 46 T -> K (IN STRAIN ML 308-225).
FT VARIANT 157 157 W -> L (IN STRAIN ML 308-225).
FT VARIANT 188 188 V -> F (IN STRAIN ML 308-225).
FT VARIANT 303 305 ATN -> STI (IN STRAIN ML 308-225).
FT VARIANT 320 320 A -> T (IN STRAIN ML 308-225).
FT VARIANT 372 372 N -> Q (IN STRAIN ML 308-225).
FT VARIANT 493 493 E -> V (IN STRAIN ML 308-225).
FT VARIANT 497 497 S -> N (IN STRAIN ML 308-225).
FT VARIANT 585 585 H -> Y (IN STRAIN ML 308-225).
FT VARIANT 709 709 E -> K (IN STRAIN ML 308-225).
FT VARIANT 721 721 M -> T (IN STRAIN ML 308-225).
FT VARIANT 751 753 GHL -> SHF (IN STRAIN ML 308-225).
FT VARIANT 803 803 S -> P (IN STRAIN ML 308-225).
FT VARIANT 815 815 A -> V (IN STRAIN ML 308-225).
FT VARIANT 824 824 C -> S (IN STRAIN ML 308-225).
FT VARIANT 829 835 LNLVHTS -> MNLINYA (IN STRAIN ML 308-225).
FT VARIANT 845 847 QGT -> LGA (IN STRAIN ML 308-225).
FT VARIANT 855 855 S -> T (IN STRAIN ML 308-225).
FT VARIANT 888 888 Q -> L (IN STRAIN ML 308-225).
FT VARIANT 1025 1025 S -> I (IN STRAIN ML 308-225).
FT CONFLICT 61 63 ENV -> TTT (IN REF. 5).
SQ SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEEBE0 CRC64;

Query Match
Best Local Similarity 7.5%; Score 177; DB 1; Length 1039;
Matches 114; Conservative 84; Mismatches 206; Indels 144; Gaps 28;

QY 5 GLINVETKLSFG-ANGKVNIIISDTKGLNFAKET-----AGTNGDTTHLNGI 52
DB 66 GTLANHDNIQVFTGTMGI-----STGLEYPDNEANTGGQVDDGGTANTTTSGL 120
QY 53 -----GSTLIDMLLTGATTNV-----TNDNVTDDEK---KRAASVKDLN-AGWNKGVK 99
DB 121 QRNVNPGGSDIVISAGGQSLOGRAVNTLNGGEQWHEGAIATGTVINDKGWQV--VK 178
QY 100 PGTASDNDVDFRT-----YDTVEFLSADTKTTVN-----VESKDKGKTEYK 143
DB 179 PGTATDTV--VNTGAEGGPDANGDTGQFVRGDVARTTINKNGRIQVRAEGTANTTVVY 236
QY 144 ICAKTSV-----IKEKDKLVTGKKGKNGSGSTDEBEGLV 178
DB 237 AGGDQTVHGHALDTTLNGSYQYVHNGGTASDTVYVNSDGMQIVKNG-GVAGNTTVNQKGR 295
QY 179 TAKEVIDAVN---KAGWRMKTITANGQT-----GOADKFETVTSKVTTFASG 223
DB 296 QVDAGGTATNVILKQGGALVTSTAATVGTGIRLGAFFSVVEGRADNV-VLENGGRDLVLTG 354
QY 224 NGTTATVSKDDGNTITVKYDVNVDALNVQNLQNSGWNLDKAVAGSSGKVIISGNVSPK 283
DB 355 HTATNT-RVDDGDTLDR---NGGTATTVS-MNGGG-----VLLADSGAAVSGTSDCK 403
QY 284 -----GKMDETVNIAGNIEITRNGKNIDIAITMTPOFSSVSLGAGADAPLSVDDEGA 338
DB 404 AFSIGGGQADALMLEKSSFTLNAG-----DTATDTTVNGGLTFARGGTLAGTTLNNGAI 459
QY 339 LNVGSKDANKPVRIJTVNAPVKGEGDVTNVAQLKGVAQNINLRDINNVNGNARAGIAQAIAT 398
DB 460 LFLSKTVN-----NDTLITREGD-----ALLQGSGLTNGSGVEK-SGSGTLTVTSNTT 508
QY 399 AGLVQAYLPKGMMAIGGTT-----YLGEAGYAIYS-----SISAGGNWII 440
DB 509 QRAVNL---NEGTFLINDSTVTVDVIAQRGTALKTGTVNLGAIADPTNVLASGATWNI 565
QY 441 KGTASGNS 448
|: |

Db 566 PDNATVQS 573
RESULT 8
OMP_B_RICJA STANDARD; PRT; 1656 AA.
AC 006653;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rompB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia japonica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=35790;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YH;
RA Uchiyama T.;
RT "Sequencing of the gene encoding the protein romp B of Rickettsia japonica";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY SIMILARITY).
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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DR EMBL; AB003681; BAA20138.1; -
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRFAMS; TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1338 120 kDa SURFACE-EXPOSED PROTEIN.
FT CHAIN 1339 1656 32 kDa BETA PEPTIDE.
FT DOMAIN 528 533 POLY-GLY
FT SEQUENCE 1656 AA; 168097 MW; 3132A69C9DD5999F CRC64;
SQ

Query Match
Best Local Similarity 7.5%; Score 177; DB 1; Length 1656;
Matches 138; Conservative 61; Mismatches 212; Indels 208; Gaps 30;

QY 1 TDETGLINVETKLSFGANG-----KKVNIISDTKGLNFAKETAGT 41
DB 193 TOKAPULADNALIVNGANGTLNVTNGFTIQVSDKSFATVKAIN-IGDGGGFMTNATNA 251
QY 42 N-----GDTTVHLNCGIGSTLTDMLLN-TGATTNVTNDNVTDDKRAASVKDVLNAGWN 94
DB 252 NALNLQAGGTTTINFTDGTGRLVLLSKNGAATDF---NVTG-----SLGN 295
QY 95 IKGKVPGGTTASDNVDFRTYDVEFLSADTKTTTVN-----VESKDKGKTEY--KI 144
DB 296 LKGIIELTNVAINGQLIANAG-----PANAVICTNNGAGRAAGFVVSVDNGRAATIDGOV 350
QY 145 GAKTSVIKE-----KDKLVTKGKGKNGSGSTDEBEGLVTA 181
|: |

Db 351 YAKDMVIOANANGQVNRHIVDVGDIGTGTAFKTAASIVAITONSNGFTDFG-NLAAQV 409
Qy 182 EVIDAVNKAQWRMKTITTTANGQTQADKFEVTISGTVTFASNGTGTATVSKDQGNITVK 241
Db 410 TVPDTM-----TLTGN-FTGDANN-PGNTAGV-ITPAA-NGTLASASAD--ANVAVT 455
Qy 242 YDYNVGDALNVNQLNGWNLDSKAV--AGSSKSVISGNSVPSKGMDETIV----- 290
Db 456 NNITAIEASGVGVQLSGTHTABLRNLGNAGSVEFLADGTV--INGKVNQTVLVGGVLAAG 513
Qy 291 -----NINA-GNNI 298
Db 514 AITLDSGATITDIGNGGGGAALQSTILTANDATKTLTLCGANIISANGGTINFQANGGTI 573
Qy 299 EITRNGKNI-----DIATSMTPQFSSVSLGAGADAPTLSVDDE-----GALNVS 343
Db 574 KLIFSTONNIVVDCDLATA-TDQGVVDASSLTNAQTLTISGTIGIIGANNNTTLGQFNIGS 632
Qy 344 KDA---NKPVRITNVPAGVEGDV-----TNVAQLKGVAQNLNRRIDNVNGNARAG 391
Db 633 SKTTLNGGNVAINELVIG-NGGSVQFAHNTYLTIRTTNAAAGQGIIFNPVYVNNNTTLAAG 691
Qy 392 IAQAIATAGLVQVLPCK-----SMMAIGGGTVLGEAGYA-----IGYSSISAGGN 437
Db 692 TNLGSAANPLAEINFGSKGARADTVLVNGGVNL-----YATNITTTDANVGSFVNAGGK 747
Qy 438 WIIKGTASNGSRGHFGASA 456
Db 748 NIVSGTVGGQGNKENTVA 766

RESULT 9

HLVA_PROMI STANDARD; PRT; 1577 AA.
ID HLVA_PROMI
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN=Isolate 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serattia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
CC -----
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CC -----
DR EMBL; M30186; AAA25657.1; -.

DR PIR; A35140; A35140.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 7.4%; Score 173.5; DB 1; Length 1577;
Best Local Similarity 22.6%; Pred. No. 0.12;
Matches 132; Conservative 85; Mismatches 168; Indels 199; Gaps 35;

Qy 8 NVETKLSFGANGKKNYIISDTKGLNFA---KETAGT-----NG 43
Db 711 STTEQANSTISGANDVLOAN-KDVTAGSDLTATTAGNASITGDNVAFVSTENKKQTDNT 769
Qy 44 DTFVH-----LNGIGS-----TLTDLMLLTGATTNVTND-NVTDDEKKRAAS 84
Db 770 DTTISGFSYTGVDKVGKADFOYDKQHTQTEVTKNRGSOEAVAGDLTITAN----- 822
Qy 85 VKDVLNAGWNIGVKPGCTTASDNVD--FVPTYDTVEFL---SADTKTTTVN----- 131
Db 823 -KDLLHEG-----ASHVEGKYQESGENIOHLAVNDSETSKTDSLNVGIDVGVN 870
Qy 132 -----ESKDNKGKTEVKIGARTSVIKE---KD-----GKLVTG 161
Db 871 LDYSGVTKPKVKAIEDGVNT-TKPGNNTDLTKVTARDAITANLANLSNLETNPNGVEGI 929
Qy 162 KKGKENGSSDE---GEGLVTAKEVIDAVNK---AGWRMKT-----TANGOTGQA--D 207
Db 930 KGGGSOQSDSQAVSTSIINAGKIDIDSNKHLHQDQGHYQSTQEGISLTANTHTSEATLD 989
Qy 208 KFETVTSGTK-----VTFASNGTITATVSKDDQGNITVKYDVNVGDALNVNQLNSGW--N 261
Db 990 KHQTTTHETKGGQIGVSTRTGSDITVAIKGEQTT-----DNALMETKAGSOFTSN 1042
Qy 262 LDSKAVAGSSCKVISGNVSPSKGMDTVAINAGNIEITR-----NGK-NID 308
Db 1043 GDISINVENAHYEGAQFDQKCK---TV-INAGGDLTLAQATDTHSESQSNVNGSANLK 1098
Qy 309 IATSMTPQFSSVSLGAGADAPTIL-SVDDEGALNVGSKDANKPVRTNVPAGVKEGDTNV 367
Db 1099 VGT--TPE--SKDYGGGFNAGTTHHSKEQTTAKVGTITGSGQIELNAGHNLTLQG--THL 1152
Qy 368 AOLKGVAQNLNRRID-----NVNGNARAGIAQAIATAGLVQVLPCKSM--- 411
Db 1153 SSEQDIALNATNKVDLOSASSEHTEKGNLSGGVQAGF-----GKKMTDD 1197
Qy 412 -MAIGGTVLGEAGYAIG---YSSISAGGNWIKG---TASGNS 448
Db 1198 ASSVNG---LGSQAQFALGKODEKSVSREGGTINNSGNLTNGNS 1238

RESULT 10

ICEN_XANCT STANDARD; PRT; 1567 AA.
AC P18127; 1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X56S;
RX MEDLINE=91080859; PubMed=2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from Xanthomonas campestris pv. translucens.";
RL Mol. Gen. Genet. 223:163-166(1990).
CC -!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE

"Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";
Gene 140:115-119(1994).

[2]
RT STRAIN=Malish 7;
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";
RL Science 293:2093-2098(2001).
RN [3]
RN SEQUENCE OF 8-204 FROM N.A.
RC STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;
RX STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;
RA Roux V., Fournier P.-E., Raoult D.;
RT "Differentiation of spotted fever group rickettsiae by sequencing and
analysis of restriction fragment length polymorphism of PCR-amplified
DNA of the gene encoding the protein rOmpA";
RL J. Clin. Microbiol. 34:2058-2065(1996).
RN [4]
RN SEQUENCE OF 953-2012 FROM N.A.
RC STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;
RA Raoult D., Fournier P.-E., Roux V.;
RT "Phylogenetic analysis of spotted fever group rickettsiae by study
of the outer surface protein rOmpA";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- PTM: GLYCOSYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC -----
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CC -----
DR EMBL: U01028; AAA17405.1; -;
DR EMBL: AE008674; AAL03811.1; -;
DR EMBL: U43794; AAB49549.1; -;
DR EMBL: U43798; AAB49550.1; -;
DR EMBL: U43806; AAB49551.1; -;
DR EMBL: U45244; AAB49556.1; -;
DR EMBL: U46918; AAB46663.1; -;
DR EMBL: U83440; AAC35176.1; -;
DR EMBL: U83443; AAC35179.1; -;
DR EMBL: U83448; AAC35184.1; -;
DR EMBL: U83453; AAC35189.1; -;
DR InterPro: IP006315; Autotransport.
DR Pfam: PF03797; Autotransporter; 1.
DR TIGRfams: TIGR01414; autotrans_baril; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;
KW Complete proteome.
FT SIGNAL 1 38
FT CHAIN 39 2021
FT DOMAIN 238 946
FT DOMAIN 1424 1528
FT VARIANT 60 60
FT VARIANT 76 76
FT VARIANT 86 137
FT VARIANT 126 133
FT VARIANT 953 954
FT VARIANT 1245 1245
FT VARIANT 1308 1308
FT VARIANT 1877 1877
FT CONFLICT 10 10
FT CONFLICT 92 92

FT CONFLICT 126 126
FT CONFLICT 137 137
FT CONFLICT 157 157
FT CONFLICT 368 368
FT CONFLICT 374 388
FT
FT CONFLICT 640 640
FT CONFLICT 669 669
FT CONFLICT 793 793
FT CONFLICT 803 804
FT CONFLICT 809 823
FT
FT CONFLICT 898 898
FT CONFLICT 908 908
FT CONFLICT 985 985
FT CONFLICT 1009 1009
FT CONFLICT 1013 1013
FT CONFLICT 1182 1182
FT CONFLICT 1314 1314
FT CONFLICT 1451 1451
FT CONFLICT 1624 1624
FT CONFLICT 1628 1628
FT CONFLICT 1872 1872
FT CONFLICT 1875 1875
FT CONFLICT 1878 1879
FT CONFLICT 1936 1936
FT CONFLICT 1965 1970
FT CONFLICT 1997 1997
SQ SEQUENCE 2021 AA; 203328 MW; 327FC42D7CB24668 CRC64;

Query Match 7.1%; Score 168; DB 1; Length 2021;
Best Local Similarity 21.8%; Pred. No. 0.29;
Matches 134; Conservative 65; Mismatches 209; Indels 208; Gaps 30;

QY 2 DETGLINVEKLSFGANGKKVNIISDTKGLNFAKETAGTAGNGDTTHVNLGIGSTLTDMLL 61
DB 625 DNTGNAN-----NG---IVTFTGNSTVTGNTGNATATVNV-GAGIATLEGAV 669
QY 62 NTCATTNVTNDVNTDDEKKRAASVKDVLNAGWKVKGPGTASDNDVDFVRYDTVEFLS 121
DB 670 IKATTKLYN-----AASVLTITNVNAVLTGAIDNTTGVDNVGVNLNAGLSQVT 719
QY 122 ADTKTT-----TVNV-----ESKDNG---KKEVTKIGAKTSVIKERDGLVGTG---KKGGEN 167
DB 720 GNIGNTNALATISVGAGKATLGGAVIKATTTKLTDNASAVTFNPVVVTGAI DNTGNANN 779
QY 168 GSSTDEGEGLVTAK-----EVIDAVNKA-----GWRMKTITAN----- 200
DB 780 GIATFTGDSVTGNTGNATATVNVGAGLLRVQGGVYKSNNTINLTDNASAVTFNPVVV 839
QY 201 ---GOTGOADK-FETVTSKTKVTFASGN-GTTATVS-----KDD 234
DB 840 TGAIDNTGNANGIVTFTGDSVTGNTGNATATISVGAGKATLGGAIKATTTKLTDN 899
QY 235 QGNITVKYDVNVGDALNVNQLNSKAVAGSGKVISGNVSPSKGMBDET VINA 294
DB 900 ASAVTFTNPVVTGAID-----NTG-NANGNIVTFTGDSVTGNTGNATNAL--ATVNVGA 951
QY 295 GNNIEI--FRNGKNIDIATSMTPQFSVSLGACADAP-----TSLVDDEGALNVGSK--- 344
DB 952 GVTLOAGGSLDANNIDFGARSTLEFNGLDGGGNAIPYKPGAINGNNAILNVNTKLLT 1011
QY 345 -----DANK-PVRITN----- 354
DB 1012 AYHLTGTVAEINIGAGNLFAIDASAGDVTILNAQDIHFALDSALVLSNLTGVVNNIL 1071
QY 355 -----VAPGYKEGDV-----TNVAQLKGVAQNLRNIDVNGNA-----R 389
DB 1072 LAADLVAPGVDEGTVVFDGGVGNLIGSNVA---GAARN---IGDVGNGKFTLLIYNA 1124
QY 390 AGTAQAIATAGLVQAVLPKG-----SMATGGGT-YLGEAGYAI-----GYSSISAGG----- 436
DB 1125 VTITDDVNLEGIONVLINNADFTSSTAFNAGTIQINDATYTTIDANNGLNIPAGNIKFA 1184

Qy 437 ---NWIIKGTASNSR 449
 Db 1185 HADAQLILQSSGND 1200

RESULT 14
 OMPB_RICTY STANDARD; PRT; 1645 AA.
 AC P6989;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)
 DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOMPb)
 DE (rOMP B) [Contains: 120 kDa surface-exposed protein (Surface protein
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
 GN OMPB OR SLP.

OS Rickettsia typhi.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=785;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wilmington;
 RX MEDLINE=94040787; PubMed=8224886;
 RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
 RT "Cloning and sequence analysis of the gene encoding the crystalline
 surface layer protein of Rickettsia typhi.";
 RL Gene 133:129-133(1993).
 RN [2]
 RP PARTIAL SEQUENCE.
 RC STRAIN=Wilmington;
 RX MEDLINE=92114896; PubMed=1370573;
 RA Ching W.M., Carl M., Dasch G.A.;
 RT "Mapping of monoclonal antibody binding sites on CNBR fragments of
 the S-layer protein antigens of Rickettsia typhi and Rickettsia
 prowazekii.";
 RL Mol. Immunol. 29:95-105(1992).
 RN [3]
 RP IDENTIFICATION OF CLEAVAGE SITE.
 RX MEDLINE=92104668; PubMed=1729180;
 RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
 RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
 membrane protein of rickettsiae: identification of an avirulent
 mutant deficient in processing.";
 RL Infect. Immun. 60:159-165(1992).
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
 CC S-LAYER WITH HEXAGONAL SYMMETRY.
 CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPb FAMILY.

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CC EMBL; L04661; AAB48987.1; -
 CC PIR; JN0896; JN0896.
 CC InterPro; IPR006315; Autotransport.
 CC InterPro; IPR005546; Autotransporter.
 CC Pfam; PF03797; Autotransporter; 1.
 CC TIGRFAMs; TIGR01414; autotrans_bar1; 1.
 CC Antigen; S-layer; Transmembrane; Cell wall.
 CC CHAIN 1 1353 120 kDa SURFACE-EXPOSED PROTEIN.
 CC FT CHAIN 1354 1645 32 kDa BETA PEPTIDE.
 CC FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).

FT CONFLICT 657 657 H -> N (IN REF. 2).
 FT CONFLICT 842 842 V -> I (IN REF. 2).
 FT CONFLICT 1071 1071 G -> A (IN REF. 2).
 FT CONFLICT 1306 1306 G -> S (IN REF. 2).
 SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;

Query Match 7.1%; Score 166; DB 1; Length 1645;
 Best local similarity 22.4%; Pred. No. 0.29;
 Matches 136; Conservative 59; Mismatches 209; Indels 204; Gaps 31;

Qy 1 TDEGLINVEKLSFGANG-----KKVNIISDTKGLNFAKETAGT 41
 Db 193 TQEAPLTLGNNAKIVANGANGLLNTNGFVKVSKDTFAGIKTIN-IGNQGLMFWTTDDAA 251
 Qy 42 N-----GDTTVHLNGIGSLTLLMLNTGATNTVNDVTDDEKKRAASVKDVLNAGWNI 95
 Db 252 NALNLOGGGNTINFNGRDG--TGKLVLSKNGNATEFNVTG-----SLGNNL 296
 Qy 96 KGV-KPOTTA-----SDN-----VDFVRYTYVEFLSADTKTTTVNVE 132
 Db 297 KGVIEFDTTAAAGKLIANGGAANAVIDGNGAGRAAGFIVSD-----NGNAATISGVY 351
 Qy 133 SKD-----NGKKT-----EVKIGAKTSVIKEKDKLVTKGKGGENGS--STDEG-- 174
 Db 352 AKDIVIOSANAGQVTFEHLVDVGLGKTN-FKTADSKVII-----TENASFGSTDFGNLA 406
 Qy 175 -----EGLVTAKEVIDAVNK---AGWRMKTITTANGO--TGQADKPFETVIS-----G 215
 Db 407 VQIVVPPNKKILTGNFIDGAKNNGTAG--VITFNANGTLVSGNDPNIVVTINIKAEIVEG 464
 Qy 216 TKVTFASG-----NGTTATVSKDDOGNITVKYDVNVGDALNVQNLQNSGNWLDKAVA 268
 Db 465 AGIVQLSGIHGAELRLGNAGSIEFKLDGTV-INGPVNQNPVNNALAAAGSIQDGSAIL 523
 Qy 269 GSSGKVLISGVNSPSKGMDET-----VNTNAGNIIETTRNGKI----- 307
 Db 524 --TGDI--GNCVNAALQDITLANDASKILTSLGANIIGANAGAIHFQANGTIQTST 579
 Qy 308 -----DIATSMTPQFSSVSL-----GAGADAPTLSVDDEGALNYGSK 344
 Db 580 QNNILVDFDLDTTQDTQGVVDASSLTNNQTLINGSIGTIGANTKL-----GRFNVGSS 634
 Qy 345 -----DANKPVKIT-NVAPGVKEGDTNVVAOLKGVQNLNRRIDNVNGN 387
 Db 635 KTLNAGDVAINELVMENDGSVHLTHNTYLTITKTINAANOGLIIVAADPINTDTALADGT 694
 Qy 388 ARAGIAQAIATAGLVQVLYLPGKSMMAIGGGYGLGEAGY-----IGYSSISAGSNW 438
 Db 695 NLGSAESPLNIIHFATKAANGDSILHIGKGVNL-----YANNITTDANVGLSHFRSGTS 750
 Qy 439 IIRGTASG 446
 Db 751 IVSGTVGG 758

RESULT 15
 YDEK_ECOLI STANDARD; PRT; 1325 AA.
 ID YDEK_ECOLI
 AC P32051; P76140; P77168;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical lipoprotein ydek precursor (ORFT).
 GN YDEK OR ORFT OR B1510.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of *Escherichia coli* K-12.";
RL Science 277:1453-1474(1997).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3];
RX SEQUENCE OF 595-1325 FROM N.A.
RA MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
RT "An *Escherichia coli* gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC (Potential).
CC -!- SIMILARITY: TO E.COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
ISP42 AND MOM38.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 653.
CC -----
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CC -----
DR EMBL; AF000248; AAC74583.1; -
DR EMBL; D90793; BAA15190.1; ALT_INIT.
DR EMBL; D90794; BAA15197.1; ALT_INIT.
DR EMBL; X73295; CAA51730.1; ALT_FRAME.
DR PIR; A64905; A64905.
DR Ecogene; EG11780; Ydek.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; signal;
KW Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1325 HYPOTHELICAL LIPOPROTEIN YDEK.
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
FT CONFLICT 884 884 M -> K (IN REF. 3).
FT CONFLICT 1317 1317 M -> S (IN REF. 3).
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;

Query Match 7.0%; Score 165; DB 1; Length 1325;
Best Local Similarity 24.3%; Pred. No. 0.26;
Matches 125; Conservative 54; Mismatches 218; Indels 117; Gaps 27;

QY 4 TGLINVEKLSFGANGKKVNIISDTKGLNFAKTAGTNGDTTVHLNGTGST--LTD--- 58
DB 90 TGVNLILA-----GGNASLTITTSVIGAN--EDSEGI-----VNLGGTWRLYDSGN 135
QY 59 --MLNTG----ATTNVTNDNVNVDDEKKRAASVKDLNAGWNKIGVKPGTTASDNVDFVR 112
DB 136 NARPLNVGSGSGTGLNIQKGVHDG-----GYLRIGSGTGGV--GTNVNVEGDSVL 184
QY 113 TYDVEFFLSADTKTTVNVESKDNKKTE-----VKIGAKTSVIKEKDGK-LVTGK-- 162
DB 185 TTLEFEGISGTGSLNIT----DKGYVTSSIVAILGYQAGSNQVWVVEKGEWLKNNDS 240

QY 163 -----GKGENSGSTDEGEGLVTAKEVIDAVNKAQWRMKTITTTANGQTQADKPEVTSGT 216
DB 241 SIEFQIGNOGTGEATIREGGLVTAENTIIIGNATG---IGTLNVQ-----DQDSVITVRR 292
QY 217 KYTFASNGTGTATVSKDDOGNITVK-YD-VNVDGALN--VNQLQNSGWNL----- 262
DB 293 LXYGYFENG---TVNISNGLINNKKEYSLVGVODSGHVVNVDKGHWNFLGTGEAFRYI 349
QY 263 -----DSKAVAGSSGKVISGNVSPSKGMDETVNIAGN-----NIETRNGKNIDIA 310
DB 350 YICDAGDGEINLVSSSEKGVDSGIITAG---MKET---GTGNITVTKDNKSNVITNLGTNLGYD 403
QY 311 TSMTPQFSSVSLCAGADAPTLSDDEGALNV-----GSKDANKPVRITTNVAPGVKEGDVT 365
DB 404 GHCEMNISNOGLVSVNGSSSLGYGETGVGNVSITTTGGMHEVKNVYTTTIGVAGVGNLNIS 463
QY 366 NVAQLKGVAONLNRRINDYNGNARAGIAQAIATAGLVQAYLP--GKSMAIGGGTYLGEA 423
DB 464 DGG--KFSQNTITFLGDKASGIGTLNMDATSSFTDVGINVGFGSGIVNVSNGATLNST 521
QY 424 GYAI-----GYSSISAGGNWIIKGTASGNSR 449
DB 522 GYGFIGNASGKIVNISTDSLWNLK-TSSTNAQ 554

Search completed: October 6, 2003, 09:24:17
Job time : 10.1345 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 ; Search time 33.9322 Seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-36

Perfect score: 2350

Sequence: 1 TDEGLINVTETKLSFGANG.....TASGNRHFSGASVGYQW 462

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2337	99.4	592	2 Q93QY2	Q93QY2 neisseria m
2	2299	97.8	592	2 Q9JPS9	Q9JPS9 neisseria m
3	2280	97.0	594	2 Q9JPI3	Q9JPI3 neisseria m
4	2280	97.0	594	2 Q9JPS2	Q9JPS2 neisseria m
5	2261	96.2	598	2 Q9JPS0	Q9JPS0 neisseria m
6	2261	96.2	598	2 Q93QY5	Q93QY5 neisseria m
7	2261	96.2	598	2 Q9JPT0	Q9JPT0 neisseria m
8	2260	96.2	590	2 Q9JPS3	Q9JPS3 neisseria m
9	2260	96.2	599	2 Q9JPR8	Q9JPR8 neisseria m
10	2247	95.6	594	2 Q9JPH7	Q9JPH7 neisseria m
11	2247	95.6	598	2 Q9JPR9	Q9JPR9 neisseria m
12	2228.5	94.8	600	2 Q9JPS6	Q9JPS6 neisseria m
13	2224.5	94.7	526	2 Q9JPS4	Q9JPS4 neisseria m
14	2224.5	94.7	530	2 Q9JPS1	Q9JPS1 neisseria m
15	2213	94.2	594	2 Q93QY4	Q93QY4 neisseria m
16	2210.5	94.1	591	2 Q93QY3	Q93QY3 neisseria m

17	2210.5	94.1	591	2 Q9JPS7	Q9JPS7 neisseria m
18	2210.5	94.1	591	16 Q9JRI8	Q9JRI8 neisseria m
19	2206.5	93.9	592	2 Q9AQF0	Q9AQF0 neisseria m
20	2156	91.7	600	2 Q9JPS5	Q9JPS5 neisseria m
21	2136	90.9	592	16 Q9JQW4	Q9JQW4 neisseria m
22	2119	90.2	598	2 Q9JPR7	Q9JPR7 neisseria m
23	2116	90.0	589	2 Q93QY1	Q93QY1 neisseria m
24	2114	90.0	599	2 Q9JPS8	Q9JPS8 neisseria m
25	2105	89.6	589	2 Q9JPI0	Q9JPI0 neisseria m
26	2104	89.5	595	2 Q9JPH0	Q9JPH0 neisseria m
27	876	37.3	2353	2 P71401	P71401 haemophilus
28	851	36.2	1096	2 Q8GM79	Q8GM79 haemophilus
29	849.5	36.1	1098	2 Q48152	Q48152 haemophilus
30	832	35.4	1210	2 Q8GM74	Q8GM74 haemophilus
31	829	35.3	1210	2 Q8GM75	Q8GM75 haemophilus
32	821.5	35.0	1204	2 Q8GM76	Q8GM76 haemophilus
33	574.5	24.4	1002	2 Q8GM78	Q8GM78 haemophilus
34	573.5	24.4	1004	2 Q8GM77	Q8GM77 haemophilus
35	390.5	16.6	1299	16 Q9F3X6	Q9F3X6 pasteurella
36	372	15.8	2314	2 Q8QM8	Q8QM8 moraxella c
37	360	15.3	1588	16 Q8XDG4	Q8XDG4 escherichia
38	359.5	15.3	2059	16 Q9PD50	Q9PD50 xyliella fas
39	357	15.2	1190	16 Q9PC04	Q9PC04 xyliella fas
40	352.5	15.0	1461	16 Q8ZL64	Q8ZL64 salmonella
41	351	14.9	1964	2 Q8QM9	Q8QM9 moraxella c
42	349	14.9	1778	16 Q8FCB2	Q8FCB2 escherichia
43	348.5	14.8	1107	16 Q9F2D8	Q9F2D8 salmonella
44	317.5	13.5	2712	16 Q9F3X5	Q9F3X5 pasteurella
45	317	13.5	641	16 Q8CKM1	Q8CKM1 yersinia pe

ALIGNMENTS

RESULT 1

Q93QY2

ID Q93QY2 PRELIMINARY; PRT; 592 AA.

AC Q93QY2;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE NHA outer membrane protein.

GN NHA.

OS Neisseria meningitidis.

OC Bacteria: Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H41;

RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer

RT membrane protein of Neisseria meningitidis.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF157609; AAK68870.1; -

DR InterPro; IPR005594; Yada.

DR Pfam; PF03895; Yada; 1.

SQ SEQUENCE 592 AA; 61869 MW; F9403A0B4A18EEA7 CRC64;

Query Match 99.4%; Score 2337; DB 2; Length 592;

Best Local Similarity 99.8%; Pred. No. 2.7e-94;

Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2	DEGLINVTETKLSFGANGKKNIIISDTKGLNFAKETAGTNGDTTVHLNIGISTLDMLL	61
Db	132	DUTGLINVTETKLSFGANGKKNIIISDTKGLNFAKETAGTNGDTTVHLNIGISTLDMLL	191
QY	62	NTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEFLS	121
Db	192	NTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEFLS	251
QY	122	ADTKTTTVNVEKNDGKTEVKIGAKTSVIKEKDGKLVTKGKGNGSSSTDEGEGLVTAK	181

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Db 252 ADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGKGNGSSSTDEGEGLVTAK 311
QY 182 EVIDAVNKAGWRMKTITANGOTQADKFEFVTSCTKVTFAAGNGTTATVSKDDQGNITVK 241
Db 312 EVIDAVNKAGWRMKTITANGOTQADKFEFVTSCTKVTFAAGNGTTATVSKDDQGNITVK 371
QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTVINAGNIEIT 301
Db 372 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTVINAGNIEIT 431
QY 302 RNGKNIDDIATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSKDANKPVRITNVAPGVKE 361
Db 432 RNGKNIDDIATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSKDANKPVRITNVAPGVKE 491
QY 362 GDTVNTVAQLKGVAQNLRNIDNVNGNARAGIAQAIATAGLVQVAYLPCKSMMAIGGGTYLG 421
Db 492 GDTVNTVAQLKGVAQNLRNIDNVNGNARAGIAQAIATAGLVQVAYLPCKSMMAIGGGTYLG 551
QY 422 EAGYATGYSSISAGGNNIIKGTASGNSRHFHGASASVGYOW 462
Db 552 EAGYATGYSSISAGGNNIIKGTASGNSRHFHGASASVGYOW 592
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RESULT 2

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Q9JPS9 ID Q9JPS9 PRELIMINARY; PRT; 592 AA.
AC Q9JPS9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OX Neisseriaceae; Neisseria.
NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;
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Query Match 97.8%; Score 2299; DB 2; Length 592;

Best Local Similarity 98.3%; Pred. No. 1.2e-92;

Matches 453; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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QY 2 DETGLINVETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 61
Db 132 DLRLGLINVETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 191
QY 62 NTGATTNVTNDVTDDEKRAASVKDVLNAGWNIGKVGKGTASDNDVDFVRYDVEFLS 121
Db 192 NTGATTNVTNDVTDDEKRAASVKDVLNAGWNIGKVGKGTASDNDVDFVRYDVEFLS 251
QY 122 ADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGKGNGSSSTDEGEGLVTAK 181
Db 252 ADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGKGNGSSSTDEGEGLVTAK 311
QY 182 EVIDAVNKAGWRMKTITANGOTQADKFEFVTSCTKVTFAAGNGTTATVSKDDQGNITVK 241
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Db 312 EVIDAVNKAGWRMKTITANGOTQADKFEFVTSCTKVTFAAGNGTTATVSKDDQGNITVM 371
QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTVINAGNIEIT 301
Db 372 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTVINAGNIEIT 431
QY 302 RNGKNIDDIATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSKDANKPVRITNVAPGVKE 361
Db 432 RNGKNIDDIATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSKDANKPVRITNVAPGVKE 491
QY 362 GDTVNTVAQLKGVAQNLRNIDNVNGNARAGIAQAIATAGLVQVAYLPCKSMMAIGGGTYLG 421
Db 492 GDTVNTVAQLKGVAQNLRNIDNVNGNARAGIAQAIATAGLVQVAYLPCKSMMAIGGGTYRG 551
QY 422 EAGYATGYSSISAGGNNIIKGTASGNSRHFHGASASVGYOW 462
Db 552 EAGYATGYSSISAGGNNIIKGTASGNSRHFHGASASVGYOW 592
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RESULT 3

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Q9JPI3 ID Q9JPI3 PRELIMINARY; PRT; 594 AA.
AC Q9JPI3
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OX Neisseriaceae; Neisseria.
NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, and BZ232;
RX MEDLINE=20175756; PubMed=10710308;
RX Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -.
DR EMBL; AF226369; AAF42518.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D0D4B46 CRC64;
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Query Match 97.0%; Score 2280; DB 2; Length 594;

Best Local Similarity 97.8%; Pred. No. 8.1e-92;

Matches 450; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

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QY 2 DETGLINVETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDMLL 61
Db 134 DLTDLISVETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDLL 193
QY 62 NTGATTNVTNDVTDDEKRAASVKDVLNAGWNIGKVGKGTASDNDVDFVRYDVEFLS 121
Db 194 NTGATTNVTNDVTDDEKRAASVKDVLNAGWNIGKVGKGTASDNDVDFVRYDVEFLS 253
QY 122 ADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGKGNGSSSTDEGEGLVTAK 181
Db 254 ADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTKGKGNGSSSTDEGEGLVTAK 313
QY 182 EVIDAVNKAGWRMKTITANGOTQADKFEFVTSCTKVTFAAGNGTTATVSKDDQGNITVK 241
Db 314 EVIDAVNKAGWRMKTITANGOTQADKFEFVTSCTKVTFAAGNGTTATVSKDDQGNITVK 373
QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDVTVINAGNIEIT 301
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Db 374 YDYNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNEIT 433
QY 302 RGNKNIDIIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPCVKE 361
Db 434 RGNKNIDIIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPCVKE 493
QY 362 GDVTNVAQLKGVQAOINLNNRIDNVGNARAGIAQIAIATAGLVQAYLPCKSMMAIGGGTYLG 421
Db 494 GDVTNVAQLKGVQAOINLNNRIDNVGNARAGIAQIAIATAGLVQAYLPCKSMMAIGGGTYRG 553
QY 422 EAGYATGYSSISAGGNIWIKGTASGNSRGHFGASASVGYOW 462
Db 554 EAGYATGYSSISDGGNIWIKGTASGNSRGHFGASASVGYOW 594

RESULT 4
Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226379; AAF42528.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 97.0%; Score 2280; DB 2; Length 594;
Best Local Similarity 97.6%; Pred. No. 8.1e-92;
Matches 450; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 DETGLNVEVEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGISGTLTDLML 61
Db 134 DLTLDSVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGISGTLTDLML 193
QY 62 NTGATTNVTNDVTDDEKRAASVKDVLNAGWIKGVKPGTTASDNDVDFVRTYDVEFLS 121
Db 194 NTGATTNVTNDVTDDEKRAASVKDVLNAGWIKGVKPGTTASDNDVDFVRTYDVEFLS 253
QY 122 ADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTKGKGGNGSSSTDEGEGLVTAK 181
Db 254 ADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTKGKGGNGSSSTDEGEGLVTAK 313
QY 182 EVIDAVNKGAWRMKTTTANGQTQADKFETVTSCTKVTASGNGTTATVSKDDQGNITVK 241
Db 314 EVIDAVNKGAWRMKTTTANGQTQADKFETVTSCTKVTASGNGTTATVSKDDQGNITVK 373
QY 242 YDYNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNEIT 301
Db 374 YDYNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNEIT 433
QY 302 RGNKNIDIIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPCVKE 361
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Db 434 RGNKNIDIIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPCVKE 493
QY 362 GDVTNVAQLKGVQAOINLNNRIDNVGNARAGIAQIAIATAGLVQAYLPCKSMMAIGGGTYLG 421
Db 494 GDVTNVAQLKGVQAOINLNNRIDNVGNARAGIAQIAIATAGLVQAYLPCKSMMAIGGGTYRG 553
QY 422 EAGYATGYSSISAGGNIWIKGTASGNSRGHFGASASVGYOW 462
Db 554 EAGYATGYSSISDGGNIWIKGTASGNSRGHFGASASVGYOW 594

RESULT 5
Q9JPS0 PRELIMINARY; PRT; 598 AA.
AC Q9JPS0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NGH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226381; AAF42530.1; -.
DR EMBL; AF157607; AAK68868.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0BB8A63CB CRC64;

Query Match 96.2%; Score 2261; DB 2; Length 598;
Best Local Similarity 96.7%; Pred. No. 5.5e-91;
Matches 446; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 2 DETGLNVEVEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGISGTLTDLML 61
Db 138 DLTLDSVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGISGTLTDLML 197
QY 62 NTGATTNVTNDVTDDEKRAASVKDVLNAGWIKGVKPGTTASDNDVDFVRTYDVEFLS 121
Db 198 NTGATTNVTNDVTDDEKRAASVKDVLNAGWIKGVKPGTTASDNDVDFVRTYDVEFLS 257
QY 122 ADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTKGKGGNGSSSTDEGEGLVTAK 181
Db 258 ADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTKGKGGNGSSSTDEGEGLVTAK 317
QY 182 EVIDAVNKGAWRMKTTTANGQTQADKFETVTSCTKVTASGNGTTATVSKDDQGNITVK 241
Db 318 EVIDAVNKGAWRMKTTTANGQTQADKFETVTSCTKVTASGNGTTATVSKDDQGNITVK 377
QY 242 YDYNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNEIT 301
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Db 378 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVLISGNVSPSKGMDFTVINAGNNIEIT 437
QY 302 RNKGNIDIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVE 361
Db 438 RNKGNIDIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVE 497
QY 362 GDVTNVAQLKGVQAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAAYLPCKSMMAIGGGTYLG 421
Db 498 GDVTNVAQLKGVQAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAAYLPCKSMMAIGGGTYRG 557
QY 422 EAGYATGYSSISAGGNWIIKGTASGNSRGRHFGASASVGYOW 462
Db 558 EAGYATGYSSISDTGNWVIKGTASGNSRGRHFGASASVGYOW 598

RESULT 6
Q93QY5 PRELIMINARY; PRT; 598 AA.
AC Q93QY5;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DE 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE NHHA outer membrane protein.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B210;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157603; AAK68864.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62687 MW; 18CEFF6410A15DF CRC64;

Query Match 96.2%; Score 2261; DB 2; Length 598;
Best Local Similarity 96.5%; Pred. No. 5.5e-91;
Matches 445; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 DETGLINVETEKLSPFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSLTDLML 61
Db 138 DLTLDSVETEKLSPFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSLTDLML 197
QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRTYDTVEFLS 121
Db 198 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRTYDTVEFLS 257
QY 122 ADTKTTTVNYESKDNKKTEVKIGAKTSVKEKDGKLVTKGKGNGSSDDEGLVTAK 181
Db 258 ADTKTTTVNYESKDNKKRTVEKIGAKTSVKEKDGKLVTKGKGNGSSDDEGLVTAK 317
QY 182 EVIDAVNKAGWRMKTITANGOTQADKFEVTSKVTTFASGNGTTATVSKDDQGNITVK 241
Db 318 EVIDAVNKAGWRMKTITANGOTQADKFEVTSKVTTFASGNGTTATVSKDDQGNITVK 377
QY 182 EVIDAVNKAGWRMKTITANGOTQADKFEVTSKVTTFASGNGTTATVSKDDQGNITVK 241
Db 318 EVIDAVNKAGWRMKTITANGOTQADKFEVTSKVTTFASGNGTTATVSKDDQGNITVK 377
QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVLISGNVSPSKGMDFTVINAGNNIEIT 301
Db 378 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVLISGNVSPSKGMDFTVINAGNNIEIT 437
QY 302 RNKGNIDIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVE 361
Db 438 RNKGNIDIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVE 497
QY 362 GDVTNVAQLKGVQAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAAYLPCKSMMAIGGGTYLG 421
Db 498 GDVTNVAQLKGVQAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAAYLPCKSMMAIGGGTYRG 557
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QY 422 EAGYATGYSSISAGGNWIIKGTASGNSRGRHFGASASVGYOW 462
Db 558 EAGYATGYSSISDTGNWVIKGTASGNSRGRHFGTSASVGYOW 598

RESULT 7
Q9JPT0 PRELIMINARY; PRT; 598 AA.
AC Q9JPT0;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226359; AAF42508.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 96.2%; Score 2261; DB 2; Length 598;
Best Local Similarity 96.5%; Pred. No. 5.5e-91;
Matches 445; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 2 DETGLINVETEKLSPFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSLTDLML 61
Db 138 DLTLDSVETEKLSPFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSLTDLML 197
QY 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRTYDTVEFLS 121
Db 198 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTTASDNVDFVRTYDTVEFLS 257
QY 122 ADTKTTTVNYESKDNKKTEVKIGAKTSVKEKDGKLVTKGKGNGSSDDEGLVTAK 181
Db 258 ADTKTTTVNYESKDNKKRTVEKIGAKTSVKEKDGKLVTKGKGNGSSDDEGLVTAK 317
QY 182 EVIDAVNKAGWRMKTITANGOTQADKFEVTSKVTTFASGNGTTATVSKDDQGNITVK 241
Db 318 EVIDAVNKAGWRMKTITANGOTQADKFEVTSKVTTFASGNGTTATVSKDDQGNITVK 377
QY 242 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVLISGNVSPSKGMDFTVINAGNNIEIT 301
Db 378 YDYNVGDALNVNQLNSGWNLDKAVAGSSGKVLISGNVSPSKGMDFTVINAGNNIEIT 437
QY 302 RNKGNIDIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVE 361
Db 438 RNKGNIDIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVE 497
QY 362 GDVTNVAQLKGVQAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAAYLPCKSMMAIGGGTYLG 421
Db 498 GDVTNVAQLKGVQAQNLNRRIDNVNGNARAGIAQAIAATAGLVQAAYLPCKSMMAIGGGTYRG 557
QY 422 EAGYATGYSSISAGGNWIIKGTASGNSRGRHFGASASVGYOW 462
Db 558 EAGYATGYSSISDTGNWVIKGTASGNSRGRHFGTSASVGYOW 598
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RESULT 10
Q9JPH7 PRELIMINARY; PRT; 594 AA.
AC Q9JPH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (NhA outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=B2198, and 297-0;
RC MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masighani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=B2198;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226368; AAF42517.1; -
DR EMBL; AF226368; AAF42507.1; -
DR EMBL; AF157604; AAK68865.1; -
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62361 MW; 436BDE68263C5C CRC64;

Query Match 95.6%; Score 2247; DB 2; Length 594;
Best Local Similarity 96.3%; Pred. No. 2.2e-90;
Matches 444; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 2 DETGLINVETEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGISGLTDLML 61
Db 134 DLTDLTSVETEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGISGLTDLML 193
Qy 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGKVGKPGTTASDNVDVFRYDVTVEFLS 121
Db 194 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGKVGKPGTTASDNVDVFRYDVTVEFLS 253
Qy 122 ADTKTTTVNVEKSDNGKKTVEKIGAKTSVKEKDKGLVTGKKGKENGSSSTDEGEGLVTAK 181
Db 254 ADTKTTTVNVEKSDNGKKTVEKIGAKTSVKEKDKGLVTGKKGKENGSSSTDEGEGLVTAK 313
Qy 182 EVIDAVNKAGWRMKTTTANGOTGQADKFETVTSCTNVTNVTASGKGTATVSKDDOGNITVK 241
Db 314 EVIDAVNKAGWRMKTTTANGOTGQADKFETVTSCTNVTNVTASGKGTATVSKDDOGNITVK 373
Qy 242 YDENVGDAENVNLQNSGNWLDKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIEIT 301
Db 374 YDENVGDAENVNLQNSGNWLDKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIEIT 433
Qy 302 RGNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
Db 434 RGNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 493
Qy 362 GDVTNVAQLKGVAQNLRNDNVNGNARAGIAQAIAATAGLVQVAYLPCKSMAIGGGTYLG 421
Db 494 GDVTNVAQLKGVAQNLRNDNVNGNARAGIAQAIAATAGLVQVAYLPCKSMAIGGGTYLG 553

Query Match 95.6%; Score 2247; DB 2; Length 598;
Best Local Similarity 96.3%; Pred. No. 2.2e-90;
Matches 444; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 2 DETGLINVETEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGISGLTDLML 61
Db 138 DLTDLTSVETEKLSFGANGKKNVITSDTKGLNFAKETAGTNGDPTVHLNGISGLTDLML 197
Qy 62 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGKVGKPGTTASDNVDVFRYDVTVEFLS 121
Db 198 NTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGKVGKPGTTASDNVDVFRYDVTVEFLS 257
Qy 122 ADTKTTTVNVEKSDNGKKTVEKIGAKTSVKEKDKGLVTGKKGKENGSSSTDEGEGLVTAK 181
Db 258 ADTKTTTVNVEKSDNGKKTVEKIGAKTSVKEKDKGLVTGKKGKENGSSSTDEGEGLVTAK 317
Qy 182 EVIDAVNKAGWRMKTTTANGOTGQADKFETVTSCTNVTNVTASGKGTATVSKDDOGNITVK 241
Db 318 EVIDAVNKAGWRMKTTTANGOTGQADKFETVTSCTNVTNVTASGKGTATVSKDDOGNITVK 377
Qy 242 YDENVGDAENVNLQNSGNWLDKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIEIT 301
Db 378 YDENVGDAENVNLQNSGNWLDKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIEIT 437
Qy 302 RGNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 361
Db 438 RGNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKE 497
Qy 362 GDVTNVAQLKGVAQNLRNDNVNGNARAGIAQAIAATAGLVQVAYLPCKSMAIGGGTYLG 421
Db 498 GDVTNVAQLKGVAQNLRNDNVNGNARAGIAQAIAATAGLVQVAYLPCKSMAIGGGTYLG 557
Qy 422 EAGYAIQYSSISAGGNWIIKGTASGNSRGRHFGASASVGYQW 462
Db 558 EAGYAIQYSSISAGGNWIIKGTASGNSRGRHFGASASVGYQW 598
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RESULT 12
Q9JPS6 PRELIMINARY; PRT; 600 AA.
AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226371; AAF42520.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 94.8%; Score 2228.5; DB 2; Length 600;
Best Local Similarity 96.3%; Pred. No. 1.4e-89;
Matches 442; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 4 TGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDITVHLNGIGSTLTDMLNT 63
DB 143 TDLTSVGTETKLSFGANGKNVNIISDTKGLNFAKETAGTNGDITVHLNGIGSTLTDMLNT 202

QY 64 GATTNTVNDVTDDEKRAASVKDVLNAGNIRKGVKPGTTASDNVDFVRYDVEFLSAD 123
DB 203 GATTNTVNDVTDDEKRAASVKDVLNAGNIRKGVKPGTTASDNVDFVRYDVEFLSAD 262

QY 124 TKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGKGGKNGSTDEGEGLVTAKEV 183
DB 263 TKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGKGGKNGSTDEGEGLVTAKEV 322

QY 184 IDAVNKAGWRMKTITANGOTGQADKFETVTSKVTFTASNGTATVSKDDQGNITVKYD 243
DB 323 IDAVNKAGWRMKTITANGOTGQADKFETVTSKVTFTASNGTATVSKDDQGNITVKYD 382

QY 244 VNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRN 303
DB 383 VNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEITRN 442

QY 304 GKNDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRIINVPAGVKEG 363
DB 443 GKNDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRIINVPAGVKEG 501

QY 364 VTNVAQLKGAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKGSMAIIGGGTYLGEA 423
DB 502 VTNVAQLKGAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKGSMAIIGGGTYRGEA 561

QY 424 GYAIGYSSISAGGNWIKGTASGNSRGRHFGASASVGYQW 462
DB 562 GYAIGYSSISAGGNWIKGTASGNSRGRHFGASASVGYQW 600

RESULT 13
Q9JPS4 PRELIMINARY; PRT; 526 AA.
AC Q9JPS4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG6788;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226377; AAF42526.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;

Query Match 94.7%; Score 2224.5; DB 2; Length 526;
Best Local Similarity 95.7%; Pred. No. 1.8e-89;
Matches 441; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 2 DETGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDITVHLNGIGSTLTDMLL 61
DB 67 DLTDLTSVETETKLSFGANGKNVNIISDTKGLNFAKETAGTNGDITVHLNGIGSTLTDMLL 126

QY 62 NTGATTNTVNDVTDDEKRAASVKDVLNAGNIRKGVKPGTTASDNVDFVRYDVEFLS 121
DB 127 NTGATTNTVNDVTDDEKRAASVKDVLNAGNIRKGVKPGTTASDNVDFVRYDVEFLS 186

QY 122 ADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGKGGKNGSTDEGEGLVTAKE 181
DB 187 ADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGKGGKNGSTDEGEGLVTAKE 246

QY 182 EVIDAVNKAGWRMKTITANGOTGQADKFETVTSKVTFTASNGTATVSKDDQGNITVK 241
DB 247 EVIDAVNKAGWRMKTITANGOTGQADKFETVTSKVTFTASNGTATVSKDDQGNITVK 306

QY 242 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEIT 301
DB 307 YDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIEIT 366

QY 302 RNKKNIDIAVSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRIINVPAGVKE 361
DB 367 RNKKNIDIAVSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRIINVPAGVKE 425

QY 362 GDVTNVAQLKGAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKGSMAIIGGGTYLGE 421
DB 426 GDVTNVAQLKGAQNLRIDNVGNARAGIAQAIAATAGLVQAYLPKGSMAIIGGGTYRGE 485

QY 422 EAGYAGYSSISAGGNWIKGTASGNSRGRHFGASASVGYQW 462
DB 486 EAGYAGYSSISAGGNWIKGTASGNSRGRHFGASASVGYQW 526

RESULT 14
Q9JPS1 PRELIMINARY; PRT; 530 AA.
AC Q9JPS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGF26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tetzelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
 meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226380; AAF42529.1; --
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1
SQ SEQUENCE 530 AA; 55190 MW; 1F836CA57598515B CRC64;

Query Match 94.7%; Score 2224.5; DB 2; Length 530;
Best Local Similarity 95.7%; Pred. No. 1.8e-89;
Matches 441; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 2 DETGLINVEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDITVHLNGIGSLTDMLL 61
DB 71 DLDTLSVTEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDITVHLNGIGSLTDMLL 130
QY 62 NTGATTNTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTASDNVDFVRYDTVEFLS 121
DB 131 NTGATTNTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTASDNVDFVRYDTVEFLS 190
QY 122 ADTKTTTVNVEKDKNGKTEVKGKAKTSVKEKDKGLVTGKGGKNGSGSTDEGEGLVTAK 181
DB 191 ADTKTTTVNVEKDKNGKTEVKGKAKTSVKEKDKGLVTGKGGKNGSGSTDEGEGLVTAK 250
QY 182 EVIDAVNKAGWRMKTITANGOTGQADKFEVTSCTKVTFSAGNGTATTATVSKDDQGNITVK 241
DB 251 EVIDAVNKAGWRMKTITANGOTGQADKFEVTSCTKVTFSAGNGTATTATVSKDDQGNITVK 310
QY 242 YDNNVQDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIT 301
DB 311 YDNNVQDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIT 370
QY 302 RGNKNIDIATSMTPQFSVSLGAGADAPTLSVDDEGALNVGSKDKANKPVRITNVAPGVKE 361
DB 371 RGNKNIDIATSMTPQFSVSLGAGADAPTLSVDDEGALNVGSKDKANKPVRITNVAPGVKE 429
QY 362 GDVTNVAQLKGVAQNLRNNDVNGNARAGIAQAIAATAGLVQAYLPKGSMMIAIGGGTYLG 421
DB 430 GDVTNVAQLKGVAQNLRNNDVNGNARAGIAQAIAATAGLVQAYLPKGSMMIAIGGGTYLG 489
QY 422 EAGYAIQYSSISAGGNWIIKGTASGNSRGHFGASASVGYOW 462
DB 490 EAGYAIQYSSISAGGNWIIKGTASGNSRGHFGASASVGYOW 530

RESULT 15
Q93QY4
ID Q93QY4 PRELIMINARY; PRT; 594 AA.
AC Q93QY4
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
 membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1; --
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 94.2%; Score 2213; DB 2; Length 594;
Best Local Similarity 95.0%; Pred. No. 5.7e-89;
Matches 438; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 2 DETGLINVEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDITVHLNGIGSLTDMLL 61
DB 134 DLDTLSVTEKLSFGANGKKNVNIISDTKGLNFAKETAGTNGDITVHLNGIGSLTDMLL 193
QY 62 NTGATTNTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTASDNVDFVRYDTVEFLS 121
DB 194 NTGATTNTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTASDNVDFVRYDTVEFLS 253
QY 122 ADTKTTTVNVEKDKNGKTEVKGKAKTSVKEKDKGLVTGKGGKNGSGSTDEGEGLVTAK 181
DB 254 ADTKTTTVNVEKDKNGKTEVKGKAKTSVKEKDKGLVTGKGGKNGSGSTDEGEGLVTAK 313
QY 182 EVIDAVNKAGWRMKTITANGOTGQADKFEVTSCTKVTFSAGNGTATTATVSKDDQGNITVK 241
DB 314 EVIDAVNKAGWRMKTITANGOTGQADKFEVTSCTKVTFSAGNGTATTATVSKDDQGNITVK 373
QY 242 YDNNVQDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIT 301
DB 374 YDNNVQDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIT 433
QY 302 RGNKNIDIATSMTPQFSVSLGAGADAPTLSVDDEGALNVGSKDKANKPVRITNVAPGVKE 361
DB 434 RGNKNIDIATSMTPQFSVSLGAGADAPTLSVDDEGALNVGSKDKANKPVRITNVAPGVKE 493
QY 362 GDVTNVAQLKGVAQNLRNNDVNGNARAGIAQAIAATAGLVQAYLPKGSMMIAIGGGTYLG 421
DB 494 GDVTNVAQLKGVAQNLRNNDVNGNARAGIAQAIAATAGLVQAYLPKGSMMIAIGGGTYLG 553
QY 422 EAGYAIQYSSISAGGNWIIKGTASGNSRGHFGASASVGYOW 462
DB 554 EAGYAIQYSSISAGGNWIIKGTASGNSRGHFGASASVGYOW 594

Search completed: October 6, 2003, 09:30:51
Job time : 34.9322 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 ; Search time 30.5718 Seconds
(without alignments)
1848.329 Million cell updates/sec

Title: US-09-771-382-37

Perfect score: 1813

Sequence: 1 NNVDVRYTYDTVEFLSADTK.....TASGSRGHFGASVGYQW 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1813	100.0	407	22 AAU06184	N. meningitidis PM
2	1808	99.7	433	22 AAU06185	N. meningitidis PM
3	1808	99.7	512	22 AAU06182	N. meningitidis PM
4	1808	99.7	591	20 AAY27202	Amino acid sequenc
5	1808	99.7	591	20 AAY23741	A surface protein
6	1808	99.7	591	20 AAY23746	A surface protein
7	1808	99.7	591	22 AAU06171	N. meningitidis PM
8	1808	99.7	591	22 AAU06175	N. meningitidis EG
9	1807	99.7	502	22 AAU06186	N. meningitidis PM

10	1805	99.6	591	21 AAY57045	BASB029 amino acid
11	1804	99.5	592	20 AAY23737	A surface protein
12	1753.5	96.7	594	20 AAY23740	A surface protein
13	1753.5	96.7	594	21 AAY57044	BASB029 amino acid
14	1753.5	96.7	594	22 AAU06174	N. meningitidis EG
15	1752.5	96.7	592	22 AAU06180	N. meningitidis Z2
16	1748.5	96.4	599	20 AAY23743	A surface protein
17	1748.5	96.4	599	22 AAU06176	N. meningitidis H3
18	1741.5	96.1	594	20 AAY23739	A surface protein
19	1741.5	96.1	594	22 AAU06179	N. meningitidis BZ
20	1736.5	95.8	592	20 AAY27203	Amino acid sequenc
21	1728.5	95.3	513	22 AAU06183	N. meningitidis H4
22	1728.5	95.3	592	20 AAY23744	A surface protein
23	1728.5	95.3	592	22 AAU06172	N. meningitidis H4
24	1728.5	95.3	598	20 AAY23738	A surface protein
25	1728.5	95.3	598	20 AAY23742	A surface protein
26	1728.5	95.3	598	22 AAU06177	N. meningitidis H1
27	1728.5	95.3	598	22 AAU06178	N. meningitidis BZ
28	1715.5	94.6	589	20 AAY23745	A surface protein
29	1715.5	94.6	589	22 AAU06173	N. meningitidis P2
30	1647.5	90.9	604	22 AAU06181	N. meningitidis su
31	608	33.5	1098	17 AAR99392	Haemophilus adhesi
32	600	33.1	116	21 AAB37832	Neisserial conserv
33	581.5	32.1	1094	21 AAB23858	Haemophilus influe
34	569	31.4	2353	17 AAR99393	Haemophilus adhesi
35	569	31.4	2411	21 AAB23860	Haemophilus influe
36	412.5	22.8	679	17 AAR99394	Haemophilus adhesi
37	412.5	22.8	679	21 AAB23855	Haemophilus influe
38	366	20.2	72	21 AAB37830	Neisserial conserv
39	339	18.7	1004	21 AAB23857	Haemophilus influe
40	331.5	18.3	1002	21 AAB23854	Haemophilus influe
41	325	17.9	1104	21 AAB23856	Haemophilus influe
42	325	17.9	1104	21 AAB23859	Haemophilus influe
43	318	17.5	1778	22 ABB52677	Escherichia coli p
44	314	17.3	2139	24 ABB71294	M. catarrhalis sur
45	312.5	17.2	2314	22 AAB69136	M. catarrhalis les

ALIGNMENTS

RESULT 1
AAU06184
ID AAU06184 standard; Protein: 407 AA.

XX AC AAU06184;

XX DT 24-OCT-2001 (first entry)

XX DE N. meningitidis PMC21 Nhha deletion mutant #2.

XX DE Surface antigen Nhha; meningococcal disease; meningitis vaccine;
mutant; muten.

XX OS Neisseria meningitidis strain PMC21.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Peptide 1..51

XX FT /label= Signal_peptide

XX FT 52..407

XX FT /label= Mature_Nhha_deletion_mutant_#2

XX FT /note= "Predicted mature protein, specifically

XX FT claimed in claim 12"

XX XX WO200155182-A1.

XX XX 02-AUG-2001.

XX XX 25-JAN-2001; 2001WO-AU00069.

XX XX 25-JAN-2000; 2000US-0177917.

XX XX

PA (UYQU) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
DR N-PSDB; AAS09174.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 7; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #2.
XX
SQ Sequence 407 AA;

Query Match 100.0%; Score 1813; DB 22; Length 407;
Best Local Similarity 100.0%; Pred. No. 9.1e-118;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNVDVFRYDTVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVIREKDGKLVTKGDKG 60
DB 52 NNVDVFRYDTVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVIREKDGKLVTKGDKG 111

QY 61 ENGSTDGEGELVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSCTNVTFSAGKG 120
DB 112 ENGSTDGEGELVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSCTNVTFSAGKG 171

QY 121 TTATVSKDDQGNITVMYDVNVDGALNVQNLQNSGWNLDKAVAGSSGKVISGNYSPSKGK 180
DB 172 TTATVSKDDQGNITVMYDVNVDGALNVQNLQNSGWNLDKAVAGSSGKVISGNYSPSKGK 231

QY 181 MDETVINAGNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDGALNVGSKKD 240
DB 232 MDETVINAGNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDGALNVGSKKD 291

QY 241 NKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNDVNDGNARAGIAQAATAGLVQAYL 300
DB 292 NKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNDVNDGNARAGIAQAATAGLVQAYL 351

QY 301 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 356
DB 352 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 407

RESULT 2
AAU06185
ID AAU06185 standard; Protein; 433 AA.
XX
AC AAU06185;
XX
DT 24-Oct-2001 (first entry)
XX
DE N. meningitidis PMC21 Nhha deletion mutant #3.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutein.
XX
OS Neisseria meningitidis strain PMC21.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Peptide 1..51
FT Protein /label= Signal_peptide
FT 52..433
FT /label= Mature_Nhha_deletion_mutant_#3
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU000069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
DR N-PSDB; AAS09175.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 8; 91pp; English.
PS
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #3.
XX
SQ Sequence 433 AA;

Query Match 99.7%; Score 1808; DB 22; Length 433;
Best Local Similarity 99.7%; Pred. No. 2.2e-117;
Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNVDVFRYDTVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVIREKDGKLVTKGDKG 60
DB 78 NNVDVFRYDTVEFLSADTKTTTVNVEKONGKTEVKIGAKTSVIREKDGKLVTKGDKG 137

QY 61 ENGSTDGEGELVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSCTNVTFSAGKG 120
DB 138 ENGSTDGEGELVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSCTNVTFSAGKG 197

QY 121 TTATVSKDDQGNITVMYDVNVDGALNVQNLQNSGWNLDKAVAGSSGKVISGNYSPSKGK 180
DB 198 TTATVSKDDQGNITVMYDVNVDGALNVQNLQNSGWNLDKAVAGSSGKVISGNYSPSKGK 257

QY 181 MDETVINAGNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDGALNVGSKKD 240
DB 258 MDETVINAGNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDGALNVGSKKD 317

QY 241 NKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNDVNDGNARAGIAQAATAGLVQAYL 300
DB 318 NKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNDVNDGNARAGIAQAATAGLVQAYL 377

QY 301 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 356
DB 378 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 433


```
RESULT 3
AAU06182
ID AAU06182 standard; Protein; 512 AA.
XX
AC AAU06182;
XX
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 Nhha deletion mutant #1.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutain.
XX
OS Neisseria meningitidis strain PMC21.
OS Synthetic.
FH
FH Key Location/Qualifiers
FT Peptide 1..51
FT /label= Signal_peptide
FT Protein 52..512
FT /label= Mature_Nhha_deletion_mutant_#1
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
PN WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
DR N-PSDB; AAS09172.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis .
XX
XX Claim 12; Fig 5; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence represents N. meningitidis strain PMC21 surface
XX antigen Nhha deletion mutant #1.
XX
SQ Sequence 512 AA;
Query Match 99.7%; Score 1808; DB 22; Length 512;
Best Local Similarity 99.7%; Pred. No. 2.7e-117;
Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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:|||||
DB 157 DNVDVFRVTYDTVEFLSADTKTTTNNVESKDNGKKTVEKIGAKTSVKEKDKLVTKGDKG 216
|||||
QY 61 ENGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGQTGOADKFETVTSNTVTFASGKG 120
|||||
DB 217 ENGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGQTGOADKFETVTSNTVTFASGKG 276
|||||
QY 121 TTATVSKDDQGNITVMYDVGDLNVLNQLNSGWLDSKAVAGSSGKVTSNVSFSGKG 180
|||||
Db 277 TTATVSKDDQGNITVMYDVGDLNVLNQLNSGWLDSKAVAGSSGKVTSNVSFSGKG 336
|||||
QY 181 MDETVINAGNNIEITRNKGNIIDIAITSMTPQFSSVSLGAGADAPTILSVGDGDLNVSCKD 240
|||||
DB 337 MDETVINAGNNIEITRNKGNIIDIAITSMTPQFSSVSLGAGADAPTILSVGDGDLNVSCKD 396
|||||
QY 241 NKEPVRITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGLVQAYL 300
|||||
DB 397 NKEPVRITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGLVQAYL 456
|||||
QY 301 PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 356
|||||
DB 457 PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 512
|||||
RESULT 4
AAV27202
ID AAV27202 standard; Protein; 591 AA.
XX
AC AAV27202;
XX
DT 24-SEP-1999 (first entry)
XX
DE Amino acid sequence of N. meningitidis protein ORF40-1.
XX
XX Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
XX bacterial infection; treatment.
XX
XX Neisseria meningitidis.
OS
XX
XX WO9936544-A2.
XX
XX 22-JUL-1999.
XX
XX 14-JAN-1999; 99WO-IB00103.
XX
XX 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
XX
XX WPI; 1999-444400/37.
DR N-PSDB; AAX99124.
XX
XX New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
XX Claim 1; Page 62; 123pp; English.
XX
XX The invention provides proteins (AAV27201-245) from Neisseria
XX meningitidis (strains A and B) and nucleic acid sequences (AAV99123-167)
XX encoding the proteins. Compositions comprising the protein, nucleic acid
XX or antibody specific to the protein are useful as pharmaceuticals, e.g. a
XX vaccine composition or a diagnostic composition. The composition is also
XX useful for treating or preventing an infection due to Neisseria
XX bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 591 AA;
Query Match 99.7%; Score 1808; DB 20; Length 591;
Best Local Similarity 99.7%; Pred. No. 3.2e-117;
Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNVDVFRVTYDTVEFLSADTKTTTNNVESKDNGKKTVEKIGAKTSVKEKDKLVTKGDKG 60
:|||||
DB 236 DNVDVFRVTYDTVEFLSADTKTTTNNVESKDNGKKTVEKIGAKTSVKEKDKLVTKGDKG 295
|||||
QY 61 ENGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGQTGOADKFETVTSNTVTFASGKG 120
|||||
```

Db	296	ENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFETVTSGTNVTFSAGKG	355
Qy	121	TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK	180
Db	356	TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK	415
Qy	181	MDEVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKD	240
Db	416	MDEVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKD	475
Qy	241	NKPVRIITNVAPGVKEGDTVNVQAQLKGVAQNLNRRIDNVGDNARAGIAQAATATAGLVQAYL	300
Db	476	NKPVRIITNVAPGVKEGDTVNVQAQLKGVAQNLNRRIDNVGDNARAGIAQAATATAGLVQAYL	535
Qy	301	PGKSMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFSGASASVGYQW	356
Db	536	PGKSMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFSGASASVGYQW	591
RESULT 5			
AAAY23741			
ID	AAAY23741	standard; Protein; 591 AA.	
XX	AAAY23741;		
DT	08-SEP-1999	(first entry)	
DE	A surface protein of Neisseria meningitidis.		
KW	Surface protein; surface glycoprotein; infection; vaccine;		
KW	immunoreactive peptide.		
OS	Neisseria meningitidis.		
XX	WO9931132-A1.		
PN			
XX			
PD	24-JUN-1999.		
XX			
PF	14-DEC-1998;	98WO-AU01031.	
XX			
PR	12-DEC-1997;	97GB-0026398.	
XX			
PA	(ISIS-) ISIS INNOVATION LTD.		
PA	(UYQU) UNIV QUEENSLAND.		
XX			
PI	Jennings MP, Moxon ER, Peak IRA;		
XX			
DR	WPI; 1999-418754/35.		
DR	N-PSDB; AAX85793.		
XX			
PT	Neisseria meningitidis surface proteins useful for treating N.		
PT	meningitidis infections		
XX			
PS	Claim 1; Page 104-106; 132pp; English.		
XX			
CC	The present sequence represents a surface protein of Neisseria		
CC	meningitidis which is approximately 62 kDa. The N. meningitidis		
CC	surface glycoproteins, nucleic acids, the primers and optionally		
CC	a thermostable polymerase, or antibodies are useful in a kit for		
CC	the detection or diagnosis of N. meningitidis infection in humans.		
CC	The N. meningitidis surface glycoproteins can also be used to		
CC	prevent or treat N. meningitidis infection in humans, especially		
CC	in the form of vaccines. The proteins and antibodies can also		
CC	be used to identify immunoreactive peptides.		
XX			
SQ	Sequence	591 AA;	
Query Match			
Best Local Similarity 99.7%; Score 1808; DB 20; Length 591;			
Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	NNVDFVFTYDTVEFLSADTKTTTVNVESKDKKTEVKIGAKTSVIREKDKGLVTGDKG	60

Db	236	DNVDFVFTYDTVEFLSADTKTTTVNVESKDKKTEVKIGAKTSVIREKDKGLVTGDKG	295
Qy	61	ENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFETVTSGTNVTFSAGKG	120
Db	296	ENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFETVTSGTNVTFSAGKG	355
Qy	121	TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK	180
Db	356	TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK	415
Qy	181	MDEVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKD	240
Db	416	MDEVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDGDALNVGSKKD	475
Qy	241	NKPVRIITNVAPGVKEGDTVNVQAQLKGVAQNLNRRIDNVGDNARAGIAQAATATAGLVQAYL	300
Db	476	NKPVRIITNVAPGVKEGDTVNVQAQLKGVAQNLNRRIDNVGDNARAGIAQAATATAGLVQAYL	535
Qy	301	PGKSMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFSGASASVGYQW	356
Db	536	PGKSMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFSGASASVGYQW	591
RESULT 6			
AAAY23746			
ID	AAAY23746	standard; Protein; 591 AA.	
XX	AAAY23746;		
DT	08-SEP-1999	(first entry)	
DE	A surface protein of Neisseria meningitidis.		
KW	Surface protein; surface glycoprotein; infection; vaccine;		
KW	immunoreactive peptide.		
OS	Neisseria meningitidis.		
XX	WO9931132-A1.		
PN			
XX			
PD	24-JUN-1999.		
XX			
PF	14-DEC-1998;	98WO-AU01031.	
XX			
PR	12-DEC-1997;	97GB-0026398.	
XX			
PA	(ISIS-) ISIS INNOVATION LTD.		
PA	(UYQU) UNIV QUEENSLAND.		
XX			
PI	Jennings MP, Moxon ER, Peak IRA;		
XX			
DR	WPI; 1999-418754/35.		
DR	N-PSDB; AAX85798.		
XX			
PT	Neisseria meningitidis surface proteins useful for treating N.		
PT	meningitidis infections		
XX			
PS	Claim 1; Page 127-128; 132pp; English.		
XX			
CC	The present sequence represents a surface protein of Neisseria		
CC	meningitidis which is approximately 62 kDa. The N. meningitidis		
CC	surface glycoproteins, nucleic acids, the primers and optionally		
CC	a thermostable polymerase, or antibodies are useful in a kit for		
CC	the detection or diagnosis of N. meningitidis infection in humans.		
CC	The N. meningitidis surface glycoproteins can also be used to		
CC	prevent or treat N. meningitidis infection in humans, especially		
CC	in the form of vaccines. The proteins and antibodies can also		
CC	be used to identify immunoreactive peptides.		
XX			
SQ	Sequence	591 AA;	
Query Match			
Best Local Similarity 99.7%; Score 1808; DB 20; Length 591;			
Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	NNVDFVFTYDTVEFLSADTKTTTVNVESKDKKTEVKIGAKTSVIREKDKGLVTGDKG	60

Query Match 99.7%; Score 1808; DB 20; Length 591;

Best Local Similarity 99.7%; Pred. No. 3.2e-117;		Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1	NNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVIKEKDGKLVTKDKG	60
Db	236	DNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVIKEKDGKLVTKDKG	295
QY	61	ENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFETVTSCTNVTFFASGKG	120
Db	296	ENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFETVTSCTNVTFFASGKG	355
QY	121	TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG	180
Db	356	TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG	415
QY	181	MDETVMINAGNIEITRNKKNIDIAISMTPOFSSVSLGAGADAPTLVSDGDALNVGSKKD	240
Db	416	MDETVMINAGNIEITRNKKNIDIAISMTPOFSSVSLGAGADAPTLVSDGDALNVGSKKD	475
QY	241	NKPVRTITNVPAGVKEGDTVNVQAOLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYL	300
Db	476	NKPVRTITNVPAGVKEGDTVNVQAOLKGVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYL	535
QY	301	PKKSMMAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW	356
Db	536	PKKSMMAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW	591
RESULT 7			
AAU06171			
ID	AAU06171 standard; Protein; 591 AA.		
XX	AAU06171;		
AC			
XX			
DT	24-OCT-2001 (first entry)		
XX			
DE	N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.		
XX			
KW	Surface antigen NhhA; meningococcal disease; meningitis vaccine.		
XX			
OS	Neisseria meningitidis strain PMC21.		
XX			
FH	Key Location/Qualifiers		
FT	Peptide	1..51	
FT	/label= Signal_peptide		
FT	Region	1..50	
FT	/label= C1		
FT	/note= "Conserved region 1"		
FT	Region	51..108	
FT	/label= V1		
FT	/note= "Variable region 1"		
FT	Protein		
FT	/label= Mature_NhhA		
FT	/note= "Predicted mature protein, specifically		
FT	claimed in claim 12"		
FT	Region	109..120	
FT	/label= C2		
FT	/note= "Conserved region 2"		
FT	Region	121..124	
FT	/label= V2		
FT	/note= "Variable region 2"		
FT	Region	125..188	
FT	/label= C3		
FT	/note= "Conserved region 3"		
FT	Region	189..210	
FT	/label= V3		
FT	/note= "Variable region 3"		
FT	Region	211..229	
FT	/label= C4		
FT	/note= "Conserved region 4"		
FT	Region	230..236	
FT	/label= V4		
FT	/note= "Variable region 4"		

Region	237..591																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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ID XX AAU06175 standard; Protein; 591 AA.
AC AAU06175;
DT 24-OCT-2001 (first entry)
DE N. meningitidis EG329 surface antigen Nhha polypeptide sequence.
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.
KW Neisseria meningitidis strain EG329.
OS
FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..108
FT /label= V1
FT /note= "Variable region 1"
FT Region 109..120
FT /label= C2
FT /note= "Conserved region 2"
FT Region 121..124
FT /label= V2
FT /note= "Variable region 2"
FT Region 125..188
FT /label= C3
FT /note= "Conserved region 3"
FT Region 189..210
FT /label= V3
FT /note= "Variable region 3"
FT Region 211..229
FT /label= C4
FT /note= "Conserved region 4"
FT Region 230..236
FT /label= V4
FT /note= "Variable region 4"
FT Region 237..591
FT /label= C5
FT /note= "Conserved region 5"
XX WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09165.
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha

CC from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 591 AA;
Query Match 99.7%; Score 1808; DB 22; Length 591;
Best Local Similarity 99.7%; Pred. No. 3.2e-117;
Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NNVDVVRTYDTVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVIKEKDKLVTGKDKG 60
DB :|||||
236 DNVDVVRTYDTVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVIKEKDKLVTGKDKG 295
QY 61 ENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKFETVTSNTVTFASGKG 120
DB :|||||
296 ENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKFETVTSNTVTFASGKG 355
QY 121 TTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKGK 180
DB :|||||
356 TTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKGK 415
QY 181 MDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKD 240
DB :|||||
416 MDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKD 475
QY 241 NKPVRTTNVAPGVKEGDTVNVQNLKGAQNLRNIDNVNAGNARAGIAQAATAGLVQAYL 300
DB :|||||
476 NKPVRTTNVAPGVKEGDTVNVQNLKGAQNLRNIDNVNAGNARAGIAQAATAGLVQAYL 535
QY 301 PGKSMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 356
DB :|||||
536 PGKSMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591
RESULT 9
AAU06186
ID AAU06186 standard; Protein; 502 AA.
XX
AC AAU06186;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 Nhha deletion mutant #4.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutein.
XX
OS Neisseria meningitidis strain PMC21.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..49
FT /label= Signal_peptide
FT Protein 50..502
FT /label= Mature_Nhha_deletion_mutant_#4
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
XX
PN WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09176.
XX

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XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 9; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #4.
XX
XX SQ Sequence 502 AA;
Query Match 99.7%; Score 1807; DB 22; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.1e-117;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 NVDFVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKLVTGDKGE 61
Db 148 NVDFVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKLVTGDKGE 207
Qy 62 NGSTDGEGGLVTAKEVIDAVNKGWRMKTNTTANGQTGQADKFTVTSGTNTVTFASGKG 121
Db 208 NGSTDGEGGLVTAKEVIDAVNKGWRMKTNTTANGQTGQADKFTVTSGTNTVTFASGKG 267
Qy 122 TATVSKDDQGNITVMYDVNVGDALNVNQLNSGNWLDKSKAVAGSSGKVISGNVSPSKGM 181
Db 268 TATVSKDDQGNITVMYDVNVGDALNVNQLNSGNWLDKSKAVAGSSGKVISGNVSPSKGM 327
Qy 182 DETVINAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDN 241
Db 328 DETVINAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDN 387
Qy 242 KPVRTITNVPAGVKEGDTNVAQLKGVAQNLNNDVGNARAGIAQAIATAGLVQAYLP 301
Db 388 KPVRTITNVPAGVKEGDTNVAQLKGVAQNLNNDVGNARAGIAQAIATAGLVQAYLP 447
Qy 302 GKSMMAIGGCTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 356
Db 448 GKSMMAIGGCTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 502
RESULT 10
AA57045
ID AA57045 standard; Protein: 591 AA.
XX
XX AA57045;
XX
XX 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
XX BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX
XX Neisseria meningitidis.
XX
XX Key Location/Qualifiers
FH Misc-difference 90
FT /note= "Encoded by AAT"
FT Misc-difference 92
FT /note= "Encoded by GAT"
FT Misc-difference 98
FT /note= "Encoded by AAC"
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FT Misc-difference 108
FT /note= "Encoded by AATC"
FT Misc-difference 123
FT /note= "Encoded by ACA"
FT Misc-difference 269
FT /note= "Encoded by AAA"
FT Misc-difference 389
FT /note= "Encoded by CGT"
XX
XX WO9958683-A2.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-EP03255.
XX
XX 13-MAY-1998; 98GB-0010276.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Ruelle J;
XX
XX WPI: 2000-053103/04.
XX N-PSDB; AAZ39865.
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
XX treatment or prevention of bacterial infections in mammal -
XX
XX Claim 4; Fig 2; 74pp; English.
XX
XX This is the Neisseria meningitidis BASB029 amino acid sequence from
XX serogroup B strain H44/76. The BASB029 protein is homologous to the
XX Haemophilus influenzae surface fibril (HSF) protein. The invention
XX relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
XX polypeptide sequences (AA57044-Y57045) and their immunogenic fragments.
XX BASB029 polypeptides are useful in a method of diagnosing a Neisseria
XX meningitidis infection in a mammal. Compositions containing BASB029
XX polynucleotides and polypeptides are useful for generating an immune
XX response in an animal. A therapeutic composition comprising an antibody
XX directed against BasB029 is useful in treating humans with Neisseria
XX meningitidis disease. The polynucleotide is useful in the diagnosis of
XX the stage of infection, type of infection, susceptibility to an
XX infection which results from increased or decreased expression of the
XX polynucleotide, and for therapeutic or prophylactic purposes,
XX particularly genetic immunisation. Antibodies against BASB029
XX polynucleotides and polypeptides are also useful for treating infections
XX particularly bacterial infections. The protein is useful in the
XX screening and development of antibacterial drugs. Fused recombinant
XX protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.
XX
XX SQ Sequence 591 AA;
Query Match 99.6%; Score 1805; DB 21; Length 591;
Best Local Similarity 99.4%; Pred. No. 5.1e-117;
Matches 354; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NNVDVVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKLVTGDKG 60
Db 236 NNVDVVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKLVTGDKG 295
Qy 61 ENGSDTDEGGLVTAKEVIDAVNKGWRMKTNTTANGQTGQADKFTVTSGTNTVTFASGKG 120
Db 296 ENGSDTDEGGLVTAKEVIDAVNKGWRMKTNTTANGQTGQADKFTVTSGTNTVTFASGKG 355
Qy 121 TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNWLDKSKAVAGSSGKVISGNVSPSKGM 180
Db 356 TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNWLDKSKAVAGSSGKVISGNVSPSKGM 415
Qy 181 MDETVINAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDN 240
Db 416 MDETVINAGNNIETTRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKDN 475
Qy 241 NKPVRTITNVPAGVKEGDTNVAQLKGVAQNLNNDVGNARAGIAQAIATAGLVQAYL 300
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|||||
Db 476 NKPRITNVAPGVKEGDTNVAQLKGVAQNLNNDVGNARAGIAQAATAGLVQAYL 535
Qy 301 PGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFGASASVGYOW 356
Db 536 PGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFGASASVGYOW 591

RESULT 11
AAY23737
ID AAY23737 standard; Protein; 592 AA.
XX
AC AAY23737;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN W09931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
WPI; 1999-418754/35.
DR N-PSDB; AAX85788.
XX
Neisseria meningitidis surface proteins useful for treating N.
meningitidis infections
XX
Claim 1; Page 86-87; 132pp; English.
XX
The present sequence represents a surface protein of Neisseria
meningitidis which is approximately 62 kDa. The N. meningitidis
surface glycoproteins, nucleic acids, the primers and optionally
a thermostable polymerase, or antibodies are useful in a kit for
the detection or diagnosis of N. meningitidis infection in humans.
The N. meningitidis surface glycoproteins can also be used to
prevent or treat N. meningitidis infection in humans, especially
in the form of vaccines. The proteins and antibodies can also
be used to identify immunoreactive peptides.
XX
SQ Sequence 592 AA;
Query Match 99.5%; Score 1804; DB 20; Length 592;
Best Local Similarity 99.4%; Pred. No. 6.1e-117;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNVDVFRTYDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDKG 60
Db 237 DNVDFVRTYDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDKG 296
Qy 61 ENGSDTEGEGLVTAKEVIDAVNKGWRMKTMTTANGOTGOADKFEVTSCTNVTFSAGKG 120
Db 297 ENGSDTEGEGLVTAKEVIDAVNKGWRMKTMTTANGOTGOADKFEVTSCTNVTFSAGKG 356
Qy 121 TTATVSKDDQGNITVMYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPSKGK 180
Db 357 TTATVSKDDQGNITVMYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPSKGK 416
Qy 181 MDETNTNAGNINIEITRNGKNIDTATSWTPOFSSVSLGAGADAPTLSVDGALNVGSKKD 240
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|||||
Db 417 MDETNTNAGNINIEITRNGKNIDTATSWTPOFSSVSLGAGADAPTLSVDGALNVGSKKD 476
Qy 241 NKPRITNVAPGVKEGDTNVAQLKGVAQNLNNDVGNARAGIAQAATAGLVQAYL 300
Db 477 NKPRITNVAPGVKEGDTNVAQLKGVAQNLNNDVGNARAGIAQAATAGLVQAYL 536
Qy 301 PGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFGASASVGYOW 356
Db 537 PGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFGASASVGYOW 592

RESULT 12
AAY23740
ID AAY23740 standard; Protein; 594 AA.
XX
AC AAY23740;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN W09931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
WPI; 1999-418754/35.
DR N-PSDB; AAX85792.
XX
Neisseria meningitidis surface proteins useful for treating N.
meningitidis infections
XX
Claim 1; Page 100-101; 132pp; English.
XX
The present sequence represents a surface protein of Neisseria
meningitidis which is approximately 62 kDa. The N. meningitidis
surface glycoproteins, nucleic acids, the primers and optionally
a thermostable polymerase, or antibodies are useful in a kit for
the detection or diagnosis of N. meningitidis infection in humans.
The N. meningitidis surface glycoproteins can also be used to
prevent or treat N. meningitidis infection in humans, especially
in the form of vaccines. The proteins and antibodies can also
be used to identify immunoreactive peptides.
XX
SQ Sequence 594 AA;
Query Match 96.7%; Score 1753.5; DB 20; Length 594;
Best Local Similarity 97.2%; Pred. No. 1.9e-113;
Matches 347; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
Qy 1 NNVDVFRTYDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDKG 60
Db 238 DNVDFVRTYDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDKG 297
Qy 61 ENGSDTEGEGLVTAKEVIDAVNKGWRMKTMTTANGOTGOADKFEVTSCTNVTFSAGKG 120
Db 298 ENGSDTEGEGLVTAKEVIDAVNKGWRMKTMTTANGOTGOADKFEVTSCTNVTFSAGKG 357
Qy 121 TTATVSKDDQGNITVMYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPSKGK 180
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Db 358 TTATVSKDDGNTVMYDVGALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKG 417
QY 181 MDETVINAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTILSVDDG-ALNVGSKK 239
Db 418 MDETVINAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTILSVDDGALNVGSKD 477
QY 240 DNKPVRTITNVPAGVKEGDTNVNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAY 299
Db 478 ANKPVRTITNVPAGVKEGDTNVNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAY 537
QY 300 LPKGSMAIIGGGTYRGEAGYAGYSSISDGGNWIIRGTASGNSRGHFGASASVGYOW 356
Db 538 LPKGSMAIIGGGTYRGEAGYAGYSSISDGGNWIIRGTASGNSRGHFGASASVGYOW 594

RESULT 13
AAV57044
ID AAY57044 standard; Protein; 594 AA.
XX
AC AAY57044;
XX
DT 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
XX
KW BASB029; Nisseria meningitidis; surface fibril protein; HSP; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Misc-difference 104
FT /note= "Encoded by AATC"
XX
XX WO958683-A2.
XX
PD 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-EP03255.
XX
PR 13-MAY-1998; 98GB-0010276.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI: 2000-053103/04.
DR N-PSDB; AA239864.
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
XX treatment or prevention of bacterial infections in mammal
XX
XX Claim 4; Fig 2; 74pp; English.
XX
XX This is the Nisseria meningitidis BASB029 amino acid sequence from
XX serogroup B strain ATCC13090. The BASB029 protein is homologous to the
XX Haemophilus influenzae surface fibril (HSP) protein. The invention
XX relates to BASB029 polynucleotide sequences (AA239864-239865) and
XX polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.
XX BASB029 polypeptides are useful in a method of diagnosing a Neisseria
XX meningitidis infection in a mammal. Compositions containing BASB029
XX polynucleotides and polypeptides are useful for generating an immune
XX response in an animal. A therapeutic composition comprising an antibody
XX directed against BASB029 is useful in treating humans with Neisseria
XX meningitidis disease. The polynucleotide is useful in the diagnosis of
XX the stage of infection, type of infection, susceptibility to an
XX infection which results from increased or decreased expression of the
XX polynucleotide, and for therapeutic or prophylactic purposes,
XX particularly genetic immunisation. Antibodies against BASB029
XX polynucleotides and polypeptides are also useful for treating infections
XX particularly bacterial infections. The protein is useful in the
XX screening and development of antibacterial drugs. Fused recombinant
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CC protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.
SQ Sequence 594 AA;
Query Match 96.7%; Score 1753.5; DB 21; Length 594;
Best Local Similarity 97.2%; Pred. No. 1.9e-113;
Matches 347; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
QY 1 NNVDVFTYDTVFELSDATKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGDKG 60
Db 238 DNVDVFTYDTVFELSDATKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGDKG 297
QY 61 ENGSSTDEGELVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFETVTSNTVTFASGK 120
Db 298 ENDSSTDKGELVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFETVTSNTVTFASGK 357
QY 121 TTATVSKDDGNTVMYDVGALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKG 180
Db 358 TTATVSKDDGNTVMYDVGALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKG 417
QY 181 MDETVINAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTILSVDDG-ALNVGSKK 239
Db 418 MDETVINAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTILSVDDGALNVGSKD 477
QY 240 DNKPVRTITNVPAGVKEGDTNVNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAY 299
Db 478 ANKPVRTITNVPAGVKEGDTNVNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAY 537
QY 300 LPKGSMAIIGGGTYRGEAGYAGYSSISDGGNWIIRGTASGNSRGHFGASASVGYOW 356
Db 538 LPKGSMAIIGGGTYRGEAGYAGYSSISDGGNWIIRGTASGNSRGHFGASASVGYOW 594

RESULT 14
AAU06174
ID AAU06174 standard; Protein; 594 AA.
XX
AC AAU06174;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
XX Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain EG327.
XX
FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..104
FT /label= V1
FT /note= "Variable region 1"
FT Region 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT Region 117..126
FT /label= V2
FT /note= "Variable region 2"
FT Region 127..190
FT /label= C3
FT /note= "Conserved region 3"
FT Region 191..212
FT /label= V3
FT /note= "Variable region 3"
FT Region 213..231
FT /label= C4
FT /note= "Conserved region 4"
FT Region 232..238
FT /label= V4
FT /note= "Variable region 4"
```


CC from N. meningitidis strain 22491 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 592 AA;

Query Match	96.7%;	Score 1752.5;	DB 22;	Length 592;
Best Local Similarity	97.5%;	Pred. No. 2.2e-113;		
Matches 347;	Conservative 3;	Mismatches 5;	Indels 1;	Gaps 1;

QY	2	NVDFVRTYDTVEFLSADTKTTVNVESKDNGKTEVKIGAKTSVIKEKDGLVTGDKGE	61
Db	237	NVDFVRTYDTVEFLSADTKTTVNVESKDNGKTEVKIGAKTSVIKEKDGLVTGDKGE	296
QY	62	NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGOADKFEVTSCTNVTFFASGKGT	121
Db	297	NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGOADKFEVTSCTNVTFFASGKGT	356
QY	122	TATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKM	181
Db	357	TATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNVSPSKGKM	416
QY	182	DETVNINAGNNIEITRNKGNIDIASMTPOFSSVSLGAGADAPTLSDVDG-ALNVGSKKD	240
Db	417	DETVNINAGNNIEISRNKGNIDIASMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDA	476
QY	241	NKPVRTITNVAPGVKEGDTVNVQALKGVAQNLRINDVNDGNARAGIAQAIAITAGLVOAYL	300
Db	477	NKPVRTITNVAPGVKEGDTVNVQALKGVAQNLRINDVNDGNARAGIAQAIAITAGLVOAYL	536
QY	301	PGKSMMAIGGGTYRGEAGYAIGYSISDGGNNWIKGTASGNSRGRHFGASASVGYOW	356
Db	537	PGKSMMAIGGGTYRGEAGYAIGYSISDGGNNWIKGTASGNSRGRHFGASASVGYOW	592

Search completed: October 6, 2003, 09:22:43
Job time : 31.5718 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:14:45 ; Search time 9.52015 Seconds
(without alignments)
1582.188 Million cell updates/sec

Title: us-09-771-382-37
Perfect score: 1813
Sequence: 1 NNVDVFRVTYDTEFLSADTK.....TASGSRGHFGASASVGYQW 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued_Patents_AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1808	99.7	591	3	US-09-377-155-11
2	1808	99.7	591	3	US-09-377-155-21
3	1808	99.7	591	4	US-09-669-974-11
4	1808	99.7	591	4	US-09-669-974-21
5	1804	99.5	592	3	US-09-377-155-2
6	1804	99.5	592	4	US-09-669-974-2
7	1753.5	96.7	594	3	US-09-377-155-9
8	1753.5	96.7	594	4	US-09-669-974-9
9	1748.5	96.4	599	3	US-09-377-155-15
10	1748.5	96.4	599	4	US-09-669-974-15
11	1741.5	96.1	594	3	US-09-377-155-7
12	1741.5	96.1	594	4	US-09-669-974-7
13	1728.5	95.3	592	3	US-09-377-155-17
14	1728.5	95.3	592	4	US-09-669-974-17
15	1728.5	95.3	598	3	US-09-377-155-5
16	1728.5	95.3	598	4	US-09-377-155-13
17	1728.5	95.3	598	4	US-09-669-974-5
18	1728.5	95.3	598	4	US-09-669-974-13
19	1715.5	94.6	589	3	US-09-377-155-19
20	1715.5	94.6	589	4	US-09-669-974-19
21	608	33.5	1098	1	US-08-409-995-2
22	608	33.5	1098	3	US-08-685-467-2
23	608	33.5	1098	3	US-09-377-155-32
24	608	33.5	1098	3	US-08-913-942-2
25	608	33.5	1098	4	US-09-669-974-32
26	608	33.5	1098	4	US-09-268-347-44
27	590	32.5	658	1	US-08-409-995-5

28	590	32.5	658	3	US-08-585-467-5	Sequence 5, Appli
29	590	32.5	658	3	US-08-913-942-5	Sequence 5, Appli
30	581.5	32.1	1094	4	US-09-268-347-32	Sequence 32, Appl
31	569	31.4	2353	3	US-09-377-155-33	Sequence 33, Appl
32	569	31.4	2353	3	US-08-913-942-4	Sequence 4, Appli
33	569	31.4	2353	4	US-09-669-974-33	Sequence 33, Appl
34	569	31.4	2411	4	US-09-268-347-36	Sequence 36, Appl
35	568.5	31.4	2354	4	US-09-268-347-47	Sequence 47, Appl
36	549	30.3	1912	1	US-08-409-995-4	Sequence 4, Appli
37	549	30.3	1912	3	US-08-685-467-4	Sequence 4, Appli
38	529.5	29.2	607	1	US-08-409-995-6	Sequence 6, Appli
39	529.5	29.2	607	3	US-08-685-467-6	Sequence 6, Appli
40	529.5	29.2	607	3	US-08-913-942-6	Sequence 6, Appli
41	412.5	22.8	679	3	US-08-913-942-15	Sequence 15, Appl
42	412.5	22.8	679	4	US-09-268-347-26	Sequence 26, Appl
43	339	18.7	1004	4	US-09-268-347-30	Sequence 30, Appl
44	331.5	18.3	1002	4	US-09-268-347-24	Sequence 24, Appl
45	325	17.9	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-377-155-11
; Sequence 11, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-377-155-11

Query Match	99.7%	Score	1808;	DB	3;	Length	591;
Best Local Similarity	99.7%	Pred. No.	3.8e-141;				
Matches	355;	Conservative	1;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	NNVDVFRVTYDTEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDKG	60				
Db	236	NNVDVFRVTYDTEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDKGLVTGDKG	295				
Qy	61	ENGSSDDEGELGTAKETVIDAVNKAGWRMKTITANGOTQADKFETVTSCTNTVTFASGKG	120				
Db	296	ENGSSDDEGELGTAKETVIDAVNKAGWRMKTITANGOTQADKFETVTSCTNTVTFASGKG	355				
Qy	121	TTATVSKDDOGNTVMYDVMVGDALNVNQLONGSNLDSKAVAGSSKVTSGNVSPSKGK	180				
Db	356	TTATVSKDDOGNTVMYDVMVGDALNVNQLONGSNLDSKAVAGSSKVTSGNVSPSKGK	415				
Qy	181	MDETNNAGNNIEITRNGKNIDITATSMTPQFSVSVISGACADAPTLSDVDGALNVGSKKD	240				
Db	416	MDETNNAGNNIEITRNGKNIDITATSMTPQFSVSVISGACADAPTLSDVDGALNVGSKKD	475				
Qy	241	NKPVRTTNVAPGKGVGTNNVAQLKGVAQNNLRIDNVNVDGNARAGIAQAATAGLVOAYL	300				
Db	476	NKPVRTTNVAPGKGVGTNNVAQLKGVAQNNLRIDNVNVDGNARAGIAQAATAGLVOAYL	535				
Qy	301	PGKSMIAIGGTYRGEAGYAGYSSISDSDGNWIKGTASGNSRGHFGASASVGYQW	356				
Db		PGKSMIAIGGTYRGEAGYAGYSSISDSDGNWIKGTASGNSRGHFGASASVGYQW					

Db 536 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWI1KGTASGNSRCHFGASASVGYQW 591

RESULT 2

US-09-377-155-21

; Sequence 21, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; CURRENT FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-377-155-21

Query Match 99.7%; Score 1808; DB 3; Length 591;

Best Local Similarity 99.7%; Pred. No. 3.8e-141;

Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNVDVFRVTDYTVFELSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKLVTKGDKG 60

Db 236 DNVDFVRTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKLVTKGDKG 295

Qy 61 ENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKPFETVTSNTVTFASGKG 120

Db 296 ENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKPFETVTSNTVTFASGKG 355

Qy 121 TTATVSKDDOGNITVMYDNNVGDALNVQNSGNWLDKAVAGSSGKVISGNNVSPSKG 180

Db 356 TTATVSKDDOGNITVMYDNNVGDALNVQNSGNWLDKAVAGSSGKVISGNNVSPSKG 415

Qy 181 MDETVINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGDLNVGSKKD 240

Db 416 MDETVINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGDLNVGSKKD 475

Qy 241 NKPVRTNVPAGVKEGDTVNAQLKGVAQNINNRIDNVGNARAGIAQAATATAGLVQAYL 300

Db 476 NKPVRTNVPAGVKEGDTVNAQLKGVAQNINNRIDNVGNARAGIAQAATATAGLVQAYL 535

Qy 301 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWI1KGTASGNSRCHFGASASVGYQW 356

Db 536 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWI1KGTASGNSRCHFGASASVGYQW 591

RESULT 3

US-09-669-974-11

; Sequence 11, Application US/09669974

; Patent No. 633173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; CURRENT FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

US-09-669-974-11

Query Match 99.7%; Score 1808; DB 4; Length 591;

Best Local Similarity 99.7%; Pred. No. 3.8e-141;

Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNVDVFRVTDYTVFELSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKLVTKGDKG 60

Db 236 DNVDFVRTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKLVTKGDKG 295

Qy 61 ENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKPFETVTSNTVTFASGKG 120

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-669-974-11

Query Match 99.7%; Score 1808; DB 4; Length 591;

Best Local Similarity 99.7%; Pred. No. 3.8e-141;

Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNVDVFRVTDYTVFELSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKLVTKGDKG 60

Db 236 DNVDFVRTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKLVTKGDKG 295

Qy 61 ENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKPFETVTSNTVTFASGKG 120

Db 296 ENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKPFETVTSNTVTFASGKG 355

Qy 121 TTATVSKDDOGNITVMYDNNVGDALNVQNSGNWLDKAVAGSSGKVISGNNVSPSKG 180

Db 356 TTATVSKDDOGNITVMYDNNVGDALNVQNSGNWLDKAVAGSSGKVISGNNVSPSKG 415

Qy 181 MDETVINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGDLNVGSKKD 240

Db 416 MDETVINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGDLNVGSKKD 475

Qy 241 NKPVRTNVPAGVKEGDTVNAQLKGVAQNINNRIDNVGNARAGIAQAATATAGLVQAYL 300

Db 476 NKPVRTNVPAGVKEGDTVNAQLKGVAQNINNRIDNVGNARAGIAQAATATAGLVQAYL 535

Qy 301 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWI1KGTASGNSRCHFGASASVGYQW 356

Db 536 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWI1KGTASGNSRCHFGASASVGYQW 591

RESULT 4

US-09-669-974-21

; Sequence 21, Application US/09669974

; Patent No. 633173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; CURRENT FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-669-974-21

Query Match 99.7%; Score 1808; DB 4; Length 591;

Best Local Similarity 99.7%; Pred. No. 3.8e-141;

Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNVDVFRVTDYTVFELSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKLVTKGDKG 60

Db 236 DNVDFVRTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKLVTKGDKG 295

Qy 61 ENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKPFETVTSNTVTFASGKG 120

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Db 296 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 355
QY 121 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 180
Db 356 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 415
QY 181 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 240
Db 416 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 475
QY 241 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 300
Db 476 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 535
QY 301 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 356
Db 536 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591

RESULT 5
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6157312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 99.5%; Score 1804; DB 3; Length 592;
Best Local Similarity 99.4%; Pred. No. 8.1e-141;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNVDVFRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVKEKDGKLVTKGDKG 60
:|||||
Db 237 DNVDVFRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVKEKDGKLVTKGDKG 296
QY 61 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 120
:|||||
Db 297 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 356
:|||||
QY 121 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 180
:|||||
Db 357 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 416
QY 181 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 240
:|||||
Db 417 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 476
QY 241 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 300
:|||||
Db 477 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 536
QY 301 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 356
:|||||
Db 537 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592
:|||||

RESULT 6
US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2

Query Match 99.5%; Score 1804; DB 4; Length 592;
Best Local Similarity 99.4%; Pred. No. 8.1e-141;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNVDVFRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVKEKDGKLVTKGDKG 60
:|||||
Db 237 DNVDVFRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVKEKDGKLVTKGDKG 296
QY 61 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 120
:|||||
Db 297 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 356
:|||||
QY 121 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 180
:|||||
Db 357 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 416
QY 181 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 240
:|||||
Db 417 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 476
QY 241 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 300
:|||||
Db 477 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 536
QY 301 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 356
:|||||
Db 537 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592
:|||||

RESULT 7
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6157312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
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Db 296 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 355
QY 121 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 180
Db 356 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 415
QY 181 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 240
Db 416 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 475
QY 241 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 300
Db 476 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 535
QY 301 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 356
Db 536 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 591

RESULT 5
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6157312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 99.5%; Score 1804; DB 3; Length 592;
Best Local Similarity 99.4%; Pred. No. 8.1e-141;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNVDVFRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVKEKDGKLVTKGDKG 60
:|||||
Db 237 DNVDVFRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVKEKDGKLVTKGDKG 296
QY 61 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 120
:|||||
Db 297 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 356
:|||||
QY 121 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 180
:|||||
Db 357 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 416
QY 181 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 240
:|||||
Db 417 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 476
QY 241 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 300
:|||||
Db 477 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 536
QY 301 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 356
:|||||
Db 537 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592
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RESULT 6
US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2

Query Match 99.5%; Score 1804; DB 4; Length 592;
Best Local Similarity 99.4%; Pred. No. 8.1e-141;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNVDVFRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVKEKDGKLVTKGDKG 60
:|||||
Db 237 DNVDVFRTYDTVEFLSADTKTTTVNVESKDNGKKEVKIGAKTSVKEKDGKLVTKGDKG 296
QY 61 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 120
:|||||
Db 297 ENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFEFVTSGTNNVTFASGKG 356
:|||||
QY 121 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 180
:|||||
Db 357 TTATVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKGK 416
QY 181 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 240
:|||||
Db 417 MDETNNAGNIEITRNKNIDIAATSMTPQSSVSLGAGADAPTLVSVDGDALNVGSKKD 476
QY 241 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 300
:|||||
Db 477 NKPVRTNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNDRAGIATAGLQVAYL 536
QY 301 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 356
:|||||
Db 537 PKGSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592
:|||||

RESULT 7
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6157312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match
Best Local Similarity 96.7%; Score 1753.5; DB 3; Length 594;
Matches 347; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 NNVDVFTYDTVEFLSADTTTNNVESKONGKTEVKGIAKTSVKEKDKLVTGDKG 60
Db 238 DNVDVFTYDTVEFLSADTTTNNVESKONGKTEVKGIAKTSVKEKDKLVTGDKG 297
Qy 61 ENGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKFEVTSCTNVTFFASGK 120
Db 298 ENDSSTDKGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKFEVTSCTNVTFFASGK 357
Qy 121 TTATVSKDDOGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 180
Db 358 TTATVSKDDOGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 417
Qy 181 MDETVINAGNNIEITRNGKNIDIATSMTPQFSVSLGAGADAPTLSDVDG-ALNVGSKK 239
Db 418 MDETVINAGNNIEITRNGKNIDIATSMTPQFSVSLGAGADAPTLSDVDDEGALNVGSKD 477
Qy 240 DNKPVRTITNVPAGVKEGDTVNAQLKGVAQNLRINDVGNARAGIAQAIAATAGLVQAY 299
Db 478 ANKPVRTITNVPAGVKEGDTVNAQLKGVAQNLRINDVGNARAGIAQAIAATAGLVQAY 537
Qy 300 LPKSKMMAIGGTYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGFASASVGYQW 356
Db 538 LPKSKMMAIGGTYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGFASASVGYQW 594

RESULT 9
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match 96.4%; Score 1748.5; DB 3; Length 599;
Best Local Similarity 97.2%; Pred. No. 3.1e-136;
Matches 347; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

Qy 1 NNVDVFTYDTVEFLSADTTTNNVESKONGKTEVKGIAKTSVKEKDKLVTGDKG 60
Db 243 DNVDVFTYDTVEFLSADTTTNNVESKONGKRTVEKIGAKTSVKEKDKLVTGDKG 302
Qy 61 ENGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKFEVTSCTNVTFFASGK 120
Db 303 ENGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKFEVTSCTNVTFFASGK 362
Qy 121 TTATVSKDDOGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 180
Db 363 TTATVSKDDOGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 422
Qy 181 MDETVINAGNNIEITRNGKNIDIATSMTPQFSVSLGAGADAPTLSDVDG-ALNVGSKK 239
Db 423 MDETVINAGNNIEITRNGKNIDIATSMTPQFSVSLGAGADAPTLSDVDKALNVGSKD 482
Qy 240 DNKPVRTITNVPAGVKEGDTVNAQLKGVAQNLRINDVGNARAGIAQAIAATAGLVQAY 299
Db 483 ANKPVRTITNVPAGVKEGDTVNAQLKGVAQNLRINDVGNARAGIAQAIAATAGLVQAY 542
Qy 300 LPKSKMMAIGGTYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGFASASVGYQW 356
Db 543 LPKSKMMAIGGTYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGFASASVGYQW 599

RESULT 10
US-09-669-974-15
; Sequence 15, Application US/09669974
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; Patent No. 633173
; ORGANISM: Neisseria meningitidis
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-669-974-15

Query Match          96.4%; Score 1748.5; DB 4; Length 599;
Best Local Similarity 97.2%; Pred. No. 3.1e-136;
Matches 347; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

Qy 1 NNVDFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKDKG 60
:|||||
Db 243 DNVDVFRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKDKG 302

Qy 61 ENGSSDDEGELVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSNTVTFASGKG 120
:|||||
Db 303 ENGSSDDEGELVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSNTVTFASGKG 362

Qy 121 TTATVSKDDOQGNITVMYDNNVGDALNNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 180
:|||||
Db 363 TTATVSKDDOQGNITVMYDNNVGDALNNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 422

Qy 181 MDETVINAGNNEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKK 239
:|||||
Db 423 MDETVINAGNNEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSVDGDKGALNVGSKD 482

Qy 240 DNKPVRTITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVDCNARAGIAQAIAATAGLVQAY 299
:|||||
Db 483 ANKPVRTITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVDCNARAGIAQAIAATAGLVQAY 542

Qy 300 LPKSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 356
:|||||
Db 543 LPKSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 599

RESULT 11
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-669-974-15

Query Match          96.1%; Score 1741.5; DB 4; Length 594;
Best Local Similarity 96.9%; Pred. No. 1.2e-135;
Matches 346; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NNVDFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKDKG 60
:|||||
Db 238 DNVDVFRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKDKG 297

Qy 61 ENGSSDDEGELVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSNTVTFASGKG 120
:|||||
Db 298 ENGSSDDEGELVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSNTVTFASGKG 357

Qy 121 TTATVSKDDOQGNITVMYDNNVGDALNNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 180
:|||||
Db 358 TTATVSKDDOQGNITVMYDNNVGDALNNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 417
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; ORGANISM: Neisseria meningitidis
; US-09-377-155-7

Query Match          96.1%; Score 1741.5; DB 3; Length 594;
Best Local Similarity 96.9%; Pred. No. 1.2e-135;
Matches 346; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NNVDFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKDKG 60
:|||||
Db 238 DNVDVFRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKDKG 297

Qy 61 ENGSSDDEGELVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSNTVTFASGKG 120
:|||||
Db 298 ENGSSDDEGELVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSNTVTFASGKG 357

Qy 121 TTATVSKDDOQGNITVMYDNNVGDALNNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 180
:|||||
Db 358 TTATVSKDDOQGNITVMYDNNVGDALNNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 417

181 MDETVINAGNNEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKK 239
:|||||
418 MDETVINAGNNEITRNKGNIDIAATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKD 477

240 DNKPVRTITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVDCNARAGIAQAIAATAGLVQAY 299
:|||||
478 TNKPVRTITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVDCNARAGIAQAIAATAGLVQAY 537

300 LPKSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 356
:|||||
538 LPKSMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594

RESULT 12
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-09-669-974-7

Query Match          96.1%; Score 1741.5; DB 4; Length 594;
Best Local Similarity 96.9%; Pred. No. 1.2e-135;
Matches 346; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NNVDFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKDKG 60
:|||||
Db 238 DNVDVFRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKDKG 297

Qy 61 ENGSSDDEGELVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSNTVTFASGKG 120
:|||||
Db 298 ENGSSDDEGELVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSNTVTFASGKG 357

Qy 121 TTATVSKDDOQGNITVMYDNNVGDALNNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 180
:|||||
Db 358 TTATVSKDDOQGNITVMYDNNVGDALNNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 417
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Query Match 95.3%; Score 1728.5; DB 3; Length 598;
Best Local Similarity 95.8%; Pred. No. 1.4e-134;
Matches 342; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY	1	NNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTKGDKG	60
Db	242	DNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIKEKDGKLVTKGKG	301
QY	61	ENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTQADKFETVTSCTNVTTFASGKG	120
Db	302	ENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTQADKFETVTSCTNVTTFASGNG	361
QY	121	TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG	180
Db	362	TTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG	421
QY	181	MDETVMINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDGD-ALNVGSKK	239
Db	422	MDETVMINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDGD-ALNVGSKD	481
QY	240	DNKPVRTITNAPGVKEGDVTNVAQLKGVAQNLRNIDNVNAGIQAIAIATAGLVQAY	299
Db	482	ANKPVRTITNAPGVKEGDVTNVAQLKGVAQNLRNIDNVNAGIQAIAIATAGLAQAY	541
QY	300	LPGKSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRHFASVGYQW	356
Db	542	LPGKSMMAIGGGTYRGEAGYAIGYSSISDGTNNVVKGTASGNSRHFGTASVGYQW	598

Search completed: October 6, 2003, 09:35:59
Job time : 10.5202 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 10.1906 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-37
Perfect score: 1813
Sequence: 1 NNVDVVRTYDTVEFLSADTK.....TASGNSRGHGASASVGQW 356
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1808	99.7	591	2 G81133	adhesin NMB0992 [i
2	1752.5	96.7	592	2 A81888	probable surface f
3	332.5	18.3	2059	2 D82671	surface protein XF
4	327	18.0	1190	2 A82615	surface protein XF
5	325	17.9	1588	2 A86036	probable adhesin z
6	325	17.9	1588	2 H91188	probable adhesin E
7	314	17.3	1107	2 AC0976	probable autotrans
8	307.5	17.0	658	2 AH0110	probable surface p
9	183.5	10.1	365	2 AB3486	cell surface prote
10	176.5	9.7	1004	2 C82672	surface-exposed ou
11	167.5	9.2	585	2 F90961	flagellin [importe
12	167.5	9.2	585	2 F85809	hypothetical prote
13	163	9.0	298	2 I64138	adhesin homolog HI
14	156.5	8.6	933	2 S41539	fibrinogen-binding
15	156	8.6	584	2 C48658	flagellin - Escher
16	155.5	8.6	989	2 D89652	fibrinogen-binding
17	154	8.5	364	2 AE0169	probable exported
18	153	8.4	4919	2 T31105	hypothetical prote
19	152.5	8.4	364	2 A81019	adhesin/invasin, p
20	152	8.4	1477	2 B43855	high-molecular-we
21	151.5	8.4	2020	2 C48399	ABC-type transport
22	151	8.3	980	2 H90681	probable flagellin
23	151	8.3	980	2 D85532	probable structura
24	151	8.3	1536	2 A43855	high-molecular-we
25	148	8.2	1910	2 AF0394	probable adhesin h
26	147	8.1	1335	2 T17508	glycoprotein Vp260
27	146	8.1	1461	2 E90696	hypothetical prote
28	145	8.0	595	2 A48658	flagellin - Escher
29	144.5	8.0	936	2 I40711	sapB protein - Cam

30	144.5	8.0	1361	2 T03415	S-layer protein -
31	144	7.9	1635	2 AB0452	hemolysin [importe
32	144	7.9	2554	2 AB3528	extracellular seri
33	143.5	7.9	906	2 C85739	hypothetical prote
34	143.5	7.9	1011	2 F90879	probable BigA-like
35	143.5	7.9	1052	2 AF2959	conserved hypotet
36	143.5	7.9	1341	2 H98323	hypothetical prote
37	143	7.9	1127	2 T25804	major ring-forming
38	143	7.9	1519	2 S41525	surface array prot
39	142	7.8	920	2 I40614	hypothetical prote
40	142	7.8	1461	2 A85547	probable RTX famil
41	142	7.8	5188	2 B85547	hypothetical prote
42	142	7.8	5291	2 F90696	hypothetical prote
43	141.5	7.8	338	2 D90697	adhesin/invasin-11
44	141.5	7.8	338	2 G85547	adhesin/invasin-11
45	141.5	7.8	1035	2 AD3203	autotransporter pr

RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: G81133

R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: G81133

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <FET>

A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match 99.7%; Score 1808; DB 2; Length 591;

Best Local Similarity 99.7%; Pred. No. 4.7e-97;

Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNVDVVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVKEKDGKLVTKDKG 60

Db 236 DNVDFVRTYDTVEFLSADTKTTTVNVVESKDNGKKTEVKIGAKTSVKEKDGKLVTKDKG 295

QY 61 ENGSSSTDEGGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFEVTSCTNVTFSAGK 120

Db 296 ENGSSSTDEGGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFEVTSCTNVTFSAGK 355

QY 121 TTATVSKDQGNITVMYDVNVGDALNVNQLNSGNWLDKSKAVAGSSGKVISGNVSPSKG 180

Db 356 TTATVSKDQGNITVMYDVNVGDALNVNQLNSGNWLDKSKAVAGSSGKVISGNVSPSKG 415

QY 181 MDETVINAGNIEITRNKKNIDIAIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKD 240

Db 416 MDETVINAGNIEITRNKKNIDIAIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKD 475

QY 241 NKPVRITNVAPGKGVKEDVTNVAOLKGAONLNRIQNVGNRAGTAQAATATAGLVQAYL 300

Db 476 NKPVRITNVAPGKGVKEDVTNVAOLKGAONLNRIQNVGNRAGTAQAATATAGLVQAYL 535

QY 301 PKKSMMAIGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGQW 356

Db 536 PKKSMMAIGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGQW 591

RESULT 2

ALIGNMENTS

A81888
Probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249)
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81888
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: A81888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-references: GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1200

Query Match 96.7%; Score 1752.5; DB 2; Length 592;
Best Local Similarity 97.5%; Pred. No. 7.5e-94;
Matches 347; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
Qy 2 NVDPVRYDTVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVKEKDGKLVTKGDKGE 61
Db 237 NVDPVRYDTVEFLSADTKTTTNNVESKDKNGKTEVKIGAKTSVKEKDGKLVTKGDKGE 296
Qy 62 NGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKPFETVSGTNVTFASGKGT 121
Db 297 NGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKPFETVSGTNVTFASGKGT 356
Qy 122 TATVSKDDQGNITVMYDVNVGDALNVNOLQNSGNWLDKAVAGSSGKVIISGNVSPSKGM 181
Db 357 TATVSKDDQGNITVMYDVNVGDALNVNOLQNSGNWLDKAVAGSSGKVIISGNVSPSKGM 416
Qy 182 DETVNIAGNNIETRNKNIDTATSTPPOFSSVSLGAGADAPTLSDGDD-ALNVGSKKD 240
Db 417 DETVNIAGNNIETRNKNIDTATSTPPOFSSVSLGAGADAPTLSDGDDALNVGSKDA 476
Qy 241 NKPVRIITNAPGVKGGVDTNVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVQAYL 300
Db 477 NKPVRIITNAPGVKGGVDTNVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVQAYL 536
Qy 301 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKGTASNSRGRHFGASASVGYQW 356
Db 537 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKGTASNSRGRHFGASASVGYQW 592

RESULT 3
D82671
surface protein Xf1529 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82671
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2059 <SIM>
A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.C.R.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovskij-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1529

Query Match 18.3%; Score 332.5; DB 2; Length 2059;
Best Local Similarity 29.3%; Pred. No. 2.5e-11;
Matches 98; Conservative 53; Mismatches 112; Indels 71; Gaps 12;
Qy 28 SKDKKTEVKIGAKTSVKEKDGKLVTKG-KDKGNGSSTDEGEGLVTAKEVIDAVNKAG 86
Db 1792 AKDGRGAESYTGKYGQNVNTVGVSDGAAKGETRSISN----VADAKEMDAVN--- 1844
Qy 87 WRMKTTTANGQTGQADKPFETVSGTNVTFASGKGTATATVSKDDQGNITVMYDVNVGDALN 146
Db 1845 LRQLDAVAQKSNLOTDDM-----RHEINNIEDVFKITKGD--S 1880
Qy 147 VNOLQNSGNWLDKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIETRNKNIDTAT 206
Db 1881 ASSVKGMGVN---AMAGITNAAVSGTESVALGR---NTNVSADNAVAI--GNG----- 1925
Qy 207 SMTPOFSSVSLGAGADAPTLSDGDDALNVGSKDKNKPVRITNAPGVKGGVDTNVAQLKG 266
Db 1926 SVADRANSVSGS-----GSE-----QVTNVAAGTADTDVNVSQLNQ 1965
Qy 267 VAQNLNRIDNVGNAR----AGIAQAATAGLVQAYLPGKSMMAIGGTYRGEAGYAG 322
Db 1966 GLITAKOYTDGWNLRRTSGGVAATAATNLPQAYVQGRGTSVGVSSYQGSATAVG 2025
Qy 323 YSSTSDGNNILKGTASNSRGRHFGASASVGYQW 356
Db 2026 VSAVSEGHVWFKPGSANTRSHVGVGAGVGYQW 2059

RESULT 4
A82615
surface protein Xf1981 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82615
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1190 <SIM>
A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovskij-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1981

Query Match 18.0%; Score 327; DB 2; Length 1190;

Best Local Similarity					
Matches 108; Conservative 27.3%; Pred. No. 2.6e-11;					
Indels 92; Gaps 14;					
Mismatches 143;					
Qy	2	NVDFVRITVDFELSDTKTTTVNVEKDKGKTEVKIGAKTSVIKEKDGLVTGRDKE	61		
Dd	848	SVHYISTYD-----GCTQGNGDGCATGTRIAVGVTLSA----	EGATAVSGAAA	897	
Qy	62	NG-SSTDEGBGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKFETVTSCTNTVFASGKG	120		
Dd	898	SGKGAISAGRNASADGSVALGD-GAKDCARGAESYTGKYSGLQNNTVGTVSVDASKG	956		
Qy	121	TTATSVSKDDOGNITVMYDVNVGDALNVQL----QNSGNWLDKAVAGSSGVISGNVSP	176		
Dd	957	EIRFVS-----NVADAKEAT--DAVNLRDLRDVAODANRYRVDNKIESLSEGGTF-----	1003		
Qy	177	SKGRMDETVINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLV-----DGD	231		
Dd	1004	-----VKVNSLN-----SAIP-----IAAGVDATAIGCATAGSAD	1035		
Qy	232	ALNVGSK-----KDNKPV-----RITNVAFCKEGDYTNVAQLK	265		
Dd	1036	SIAMGNKASADNAVAIGNHVSADRANTVSVGSAGSERQVTNVAAGTADTDVAVNVSQLN	1095		
Qy	266	GVAQNLNRINDVDGNAR----AGIAQAIAATAGLVQAYLPCKSMAIGGCTGYRGEAGYAI	321		
Dd	1096	QGLITAKQYTDGVVYGLRRDTDGGVAAAIATANLPQAYIPGRGMTSYGVSSYRGQAIAV	1155		
Qy	322	GYSSISDGGNWIIKTGASGNSRHFGSASVGYOW	356		
Dd	1156	GVSSVESGRWFVKFSGANTRSQVGIGAGVGYOW	1190		
 RESULT 5					
A86036					
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain C); Species: Escherichia coli					
C; Date: 16-Feb-2001 #sequence_revision 16-feb-2001 #text_change 14-Sep-2001					
C; Accession: A86036					
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J. iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamoumis, K.; Nature 409, 529-533, 2001					
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.					
A; Reference number: A85480; MUID:21074935; PMID:11206551					
A; Accession: A86036					
A; Status: preliminary					
A; Molecule type: DNA					
A; Residues: 1-1588 <STO>					
A; Cross-references: GB:AE0051174; NID:gl2518349; PIDN:AAG58749.1; GSPDB:GN00145;					
A; Experimental source: strain O157:H7, substrain EDL933					
C; Genetics:					
A; Gene: Z5029					

Query Match	17.9%;	Score 325;	DB 2;	Length 1588;
Best Local Similarity	26.7%;	Pred. No. 4.9e-11;		
Matches 115;	Conservative 58;	Mismatches 165;	Indels 92;	Gaps 15;
Qy	1	NNYDEVITYDTVFELSADTKTTTVNVYESKNGKKTVEKIGAKTSVKEK-----D	50	
Db	1177	NAIGAVATTTKFEHANSTEDSLAVGT-----DSLAMGAKTIIVGDKIGIGICYAYVD	1230	
Qy	51	GKLVTGDKDGE-----NGSSTDEGELVTAKEVIDAVNKAGWRMKTTFANGQ	97	
Db	1231	ANALNGIAIGSNAQVIVHNSIAIGNSTTTRGATNTYATYMDAPONSVEFSVGSDGQ	1290	
Qy	98	-----TGQADKFETVTSCTNTVTFASGKGTATTVSKDDOGNITVM-----Y	137	
Db	1291	QGITNVAAGSAD-----TDVAVN--GOLKYTDAQVSQNTQ--SITNLDNRVTNLDLSRVINI	1342	
Qy	138	DVNVGDDAL-----NVNQIQLONGWNLDLSKAVAGSGSKVTISGVNVSPEKGM---DET	184	
Db	1343	ENGIGDILVTGTGSKYFKTNTDGDVDASQAQGDGSAIAGSGSTAAADNSVAVLGTGVSVAETENT	1402	
Qy	185	VNINAGNNIEITRN---GKN-----IDIATSWTQPFSSVSLGAGADAPTLSVDDGALNVGS	237	

Db	1403	ISVGSSTNQRRITNVAAGKKNATDAVNVAQLKSSSAGGVRYDTRADG---SIDYSNITLGG	1459
Qy	238	KDKNKPVRTTNVAPRGEGDVTNVAQLKGVAQ-----NLNRRIDNVDCGNARAGI	286
Db	1460	-GNGGTTTRISNVSGAVNNDDVNTVAQLKQSVQETQKYTDQRMVEMDNKLKSTESKLSGGI	1518
Qy	287	AQATATAGLQVAYLPGRSMAIGGGTYRGAGYAIGYSSISDGGNWTIKGTASGNSRGHF	346
Db	1519	ASAMAMTGLPQAYTPGASMASIGGGTYNGESAVALGYSVMSANGRWYKLGQSTNSGQY	1578
Qy	347	GASASVGQYW	356
Db	1579	SAALGAGIQW	1588
RESULT 6			
H91188			
probable adhesin ECS4480 [similarity] - Escherichia coli (strain O157:H7, subst			
C:Species: Escherichia coli			
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001			
C:Accession: H91188			
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.;			
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.			
DNA Res. 8, 11-22, 2001			
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7			
A:Reference number: A99629; MUID:21156231; PMID:11258796			
A:Accession: H91188			
A:Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-1588 <HAY>			
A:Cross-references: GB:BA000007; PIDN:BA837903.1; PID:g13363955; GSPDB:GN00154			
A:Experimental source: Strain O157:H7, substrain RIMD 0509952			
C:Genetics:			
A:Gene: ECS4480			

Query Match	17.9%	Score 325;	DB 2;	length 1588;
Best Local Similarity	26.7%	Pred. No. 4.9e-11;		
Matches 115;	Conservative 58;	Mismatches 165;	Indels 92;	Gaps 15;
Qy	1	NNVDFVITYDYVEFLSADTKTTTNNVRESKONGKKTEVKIGAKTSVIEK-----D 50		
Db	1177	NAIGAVATTPTKYFHANSTEEDSLAVGT-----DSLAMGAKTTIVNGDKGIGIGYGAYVD 1230		
Qy	51	GKLVTKDKGE-----NGSSTDEGELVTAKEVIDAVNKAWRMKTTTANGQ 97		
Db	1231	ANALNGTAIGSNAQVIHVNSIAICNGSTTTTGAQNTNTAYNMDAPQNSVEFSVGSADQG 1290		
Qy	98	-----TGQADKFETVTSNTVTFASGKGTTATVSKDDQGNITVM-----Y 137		
Db	1291	RQITNVAAGSAD-----TDAVNV--GQLKVTDAQVSQNTQ--SITNLDNRVTNLDSSRTVNI 1342		
Qy	138	DVNVGDMAL-----NVNQLONSQWNLDLSKAVAGSSKVIISGNVSPSKGM---DET 184		
Db	1343	ENGIGDITVTTCGSTRKYFKYFTNTDGDVASAQGKDSVAIGSCSIAAADNSVALGTGSVATEENT 1402		
Qy	185	VNINAGNNIETRN--GKN-----IDTASMTQFSSVSLGAGADAPTLSDVGDALNVGS 237		
Db	1403	ISVGSSTNQRRITINVAAGKATDVA NVAAQLKSSGAGGVRYDTRADG---SIDYSNITLGG 1459		
Qy	238	KDNKPVRIITNVAPGVREGDVITNVAOILKGVAQ-----NLNNRINDVDCGNARAGI 286		
Db	1460	-GNGCTTRISNVSGAVNNNDVVNYAQLKQSVQETKYQTDQBMVEMDNKLSKTESKLSGGI 1518		
Qy	287	QAQATATAGLVQOAYLPQKSMMAIGGGTYTGRGAGYAIGYSSISDGGNWTIKGTASGNRSHF 346		
Db	1519	ASAMAMTGLPQAYTPGASMASIGGGTYNGESAVALGYSMVSYANGRWYVYKLGSTNSQGEY 1578		
Qy	347	GASASGVQW 356		
Db	1579	SAALGAGIQW 1588		

RESULT 7

AC0376
probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AC0376
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moulle, S.; O'Garra, P.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AC0376
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapB

Query Match 17.3%; Score 314; DB 2; Length 1107;
Best Local Similarity 26.8%; Pred. No. 1.4e-10;
Matches 109; Conservative 55; Mismatches 165; Indels 78; Gaps 14;
QY 16 SADTKTTVNVEKDKKTEVK-----IGAKTSVIKEDKGLVTGKDKGE----- 61
DB 713 STEEDSLAVGCTSLAMGAKTIVNADAGIGIGLNTLVNADAIAGTGNARANHANSIAM 772
QY 62 -NGSSITDEG-EGLVTAKEVIDAVNKGWRKMTTANGQ-----TGQADKFTVTSGTN 112
DB 773 GNGSQTRGAOTDYTAIYNDTPONSVG-EFVSVEGSDGQRTQITVAAGSAD-----TDAVN 826
QY 113 VTEASGKGTATVSKDDOGNITVYDVN-----VGDALNVNQLNSGNWLD-- 158
DB 827 V--GQLKVTDAQVSRNTQSTINLTQVNSLDTRVTNIENGIGDIVTGSKYKFTWDGA 884
QY 159 -----SKAVAGSGKVISGNVSPSKGK---MDEVINAGNINIEIR-----NGK 200
DB 885 DANAQAGDSVAIGSGSIAAAEVALGTNSVADEANTVSGSSTQORRITNVAAGVNTD 944
QY 201 NIDIASTMTQFSSVSLGAGADAPTLSVDGDALNVGSKDKNKPVRITNVPAGVKEGDVTN 260
DB 945 AVNVAQLKASEAGSVRYETNADG---SVNYSVLNLGDSGG-TTRIGNVSAAYNDTDAVN 1000
QY 261 VAQLKGVQAQ-----NLNRRIDNVGNARAGIAQAIAATAGLVQAYLPCKSMMAIG 309
DB 1001 YAQLKRSVEANTYTDQKNGEMSKIKGIEKMSGGIASAMAGLPQAYAPGANTISIA 1060
QY 310 GGTGREGAIVAIGSYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 356
DB 1061 GGTFNESAVAIGVMVSESGGVYKLGCTSNSSQGDYSAAIGAGFOW 1107

RESULT 8

AH0110
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175
C:Genetics:

A:Gene: YPO0902

Query Match 17.0%; Score 307.5; DB 2; Length 658;
Best Local Similarity 28.4%; Pred. No. 1.7e-10;
Matches 97; Conservative 48; Mismatches 121; Indels 75; Gaps 12;
QY 40 GAKTSVIKEDKGLVTGKDKGSGSSTDEGEGLVTAKEVIDAVNKGWRKMTTANGQTG 99
DB 369 GAAASA-----DGSVAIGQSGDNGRGVENVIG-----KYSNASNTSSG 407
QY 100 QADKFTVTSGTNVTASGKGTATVSKDDOGNITVYDVNVDGALNVNQLNSGNWLD 159
DB 408 -----TVSVGNAT-----GETRTVSNVADG-----LQATDANLRLDQ----- 442
QY 160 KAVAGSGKVISGNVSPSKGMDDEVINAGNNI-EITRNGKNIDI--ATSMTPQFSSVS 216
DB 443 ---IAASIVVVENNSGLQGTDMFQVNNSSGLAKPSATGANSATGGAGSVASGNNSTA 499
QY 217 LGAGADAP-----TLSVDGDALNVGSKDKNKPVRITNVPAGVKEGDVTNVAQLKG 266
DB 500 FGSGAKATAANSAAALGANSVADRANSVSGVSGNER--QITNVAPATQGTDAVNFOLKS 557
QY 267 VAQN---LNNRIDNVGNAR-----AGIAQAIAATAGLVQAYLPCKSMMAIGGTYRG 315
DB 558 ISQTNAYTNQRYSELUKQDLRKONSVLSAGIASAMASLTQPYTSGSSMTTIGAAASYRG 617
QY 316 EAGYAIQYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 356
DB 618 QSALSLGVSSISDGRWVSKLQASNTQGDGIGVGVGYOW 658
cell surface protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AB3486
R:Belvecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov, M.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3486
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL53053.1; PID:g17983913; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11872
A:Map position: 1

Query Match 10.1%; Score 183.5; DB 2; Length 365;
Best Local Similarity 23.1%; Pred. No. 0.0012;
Matches 77; Conservative 38; Mismatches 82; Indels 137; Gaps 11;
QY 128 DDOGNIT-VMYDVNVDGALNVNQLNSGNWLDKAVAGSGKVISGNVSPSKGMDDEVIN 186
DB 29 ENLANINDILHIESGGIKYFHANSIG--ADSRALGTNSIAVGSIDSVASGEG-----S 80
QY 187 INAGNINIEIRNGKNIDIASTMTQFSSVSLGAGA-----DAP 224
DB 81 ISVNGAQAASAHGSAVALGENAAPPANASVALGAGSKTSEVVATKGTGTGTTGQYDFAGDAP 140
QY 225 -----TLSVDGDALNV----- 235
DB 141 SGTVSVGDKGAERTITNVAAGRISVESTDAVNSQLNAVNOAIENLAAGTENDKFKSVKY 200
QY 236 -----GSKKDN-----KPVRTNVPAGVKEGDVTNVAQLK-GVAQNLNRRIDNVG 280
DB 201 DRHSDGTTKNSMTLOGWDSATPVVLANVADVGHKNDVAVNSQLKAGLSTTLGEAKAYTDQ 260
QY 281 NARAGTAQA-----IATAGLVQAYL-----PKGSMMAIGGG 311

Db 261 TALQTLDOANAYTDKFKGKLNEDIVATRIEARQAAALGLAASRLRYDDRPGRISAIGGG 320
QY 312 TYRGEAGYAI-----YSSISDGGNW 332
Db 321 FWRGEGVALGLGHTSDQMRSNLSAATSGGNW 354

RESULT 10
C82672
surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain 9a
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: C82672
R:anonymouse, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2001
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: C82672
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1004 <STM>
A:Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:APF84325.1; GSPDB:GN001
A:Experimental source: strain 9aSc
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.B.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; V
A:Reference number: A59328
A:Contents: annotation
A:Genetics:
A:Gene: XF1516

Query Match 9.7%; Score 176.5; DB 2; Length 1004;
Best Local Similarity 25.8%; Pred. No. 0.01;
Matches 98; Conservative 58; Mismatches 141; Indels 83; Gaps 18;

QY 27 ESKDNCKTEVTKIGAKTSVIKEKDGKLVTKDKGE--NGSSTDEGEGLV--TAKEVI---- 79
Db 139 QSANNG-----VALGSNSTVSGVNSVALGAGSMASLNVISVGGDGVTPAVRRIRNVNGD 194
QY 80 -----DAVNKAGWRMKTITTTANGQTQADKFEV-----TSGTNTVTFASGKGTATVS-KD 128
Db 195 GIGNNDVANKSOLDGVTSVN---DYAASVKTIALTNOVTGSSVASASGKESTAIQSGAQ 251
QY 129 DGNITVTYDNNVGDALNVQNLQNSGNLDSKAVAGSKVIGSNVSPSKMKMDETVNIN 188
Db 252 AVADNTVAF-----GGRAIANAVGASALGDFDSHAKGINSTVTGTSQSVSLGQGGVSLGYNF 307
QY 189 AG-----NNTIEITNG-----KNIDIAITSMTPQSSVSLGACADAPTLSV---DGDALNVG 236
Db 308 VREGSFLNGALGSLNVLVQGV-----SVALGSGSMASEPNVSVSGDGLRGP 357
QY 237 SKKDNKPVRTITNVAPVKGEDVTINVAQLKGVAGNLRNIDNV-----DGNARAGIA 287
Db 358 AVR-----RIVNVGDIIGNDVAVKSQLDGVTSVANDVAVSNKIAGATQITGSGVASVS 412
QY 288 QATATAGLVQAYLPKGSMAIG-----GCTYRGEAGYAIQYSSISDGGNWIIGTA- 338
Db 413 GODSTAAGASQAQAAGDSIALGARSRANAIGSSALGVGDGHALCANSTALGG-----QSTAI 468
QY 339 --SGNSRGRH----FGASASVG 353
Db 469 SEGGSILGYNISFVQGSATNG 488

RESULT 11

F90961

flagellin [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: F90961
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA836085.1; PID:g13362130; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs2662
C:Superfamily: flagellin

Query Match 9.2%; Score 167.5; DB 2; Length 585;
Best Local Similarity 23.0%; Pred. No. 0.018;
Matches 85; Conservative 54; Mismatches 161; Indels 69; Gaps 16;

QY 10 DTVEFLSADTKTTTNVNESKDNKGKTEVKIGAKTSVIKEKDGKLVTKDKGKENGSTDEG 69
Db 121 DEIDRVSGQTQFNGVNVNLAKDSMK--IQVGANDGETIIDLKKIDSIDLGLNGFNVN-G 177
QY 70 EGLVTAK-EVIDAVNKGWRMKTITTTANGQTQAD-KFEVTSCTNVTTFAS-GKGTATVS 126
Db 178 KGTITNKAATVSDLTSSAGAKLNTT-----TGLYDLKTENTLLTTDAADFGLGDKVTV- 231
QY 127 KDDQGNITVMYDNNVGDALNVQNLQNSGNLDSKAVAGSS-----GKVIS 171
Db 232 ----GVDYTYNAKSGDFTTK--STAGTGVDAQAADSASKRDLAATLHADVGKSVN 285
QY 172 GNVSPSKMKMDETVNINAGNIEITRNGKNIDIAITSMTPQFSSVSLG-----G 220
Db 286 GSYTTKDGTV--SFETDSAGNITIGSQAYVDDAGNLTNNAGSAKADMKALLKAASEG 343
QY 221 ADAPTLSDVDGALNVGSKDNKPVRTITNVAPVKGEDVTINVAQLKGVAGNLRNIDNVG 280
Db 344 SDGASLTFNGTEVTIAKA---TPATTPVAPLIPGGITYQATVSKDVLS-----ET 392
QY 281 NARAGIAQAIAATAGLVQ---AYLPKGSMAI-----GGTYRGEAGYAIQYSSISDGG 330
Db 393 KAAATSSITFNSGVLSKLTIGFTAGESDAAKSYVDKGGIT--NVADYTVSYSVNKDNG 450
QY 331 NWIIKGTAS 339
Db 451 SVTVAGYAS 459

RESULT 12

F85809

hypothetical protein flic [imported] - Escherichia coli (strain O157:H7, substrain ED
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: F85809
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <STO>
A:Cross-references: GB:AE005174; NID:g12516024; PIDN:AAG56938.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933

Db 178 KCTITNKATVSDLTSAGAKLNTT--GLYGL--KTENTLLTDDAADFCKLGNQDKVTVGG 233
QY 128 DQGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSS-----GKVISG 172
Db 234 VD-----LYNAKSGDFTTK--STAGTGVDAQAQATDSAKKRDALAATLHADVGKSVNG 285
QY 173 NVSPSKGKMDFTVINAGNIEITRNGKN--IDIATSMTPQPFSSVSLGA----- 219
Db 286 SYTTTGDGV-SFVTDGAGN--ITIGGSQAYVDDAGNLTNNAGSARKADMKALLKAASE 341
QY 220 GADAPTLSDGDLNVGSKKDNKPVRTNVPVKEGVDYTNVAQLKGVAQNLNRRIDNVD 279
Db 342 GSDGASLTFNGTEYTIKA---TPATTSVAPLIPGGITYQATVSKDVLS-----E 390
QY 280 GNARAGIAQAIATAGLVQ---AYLPKSKMMAI-----GGGTYRGEAGYAICYSSISDG 329
Db 391 TKAAATSSVTNSGVLSKTIPTAGESSDAKSYVDDKGGIT--NVADYTVSYSVNKN 448
QY 330 GNVIIKGTAS 339
Db 449 GSVTVAGYAS 458

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Job time : 12.1906 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 5.49755 Seconds
(without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-37

Perfect score: 1813

Sequence: 1 NNVDVRYTVDFVFLSADTK.....TASGNSRGHFGASVGYQW 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151.5	8.4	2003	1 YDBA_ECOLI	P33666 escherichia
2	141.5	7.8	1953	1 BIGA_SALTY	P25927 salmonella
3	140	7.7	1655	1 OMPB_RICCN	Q9KX63 r outer mem
4	136.5	7.5	550	1 FLIC_SHIFL	Q08860 shigella fl
5	136.5	7.5	930	1 PMP8_CHLPN	Q92393 chlamydia p
6	136.5	7.5	1300	1 120K_RICRI	P14914 rickettsia
7	136.5	7.5	1654	1 OMPB_RICRI	Q53047 r outer mem
8	135.5	7.5	497	1 FLIC_ECOLI	P04949 escherichia
9	134.5	7.4	1286	1 AIDA_ECOLI	Q03155 escherichia
10	132.5	7.3	1608	1 HLYA_SERMA	P15320 serratia ma
11	131	7.2	434	1 YADA_YERPS	P10858 yersinia ps
12	131	7.2	1398	1 TOP2_PLAPK	P41001 plasmodium
13	130.5	7.2	1569	1 YRJA_ECOLI	P52143 escherichia
14	130	7.2	1577	1 HLYA_PROMI	P16466 proteus mir
15	130	7.2	2249	1 OMPA_RICRI	P15921 rickettsia
16	129.5	7.1	716	1 CX80_EUPOC	Q9H9X3 eploties oc
17	129	7.1	3178	1 YS89_CAEEL	Q09624 caenorhabdi
18	128.5	7.1	1567	1 ICEN_XANCT	P18127 xanthomonas
19	128	7.1	1645	1 OMPB_RICTV	P96989 r outer mem
20	126.5	7.0	575	1 FLA2_CAMEE	P22251 campylobact
21	126.5	7.0	933	1 SLAP_CAMEE	P35827 campylobact
22	126	6.9	928	1 HXA2_HAEIN	P45354 haemophilus
23	125.5	6.9	713	1 CDG2_PAEWA	P31835 paenibacill
24	125.5	6.9	760	1 AMY_CLOAB	P23671 clostridium
25	125.5	6.9	917	1 HXA3_HAEIN	P45355 haemophilus
26	125.5	6.9	928	1 PML0_CHLPN	Q9R065 chlamydia p
27	125	6.9	1656	1 OMPB_RICJA	O06653 r outer mem
28	124.5	6.9	455	1 YADA_YEREN	P31489 yersinia en
29	124	6.8	1025	1 SLAP_CAUCR	P35828 caulobacter
30	123.5	6.8	2660	1 YEEJ_ECO57	O8X8V7 escherichia
31	123	6.8	581	1 FTBP_ADE05	P1818 human adeno
32	123	6.8	860	1 VGI2_BPB03	P37893 bacterioph
33	123	6.8	1325	1 YDEK_ECOLI	P32051 escherichia

RESULT 1

YDBA_ECOLI
ID YDBA_ECOLI STANDARD; PRT; 2003 AA.
AC P33666; P76087; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydbA.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaser P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in'
Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -!- SIMILARITY: TO S-TYPHIMURIUM ORF NEAR CYSG (AC P25928).
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION: THE GENE CODING FOR
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
BETWEEN AMINO ACIDS 839 AND 840.

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ALIGNMENTS

34	122.5	6.8	1007	1	Y741_CHLMU	Q9pit6 chlamydia m
35	122.5	6.8	1153	1	PVDB_PLAKN	P50493 plasmodium
36	122.5	6.8	1861	1	APU_THETU	P38536 t anylopull
37	122.5	6.8	2021	1	OMPA_RICCN	Q52657 rickettsia
38	122	6.7	762	1	SLAP_ACEKI	P22258 acetogenium
39	121.5	6.7	367	1	FLC2_PROMI	P42273 proteus mir
40	121	6.7	670	1	GR78_YARLI	Q99170 yaerowia li
41	121	6.7	918	1	YMBJ_CAEEL	P34487 caenorhabdi
42	121	6.7	1694	1	IGA0_HAEIN	P44969 haemophilus
43	121	6.7	1702	1	IGA2_HAEIN	P45384 haemophilus
44	121	6.7	2334	1	WAPA_BACSU	Q07833 bacillus su
45	120.5	6.6	575	1	FLB2_CANJE	P22252 campylobact

```
CC -----
DR EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90778; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; ; NOT_ANNOTATED_CDS.
DR Ecogene; EG1307; ydbA.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

Query Match
Best local similarity 23.4%; Score 151.5; DB 1; Length 2003;
Matches 101; Conservative 54; Mismatches 154; Indels 123; Gaps 23;

QY 3 VDFVRYDYVEFLSADTKT-----TTVNESKDNKGKTEVKIGAKTSV---IK 47
Db 189 IDEANNVVALEGSADGATKQYNHNGELVITGDNATVNNNGKTT---VDGKDSGTSTEIN 245
QY 48 EKDKLVTKDKKGKENG-----SSTDEGEGLVTAKE-----VIDA---VNKAGW 87
Db 246 GNGKVIQDGLDVGSGGHGIDITGDSATVDNKGTMVTPESMGIDQIDGKAIVNNEG- 304
QY 88 RMTYTTANGTGQADKFETV-----SCTNVTFAFGK----- 119
Db 305 --ESTITNGTGQINGDDATANNNGKTTVDGKDSGTGTEINGNNGKVIQDGLDVGSGGH 362
QY 120 -----GTTATVSKDDGNIYVMDVNGDALNVNQ--LQNSGNLDSKAVAGSGKVISG 172
Db 363 GIDITGDSATV--DNKGTMVTPESIGIQDGDQAVNNEG---ESAITNGTGQTQING 417
QY 173 N--VSPSKGR-----MDETVNIAGNN-----IEITRNGKNIDT-ATSMTPQFSSVS 216
Db 418 DDTANNNGKTTVDGKDSGTGTEAGNKGKVIQDGLDVGSGGHGIDITGDSATVDNKGTM 477
QY 217 LGADAPLTVSDGDALNVGSKDKNPVTRITNVPAGVKGDVTVNVAQLKGAQNLRN-I 275
Db 478 TVTDPESIGIQDGDQAVNNEGES---TITNGTG-----TQINGNDATANNNGK 525
QY 276 DNVGDNARAGIAQAIATAGLVQAYLPCKSMKATGGGTGYRGEAGYATGYSISDGGNWI 335
Db 526 TVDVGKDSGT--TKIAGNIGIVN--LDG-SLTVTGG-----AHGVENIGDNGTVNNK 572
QY 336 GTASGNSRGHFG 347
Db 573 GDIVVSDTGSIG 584

RESULT 2
BIGA_SALTY STANDARD; PRT; 1953 AA.
AC P25927; P25928; O9XC03;
DT 01-MAY-1992 (Rel. 22, Created)
DE 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative surface-exposed virulence protein bigA precursor.
GN BIGA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 14028;
RA Srofiljtkovic I., Valentine P., Heffron F.;
RT "Salmonella typhimurium rhs homolog.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=LT2 / SGSC1412 / ATCC 700720;
RC MEDLINE=21534948; PubMed=11677609;
RX
```

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RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
RN [3]
RN SEQUENCE OF 1-765 FROM N.A.
RP STRAIN=LT2;
RC MEDLINE=91100301; PubMed=1987123;
RX Wu J.Y., Siegel L.M., Kredich N.M.;
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:
RT requirement for a cloned cysG plasmid to overcome limiting siroheme
RT cofactor.";
RL Bacteriol. 173:325-333(1991).
CC -/- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
CC in positions 414 and 732.
CC -----
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CC -----
CC EMBL; AF133696; AAD39458.1; -
CC EMBL; AE008859; AAL22340.1; -
CC EMBL; M64606; AAA27042.1; ALT_FRAME.
CC EMBL; M64606; AAA27043.1; ALT_FRAME.
CC StyGene; SG10437; bigA.
CC Virulence; Repeat; Signal; Complete proteome.
FT SIGNAL 1 27 POTENTIAL
FT CHAIN 28 1953 PUTATIVE SURFACE-EXPOSED VIRULENCE
FT DOMAIN 101 252 PROTEIN BIGA.
FT REPEAT 101 103 15 X 11 AA TANDEM REPEATS.
FT REPEAT 104 113 1 (INCOMPLETE).
FT REPEAT 114 122 2 (INCOMPLETE).
FT REPEAT 123 133 3 (INCOMPLETE).
FT REPEAT 134 144 4.
FT REPEAT 145 155 5.
FT REPEAT 156 166 6.
FT REPEAT 167 177 7.
FT REPEAT 178 188 8.
FT REPEAT 189 199 9.
FT REPEAT 200 210 10.
FT REPEAT 211 221 11.
FT REPEAT 222 232 12.
FT REPEAT 233 243 13.
FT REPEAT 244 252 14.
FT REPEAT 252 252 15 (INCOMPLETE).
FT CONFLICT 207 207 D -> DRGDDDDVTPDD (IN REF. 1).
FT CONFLICT 514 514 A -> R (IN REF. 3).
FT CONFLICT 1698 1698 D -> N (IN REF. 1).
FT CONFLICT 1795 1798 OYLE -> ITLO (IN REF. 1).
FT CONFLICT 1836 1837 SA -> T (IN REF. 1).
FT CONFLICT 1836 1837 SA -> T (IN REF. 1).
SQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C954D91AE CRC64;

Query Match
Best local similarity 23.6%; Score 141.5; DB 1; Length 1953;
Matches 86; Conservative 45; Mismatches 133; Indels 101; Gaps 18;

QY 9 YDTVEFL-SADTKTTVTNNVESKDNKGKTEVKIGAKTSVKEKGLVTKDKGEN----- 62
Db 333 YDSRGYLIITADNTTIVISGDDQAHNSDRGMDISG-----QDRTGVLIISG-DRVTNLTGD 386
QY 63 GSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGTCQADKFETVTSGTNVTFAFGKTT 122
Db 387 SSVTDCATGMV-----ISGDTTNTISGHSTVDNATG-ALISNGTT 427
QY 123 ATVSKD---DQGNITVMYDVNVGDLNVNQLQNSGNLDSKAVAGSGKVISGNVSPSKG 179
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Db 428 TNFAGDIASGGGTAAIIDGDNATIKNTGTSISG-----AGSTGTVIDGNARVNN 479
QY 180 KMDVTVNAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSVDGD---ALNVG 236
Db 480 DGDMTIT-DGGTGGHITGDNVVDNAGTTV-----SGADATLYIEGDNALVINEG 530
QY 237 SKKDNKPRVITNVAPCVK-EGDVTNVAQLKGVAQNLNNRINDVVDGNARAGIAQAATAGL 295
Db 531 NQ-----TISGGAAGTTRIDGDDAHTTNTGDTA-----VDGAGSAVVIINGDNGSL 575
QY 296 VQAYLPKGSMAIGGTYRGEAGYAGYSSISDGGNWIHK-GTASGNSRGHFGASA---- 350
Db 576 TOA-----GDLIVTDGAMGIITYGT--GNEAKNTGNATVRDA 610
QY 351 -SVGV 354
Db 611 DSVGF 615

RESULT 3
OMPBL_RICCN STANDARD; PRT; 1655 AA.
AC Q9KKA3; Q9KKA3; Q9KKA3;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rompB)
DE (romp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
DE OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein rompB (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
RT australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
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CC -----
DR EMBL; AE008659; AAL03623.1; -
DR EMBL; AF123721; AAF34124.1; -
DR EMBL; AF123726; AAF34129.1; -
DR EMBL; AF149110; AAD39533.1; -
DR PIR; E97835; E97835.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1 1334
FT CHAIN 1335 1655
FT VARIANT 61 1655
FT VARIANT 75 75
FT VARIANT 78 78
FT VARIANT 251 251
FT VARIANT 413 413
FT VARIANT 959 959
FT VARIANT 988 988
FT VARIANT 1139 1139
FT CONFLICT 353 354
FT CONFLICT 776 776
FT CONFLICT 1159 1159
FT CONFLICT 1177 1177
FT CONFLICT 1492 1492
FT SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;
QY 2 NVDFVRYTD---TVFELSADTKTTTVN-----VESKDNG-----KKTEVKIKAKTSVIK 47
Db 430 NTAGVITFDANGTLASASADANVAVTNITATEASGAGVQLSGTHAAELRLGNAGSVFK 489
QY 48 EKDGKLVTKCKDG-----ENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTC 99
Db 490 LADGTGVINGKNOTALVGGALAAAGTITLDGSATITG-----DIGNAGG-----AAALOGITL 541
QY 100 QADKFEVTV-----SGTNVTFASGKGTATVSKDDQGNITVMVDV-----NVGD 143
Db 542 ANDATKTLTGGAANIIGANGTINFGANGTITKLTG--TQNNIVDFDLAIAITDQTCVVD 599
QY 144 ALNVNOLQNSGWNLDKAVAGSGKVISGNVSPSKGM-DETVNIN---AGNN--IEITR 197
Db 600 ASSLTNAQTITINGKIGTVGANNKTLGQFNIGSSKTVLSGDVAINELVIGNNGAVQFAH 659
QY 198 NKNIDIAATSMTPQ-----FSSV-----SLCAGADAPTLSVDGDALNVGSKDKPKVRIIN 248
Db 660 NTYLITRTTNAAGQGGKIIFNPVNNNTTTLATGTNLGSATNPLAEINFGSKGAANVDVTLN 719
QY 249 VAPGVKEGDTVNVVAQLKGVAQNLNNRINDVVDG--NARAGIAQAATATAGLVQ-----AYL 300
Db 720 VKGVNL-YATNITTTDA---NVGSFIFNAGGNTIVSG-----TVGGQOGCNKFNITVALD 769
QY 301 PKGSMAIGGTYRGEAGYAGYSSISDGGNWIHKGTASGNSRG 344
Db 770 NGTIVKFLGNATPFGNTTIAAN-STLQIGGNTYADFVASADGTG 812

RESULT 4
FLIC_SHIFL STANDARD; PRT; 550 AA.
AC Q08860;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Flagellin.
```

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GN FLIC OR SF1966.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IID642;
RX MEDLINE=94335647; PubMed=8057852;
RA Tomimaga A., Mahmoud M.A.-H., Mukaihara T., Enomoto M.;
RT "Molecular characterization of intact, but cryptic, flagellin genes
RL in the genus Shigella";
RN Mol. Microbiol. 12:277-285(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
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CC -----
DR EMBL; D16819; BAA04093.1; -.
DR EMBL; AE015215; BAA43516.1; -.
DR PIR; S44980; S44980.
DR InterPro; IPR001029; Flagellin.C.
DR InterPro; IPR001492; Flagellin.N.
DR Pfam; PF00700; Flagellin_C; 1.
DR Pfam; PF00669; Flagellin_N; 1.
DR PRINTS; PR00207; FLAGELLIN.
KW Flagella.
SQ SEQUENCE 550 AA; 56636 MW; CC921C9A8EF200B6 CRC64;
Query Match 7.5%; Score 136.5; DB 1; Length 550;
Best Local Similarity 21.8%; Pred. No. 0.59;
Matches 73; Conservative 50; Mismatches 161; Indels 51; Gaps 13;
QY 10 DTVEFLSADTKTTTVNVESKDNKKTEVKGIGAKTSVKEKDKGLVTKDKGKNGSSTDEG 69
Db 121 DEIDRVSGQTQFNGVNWVLAKGSKK --IQVGANDGQTITIDLKIDSITLGLNGFNNGG 178
QY 70 EGL---VTAKEIDAVNKAGWRMKTITANGQTG--QADKFETVTSCTNV--TPASGKGT 122
Db 179 GAVANTAASKADLVAAANATVVGKNTVTSAGYDAKASDLLAGVSDGDTVQATINNGFGTA 238
QY 123 ATVS--KDOGNTVTVMVDVNVGDALNVNQLNSGWNLDKAVAGSSGK---VTSGNVSPS 177
Db 239 ASATNTKYDSASKSYSDFTTASAADVQKYLTPG-----VGDTAKGTITIDGSAQDV 290
QY 178 KGKMDVTNINAGNNI-----EITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG 231
Db 291 QISSDKKITASNGDKLIYDTTGLTKNGS-----GASLITASLSTLAANTTKATITDIGT 346
QY 232 ALNVGSKDNKPKVRIITNAPVKEGVDVNTVAQLKGVAQNLN-----RIDNVGDNAR 283
Db 347 SISF-TGNSTPTPTITITYVTGAK---VDQAAEDKAVYSTGNNVDFTTAGYSVNGTGTAYT 402
QY 284 AGI-----AQAIATAGLVQAVLPCKSMMAIGGG 311
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Db 403 KGVDSSVYVDNNEALTTSDTVDFYLQDDGSVTNGSG 437
RESULT 5
PMP8_CHLPN
ID PMP8_CHLPN STANDARD; PRT; 930 AA.
AC Q9Z393; Q9RB66;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp8 precursor (Polymorphic membrane
DE protein 8) (Outer membrane protein pmp8 precursor (Polymorphic membrane
DE PMP8 OR OMP11 OR CPN0446 OR CP0307.
GN Chlamydia pneumoniae (Chlamydia pneumoniae).
OS Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Daugaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RT role in immunopathogenicity.";
RL An. Heart J. 138:S491-S495(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RN Nat. Genet. 21:385-389(1999).
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Bass S.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bowan R.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman G., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RN Nucleic Acids Res. 28:1397-1406(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; AJ133034; CAB37068.1; -.
DR EMBL; AE001627; AAD18590.1; -.
DR EMBL; AF002193; AAF38164.1; -.
DR EMBL; AF002546; BAA98654.1; -.
DR PIR; AB1591; AB1591.
DR PIR; D72078; D72078.
```



```
QY 175 -----SPSKGKMDFTVNIAGNIIETRNKNIDIATSMTPQFSSVSLGAGADAPTL 227
DB 309 LITRTTNAAGGKIIENPVPVNGTTLAA---GTNLGSATNPLAEINFGSKGVNVD 361
QY 228 VGDALNVGSKKDNKPVRII---NVAPGYKEGDTVNTVAQLKGVQAQNLNRIDNVGNAR 283
DB 362 ----VLMVGGVGLVYATNITTTDAVNGSFVFNAGGTTNIVS-GTVGGQGGKFNIV----- 411
QY 284 AGIAQAIAATAGLVQAQYLPKGSMAIGGTYRGAGYAGIYSSISDGGNWIILKGTASGNSR 343
DB 412 -----ALENGTIVKFLGNATNGNTTIAAN-STLIQISGNYTADCVASADGT 456
QY 344 G 344
DB 457 G 457

RESULT 7
OMP_RICRI
ID OMPB_RICRI STANDARD; PRT; 1654 AA.
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -I- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC
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CC
CC EMBL; X16353; CAA34403.1; -.
CC PIR; S18227; S18227.
CC InterPro; IPR006315; Autotransport.
CC InterPro; IPR005546; Autotransporter.
CC Pfam; PF03797; Autotransporter; 1.
CC TIGRfams; TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall. 120 kDa SURFACE-EXPOSED PROTEIN.
FT CHAIN 1 1333
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FT CHAIN 1334 1654 32 kDa BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 7.58; Score 136.5; DB 1; Length 1654;
Best Local Similarity 22.6%; Pred. No. 2.1;
Matches 95; Conservative 47; Mismatches 162; Indels 117; Gaps 19;

QY 2 NVDFVRYD---IWEFLSADTKTTTVN-----VESKDMG-----KKEVTKIGAKTSVIK 47
DB 430 NTAGVITFDANGTLESASADANVAVTNNITAEASGAGVVLQSLGTHAAELRLGNAGSIFK 489
QY 48 EKDKGLVTGDKK-----GENGSTDEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQA 101
DB 490 LADGTIVNGKVNQTALVGGALAAAGTITLDGSATITDIGNAGGAAALQRLITLAN----- 543
QY 102 DKFETVT-SGTNVTFASS-----KGTATVSKDDOGNITVMYDV-----NVGDALN 146
DB 544 DAKKTLTLGANTIGAGGGTIDLOANGGTIKLT-STQNNIVVDFDLAIAITDQTGVDVASS 602
QY 147 VNQLONGSWN-----LDSKAVA-----GSSGKVIS-GNV----- 174
DB 603 LTNAQILTINGKIGTIGANNKTLGQFNIGSKTIVLSNGVAINELVIGNDGAQVFAHDTY 662
QY 175 -----SPSKGKMDFTVNIAGNIIETRNKNIDIATSMTPQFSSVSLGAGADAPTL 227
DB 663 LITRTTNAAGGKIIENPVPVNGTTLAA---GTNLGSATNPLAEINFGSKGVNVD 715
QY 228 VGDALNVGSKKDNKPVRII---NVAPGYKEGDTVNTVAQLKGVQAQNLNRIDNVGNAR 283
DB 716 ----VLMVGGVGLVYATNITTTDAVNGSFVFNAGGTTNIVS-GTVGGQGGKFNIV----- 765
QY 284 AGIAQAIAATAGLVQAQYLPKGSMAIGGTYRGAGYAGIYSSISDGGNWIILKGTASGNSR 343
DB 766 -----ALENGTIVKFLGNATNGNTTIAAN-STLIQISGNYTADCVASADGT 810

RESULT 8
FLIC_ECOLI
ID FLIC_ECOLI STANDARD; PRT; 497 AA.
AC P04949;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Flagellin.
GN FLIC OR FLAF OR HAG OR B1923.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=87057066; PubMed=3536885;
RA Kuwajima G., Asaka J.-I., Fujiwara T., Fujiwara T., Node K., Kondo E.;
RT "Nucleotide sequence of the hag gene encoding flagellin of
RT Escherichia coli.";
RL J. Bacteriol. 168:1479-1483(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=89281489; PubMed=2659972;
RA Hanafusa T., Sakai A., Tomimaga A., Enomoto M.;
RT "Isolation and characterization of Escherichia coli hag operator
RT mutants whose hag48 expression has become repressible by a Salmonella
RT H1 repressor.";
RL Mol. Gen. Genet. 216:44-50(1989).
RN [3]
RP SEQUENCE FROM N.A.
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RX MEDLINE=88302441; PubMed=3043229;
RA Rosqvist R., Skurnik M., Wolf-Watz H.;
RT "Increased virulence of Yersinia pseudotuberculosis by two
RL independent mutations.";
RN Nature 334:522-525(1988).
RP SEQUENCE FROM N.A.
RC STRAIN=YPIII;
RX MEDLINE=89343638; PubMed=2761389;
RA Skurnik M., Wolf-Watz H.;
RT "Analysis of the yopA gene encoding the Yop1 virulence determinants
RL of Yersinia sp.";
CC Mol. Microbiol. 3:517-529(1989).
CC -!- FUNCTION: INVASIN IS A PROTEIN THAT ALLOWS ENTERIC BACTERIA TO
CC PENETRATE CULTURED MAMMALIAN CELLS. THE ENTRY OF INVASIN IN THE
CC CELL IS MEDIATED BY BINDING SEVERAL BETA-1 CHAIN INTEGRINS. THIS
CC PROTEIN IS AN ADHESIN FORMING A FIBRILLAR MATRIX ON THE CELL
CC SURFACE.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -----
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CC -----
CC EMBL; X13883; CAA32088.1;
CC FIR; S04534; S04534.
CC InterPro; IPR005594; Yada.
CC Pfam; PF03895; Yada; 1.
CC Plasmid; Virulence; Signal; Outer membrane.
CC SIGNAL 1 25
CC CHAIN 26 434 INVASIN.
CC SEQUENCE 434 AA; 45054 MW; E2C55F812B183D4 CRC64;

Query Match 7.2%; Score 131; DB 1; Length 434;
Best Local Similarity 21.1%; Pred. No. 0.91;
Matches 84; Conservative 51; Mismatches 137; Indels 126; Gaps 16;

QY 24 VNVESKDNKKTEVKIG-----AKTSVKEKDGKLVGT-----KDKGEN-----G 63
DB 98 LNAARKD---PYSIAIGATAEAAKPAAPAAVAVGSGSIATGVNSVAIGPLSKALGDSAVTYGA 154
QY 64 SSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEVTSGTNNVTASGKGTTA 123
DB 155 SSTAQRDGV-----AIGARASADTGVAVGFNSKVDQAQNSVAIGHSHVAADHGYSI 206
QY 124 TV---SKDDQGNITVMYDVG-DALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 179
DB 207 AIGDHSKTDREN---SVSIGHESLNRLQTLHAAGTEDTDAV-----NVAQLKK 251
QY 180 KMDETVNIAGNIEITRNGKNIDIAATSMTPQSSVSLGAGADAPLTVSDGDLNVGSKK 239
DB 252 EMAETLE-----NARKETLAQSDNDVLDAAKHH 278
QY 240 DNKPVKIT-----NVAPGVKEG-----DVT-NVAQLKGVAQ 269
DB 279 SNSVARTLTAEAHANKKSAEALVSAKVVAADSNSSHTLKTANSYTDVTVSSSTKKAISE 338
QY 270 N-----LNNRIDNDGNARAGIAQAIATAGLVQAYLPGLPKGSMMAIGGGTYRGEAGY 319
DB 339 SNQYTDHKFSQDLNRLDKLDKRVYDKGLASSAALNSLFQPYGVGVKNFTAGVGGYRSSQAL 398
QY 320 AIGYSSISDGGNWIIGKTA-SGNSRGHFGASASGVQW 356
DB 399 AIGSGYRVNSVALKAGVAYAGSSNVMYNASFNII--EW 434

RESULT 12
TOP2_PLAFK
ID TOP2_PLAFK STANDARD; PRT; 1398 AA.
```

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AC P41001;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE DNA topoisomerase II (EC 5.99.1.3).
GN TOP2.
OS Plasmodium falciparum (Isolate K1 / Thailand).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5839;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94316496; PubMed=8041616;
RA Cheesman S., McAtee S., Goman M., Johnson D., Horrocks P.,
RA Ridley R.G., Kilbey B.J.;
RT "The gene encoding topoisomerase II from Plasmodium falciparum.";
RL Nucleic Acids Res. 22:2547-2551(1994).
CC -!- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT
CC BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
CC MAKES DOUBLE-STRAND BREAKS.
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
CC NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
CC RELAX ONLY NEGATIVE SUPERCOILS.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
CC -----
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CC -----
CC EMBL; X79345; -; NOT_ANNOTATED_CDS.
CC HSSP; P06786; IBGW.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR003957; CBFA_NFYB_topis.
CC InterPro; IPR001241; DNA_topoisomI.
CC InterPro; IPR002205; DNA_topoisomIV.
CC Pfam; PF00204; DNA_gyraseB; 1.
CC Pfam; PF00521; DNA_topoisomIV; 1.
CC Pfam; PF02518; HATPase_C; 1.
CC PRINTS; PR00615; CCAATSUBUNTA.
CC PRINTS; PR00418; TP12FAMILY.
CC ProDom; PD000742; DNA_topoisomIV; 1.
CC SMART; SM00387; HATPase_C; 1.
CC SMART; SM00433; TOP2c; 1.
CC SMART; SM00434; TOP4c; 1.
CC PROSITE; PS00177; TOPOISOMERASE_II; 1.
KW Isomerase; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.
FT NP_BIND 144 149 ATP (POTENTIAL).
FT ACT_SITE 830 830 DNA CLEAVAGE (BY SIMILARITY).
FT DOMAIN 271 281 POLY-ASN.
FT DOMAIN 308 316 POLY-ASN.
FT DOMAIN 1089 1093 POLY-LYS.
FT DOMAIN 1227 1234 POLY-LYS.
SQ SEQUENCE 1398 AA; 161029 MW; BAAD7BEE88FE5BE9 CRC64;

Query Match 7.2%; Score 131; DB 1; Length 1398;
Best Local Similarity 24.2%; Pred. No. 3.5;
Matches 54; Conservative 46; Mismatches 89; Indels 34; Gaps 9;

QY 4 DFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAK---TSVKEKDGKLVTKDKG 60
DB 1190 DIEKVEEAIEFQR-----NVLSNREESNKFVKARKQGPSSMKKKKKLSSDEES 1241
QY 61 ENGSSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEVTSGTNNVTASGKG 120
DB 1242 EGGDTSDSSEFLVNTLNKNTNK-----KTTTSSNNVNNKKRLRKADDLN---SNELD 1293
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 ; Search time 26.1469 Seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-37
Perfect score: 1813
Sequence: 1 NNVDVFRVYDTVEFLSADTK.....TASGNSRGHFGASVGYQW 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_23:*
- 1: sp-archaea:*
 - 2: sp-bacteria:*
 - 3: sp-fungi:*
 - 4: sp-human:*
 - 5: sp-invertebrate:*
 - 6: sp-mammal:*
 - 7: sp-mhc:*
 - 8: sp-organelle:*
 - 9: sp-phage:*
 - 10: sp-plant:*
 - 11: sp-rodent:*
 - 12: sp-virus:*
 - 13: sp-vertebrate:*
 - 14: sp-unclassified:*
 - 15: sp-rvivirus:*
 - 16: sp-bacteriap:*
 - 17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1808	99.7	591	2 Q93QY3	Q93QY3 neisseria m
2	1808	99.7	591	2 Q9JPS7	Q9JPS7 neisseria m
3	1808	99.7	591	16 Q9JRI8	Q9JRI8 neisseria m
4	1804	99.5	592	2 Q9AQF0	Q9AQF0 neisseria m
5	1787	98.6	526	2 Q9JPS4	Q9JPS4 neisseria m
6	1787	98.6	530	2 Q9JPS1	Q9JPS1 neisseria m
7	1770	97.6	600	2 Q9JPS6	Q9JPS6 neisseria m
8	1762.5	97.2	592	2 Q9JPS9	Q9JPS9 neisseria m
9	1758.5	97.0	598	2 Q9JPR7	Q9JPR7 neisseria m
10	1758.5	97.0	599	2 Q9JPS8	Q9JPS8 neisseria m
11	1756.5	96.9	590	2 Q9JPS3	Q9JPS3 neisseria m
12	1753.5	96.7	594	2 Q93QY4	Q93QY4 neisseria m
13	1752.5	96.7	592	16 Q9JQW4	Q9JQW4 neisseria m
14	1750.5	96.6	594	2 Q9JPI3	Q9JPI3 neisseria m
15	1750.5	96.6	594	2 Q9JPS2	Q9JPS2 neisseria m
16	1750.5	96.6	595	2 Q9JPH0	Q9JPH0 neisseria m

17	1748.5	96.4	599	2 Q9JPR8	Q9JPR8 neisseria m
18	1744.5	96.2	600	2 Q9JPS5	Q9JPS5 neisseria m
19	1741.5	96.1	594	2 Q9JPH7	Q9JPH7 neisseria m
20	1741.5	96.1	598	2 Q9JPR9	Q9JPR9 neisseria m
21	1728.5	95.3	592	2 Q93QY2	Q93QY2 neisseria m
22	1728.5	95.3	598	2 Q9JPS0	Q9JPS0 neisseria m
23	1728.5	95.3	598	2 Q93QY5	Q93QY5 neisseria m
24	1728.5	95.3	598	2 Q9JPT0	Q9JPT0 neisseria m
25	1727.5	95.3	589	2 Q9JPI0	Q9JPI0 neisseria m
26	1715.5	94.6	589	2 Q93QY1	Q93QY1 neisseria m
27	608	33.5	1098	2 Q48152	Q48152 haemophilus
28	606.5	33.5	1096	2 Q8GM79	Q8GM79 haemophilus
29	586.5	32.3	1210	2 Q8GM74	Q8GM74 haemophilus
30	577.5	31.9	1210	2 Q8GM75	Q8GM75 haemophilus
31	572.5	31.6	1204	2 Q8GM76	Q8GM76 haemophilus
32	569	31.4	2353	2 P71401	P71401 haemophilus
33	369	20.4	1299	16 Q9F3X6	Q9F3X6 pasteurella
34	335.5	18.5	1004	2 Q8GM77	Q8GM77 haemophilus
35	334.5	18.5	1002	2 Q8GM78	Q8GM78 haemophilus
36	332.5	18.3	2059	16 Q9PD50	Q9PD50 xylella fas
37	327	18.0	1190	16 Q9PC04	Q9PC04 xylella fas
38	325	17.9	1588	16 Q8XDG4	Q8XDG4 escherichia
39	318	17.5	1778	16 Q8FCB2	Q8FCB2 escherichia
40	315	17.4	1461	16 Q8ZL64	Q8ZL64 salmonella
41	314	17.3	1107	16 Q9F2D8	Q9F2D8 salmonella
42	310.5	17.1	2314	2 Q8QKM8	Q8QKM8 moraxella c
43	307.5	17.0	641	16 Q8CKM1	Q8CKM1 versinia pe
44	307.5	17.0	658	16 Q8ZHJ0	Q8ZHJ0 versinia pe
45	295.5	16.3	2712	16 Q9F3X5	Q9F3X5 pasteurella

ALIGNMENTS

RESULT 1

Q93QY3	PRELIMINARY;	PRT;	591 AA.
ID	Q93QY3		
AC	Q93QY3;		
DC	01-DEC-2001 (TREMREL. 19, Created)		
DT	01-DEC-2001 (TREMREL. 19, Last sequence update)		
DT	01-OCT-2002 (TREMREL. 22, Last annotation update)		
DE	Nhha outer membrane protein.		
GN	NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
OC	Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=EG329;		
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RT	membrane protein of Neisseria meningitidis."		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF157606; AAK68867.1;		
DR	InterPro; IPR005594; YadaA.		
DR	Pfam; PF03895; YadaA; 1.		
SQ	SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;		
Query Match 99.7%; Score 1808; DB 2; Length 591;			
Best Local Similarity 99.7%; Pred. No. 2.3e-81;			
Matches 355; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
QY	1	NNVDVFRVYDTVEFLSADTKTTTVNVESKDCKKTEVKIGAKTSVTKKDGKLVTKDKGK 60	
		=====	
Db	236	NNVDVFRVYDTVEFLSADTKTTTVNVESKDCKKTEVKIGAKTSVTKKDGKLVTKDKGK 295	
QY	61	ENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFTVTSCTNVTASGKG 120	
		=====	
Db	296	ENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFTVTSCTNVTASGKG 355	
QY	121	TTATVSKDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSGKGKVISGNVSPSKG 180	
		=====	

QY 61 ENGSTDGEGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFETVTSNTVTFASGKG 120
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Db 296 ENGSTDGEGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFETVTSNTVTFASGKG 355
QY 121 TTATVSKDDQGNITVYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKG 180
|||||
Db 356 TTATVSKDDQGNITVYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKG 415
QY 181 MDETYNINAGNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLSDGDLNVGSKKD 240
|||||
Db 416 MDETYNINAGNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLSDGDLNVGSKKD 475
QY 241 NKPVRITNVAPGVKEDVTNVNQLKGVAQNLRNDVNDGNARAGIAQAIATAGLVQAYL 300
|||||
Db 476 NKPVRITNVAPGVKEDVTNVNQLKGVAQNLRNDVNDGNARAGIAQAIATAGLVQAYL 535
QY 301 PKKSMAIGGGYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 356
|||||
Db 536 PKKSMAIGGGYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 591
RESULT 4
Q9AOF0
ID Q9AOF0 PRELIMINARY; PRT; 592 AA.
AC Q9AOF0
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC58;
RA Peak I.R., Srihanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterisation of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AK09243.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;
Query Match 99.5%; Score 1804; DB 2; Length 592;
Best Local Similarity 99.4%; Pred. No. 3.7e-81;
Matches 354; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NNVDVRYDYTVDFLSADTKTTTVNVESKDNGKTEVKIGAKTSVKEKDKGLVTGKDKG 60
:|||||
Db 237 DNVDVRYDYTVDFLSADTKTTTVNVESKDNGKTEVKIGAKTSVKEKDKGLVTGKDKG 296
QY 61 ENGSTDGEGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFETVTSNTVTFASGKG 120
|||||
Db 297 ENGSTDGEGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFETVTSNTVTFASGKG 356
QY 121 TTATVSKDDQGNITVYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKG 180
|||||
Db 357 TTATVSKDDQGNITVYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKG 416
QY 181 MDETYNINAGNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLSDGDLNVGSKKD 240
|||||
Db 417 MDETYNINAGNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLSDGDLNVGSKKD 476
QY 241 NKPVRITNVAPGVKEDVTNVNQLKGVAQNLRNDVNDGNARAGIAQAIATAGLVQAYL 300
|||||
Db 477 NKPVRITNVAPGVKEDVTNVNQLKGVAQNLRNDVNDGNARAGIAQAIATAGLVQAYL 536
QY 301 PKKSMAIGGGYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 356
|||||

Db 537 PKKSMAIGGGYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 592
RESULT 5
Q9JPS4
ID Q9JPS4 PRELIMINARY; PRT; 526 AA.
AC Q9JPS4
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG6/88;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF228377; AAF42526.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;
Query Match 98.6%; Score 1787; DB 2; Length 526;
Best Local Similarity 98.6%; Pred. No. 2.2e-80;
Matches 351; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 NNVDVRYDYTVDFLSADTKTTTVNVESKDNGKTEVKIGAKTSVKEKDKGLVTGKDKG 60
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Db 171 DNVDVRYDYTVDFLSADTKTTTVNVESKDNGKTEVKIGAKTSVKEKDKGLVTGKDKG 230
QY 61 ENGSTDGEGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFETVTSNTVTFASGKG 120
|||||
Db 231 ENGSTDGEGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFETVTSNTVTFASGKG 290
QY 121 TTATVSKDDQGNITVYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKG 180
|||||
Db 291 TTATVSKDDQGNITVYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSKG 350
QY 181 MDETYNINAGNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLSDGDLNVGSKKD 240
|||||
Db 351 MDETYNINAGNIEITRNKKNIDIAATSMTPQSSVSLGAGADAPTLSDGDLNVGSKKD 410
QY 241 NKPVRITNVAPGVKEDVTNVNQLKGVAQNLRNDVNDGNARAGIAQAIATAGLVQAYL 300
|||||
Db 411 NKPVRITNVAPGVKEDVTNVNQLKGVAQNLRNDVNDGNARAGIAQAIATAGLVQAYL 470
QY 301 PKKSMAIGGGYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 356
|||||
Db 471 PKKSMAIGGGYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 526
RESULT 6
Q9JPS1
ID Q9JPS1 PRELIMINARY; PRT; 530 AA.
AC Q9JPS1
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.

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OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGF26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226380; AAF42529.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 530 AA; 51590 MW; 1F836CA57598515B CRC64;

Query Match 98.6%; Score 1787; DB 2; Length 530;
Best Local Similarity 98.6%; Pred. No. 2.2e-80;
Matches 351; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNVDVFTVDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIKEKDKLVTGKDG 60
Db :||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
175 DNVDVFHTVDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIKEKDKLVTGK 234
QY 61 ENGSSTDEGELVTAKEVIDAVNKAGRMKTTTANGTGQADKFEFTVSGTNVTFASGK 120
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
235 ENGSSTDEGELVTAKEVIDAVNKAGRMKTTTANGTGQADKFEFTVSGTNVTFASGK 294
QY 121 TTATVSKDDGNTVMDVNVGDALNVQLNSGWNLDKAVAGSSGKVIISGNVSPSKG 180
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
295 TTATVSKDDGNTVMDVNVGDALNVQLNSGWNLDKAVAGSSGKVIISGNVSPSKG 354
QY 181 MDEVTINAGNNTIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKD 240
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
355 MDEVTINAGNNTIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKD 414
QY 241 NKPVRTNVPAGYKGDVTVNAQLKGVQNLNRRIDVNDGNARAGIAQAATATAGLVQAYL 300
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
415 NKPVRTNVPAGYKGDVTVNAQLKGVQNLNRRIDVNDGNARAGIAQAATATAGLVQAYL 474
QY 301 PGKSMAIGGGTYRGAGYAGYSSISDGGNWIKTASGNSRGHFGASASVGYOW 356
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
475 PGKSMAIGGGTYRGAGYAGYSSISDGGNWIKTASGNSRGHFGASASVGYOW 530

RESULT 7
Q9JPS6 PRELIMINARY; PRT; 600 AA.
ID Q9JPS6 AC Q9JPS6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;

Query Match 97.2%; Score 1762.5; DB 2; Length 592;
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RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226371; AAF42520.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 97.6%; Score 1770; DB 2; Length 600;
Best Local Similarity 98.0%; Pred. No. 1.8e-79;
Matches 349; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 NNVDVFTVDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIKEKDKLVTGKDG 60
Db :||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
245 DNVDVFHTVDTVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIKEKDKLVTGK 304
QY 61 ENGSSTDEGELVTAKEVIDAVNKAGRMKTTTANGTGQADKFEFTVSGTNVTFASGK 120
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
305 ENGSSTDEGELVTAKEVIDAVNKAGRMKTTTANGTGQADKFEFTVSGTNVTFASGK 364
QY 121 TTATVSKDDGNTVMDVNVGDALNVQLNSGWNLDKAVAGSSGKVIISGNVSPSKG 180
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
365 TTATVSKDDGNTVMDVNVGDALNVQLNSGWNLDKAVAGSSGKVIISGNVSPSKG 424
QY 181 MDEVTINAGNNTIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKD 240
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
425 MDEVTINAGNNTIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKD 484
QY 241 NKPVRTNVPAGYKGDVTVNAQLKGVQNLNRRIDVNDGNARAGIAQAATATAGLVQAYL 300
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
485 NKPVRTNVPAGYKGDVTVNAQLKGVQNLNRRIDVNDGNARAGIAQAATATAGLVQAYL 544
QY 301 PGKSMAIGGGTYRGAGYAGYSSISDGGNWIKTASGNSRGHFGASASVGYOW 356
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
545 PGKSMAIGGGTYRGAGYAGYSSISDGGNWIKTASGNSRGHFGASASVGYOW 600

RESULT 8
Q9JPS9 PRELIMINARY; PRT; 592 AA.
ID Q9JPS9 AC Q9JPS9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;

Query Match 97.2%; Score 1762.5; DB 2; Length 592;
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Best Local Similarity 98.08; Pred. No. 4e-79;
Matches 350; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 1 NNVDVFRYTDVFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGDKG 60
Db :|||||
Db 236 DNVDVFRYTDVFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKGK 295
QY 61 ENGSSTDEGELVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEFTVSGTNVTFASGKG 120
Db :|||||
Db 296 ENGSSTDEGELVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEFTVSGTNVTFASGKG 355
QY 121 TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK 180
Db :|||||
Db 356 TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK 415
QY 181 MDETVINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKK 239
Db :|||||
Db 416 MDETVINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDKDALNVGSKD 475
QY 240 DNKPVRTNVPAGVKEGDTVNTVAQLKGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQAY 299
Db :|||||
Db 476 ANKPVRTNVPAGVKEGDTVNTVAQLKGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQAY 535
QY 300 LPKSMAAIGGTYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 356
Db :|||||
Db 536 LPKSMAAIGGTYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 592

RESULT 9
Q9JPR7 PRELIMINARY; PRT; 598 AA.
ID Q9JPR7 AC Q9JPR7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID:487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWZ107;
RX Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226385; AAF42534.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 97.08; Score 1758.5; DB 2; Length 598;
Best Local Similarity 98.08; Pred. No. 6.4e-79;
Matches 349; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 NVDFVRYTDVFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGDKGE 61
Db :|||||
Db 243 NVDFVRYTDVFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKGK 302
QY 62 NGSSTDEGELVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEFTVSGTNVTFASGKG 121
Db :|||||
Db 303 NGSSTDEGELVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEFTVSGTNVTFASGKG 362
QY 122 TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK 181
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Db :|||||
Db 363 TATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK 422
QY 182 DETVINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKK 240
Db :|||||
Db 423 DETVINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDKDALNVGSKDA 482
QY 241 NKPVRITNVPAGVKEGDTVNTVAQLKGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQAY 300
Db :|||||
Db 483 NKPVRITNVPAGVKEGDTVNTVAQLKGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQAY 542
QY 301 PGKSMAAIGGTYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 356
Db :|||||
Db 543 PGKSMAAIGGTYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 598

RESULT 10
Q9JPS8 PRELIMINARY; PRT; 599 AA.
ID Q9JPS8 AC Q9JPS8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID:487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A22;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226364; AAF42513.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 97.08; Score 1758.5; DB 2; Length 599;
Best Local Similarity 98.08; Pred. No. 6.4e-79;
Matches 349; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 NVDFVRYTDVFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGDKGE 61
Db :|||||
Db 244 NVDFVRYTDVFEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKGKE 303
QY 62 NGSSTDEGELVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEFTVSGTNVTFASGKG 121
Db :|||||
Db 304 NGSSTDEGELVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFEFTVSGTNVTFASGKG 363
QY 122 TATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK 181
Db :|||||
Db 364 TATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK 423
QY 182 DETVINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDG-DALNVGSKK 240
Db :|||||
Db 424 DETVINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDKDALNVGSKDA 483
QY 241 NKPVRITNVPAGVKEGDTVNTVAQLKGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQAY 300
Db :|||||
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QY 301 PGKSMAAIGGTYRGEAGYAIGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 356
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Db 544 PKGSMMAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 599
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RESULT 11
Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN Neisseria meningitidis.
OS Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nui S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42527.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 96.9%; Score 1756.5; DB 2; Length 590;
Best Local Similarity 97.5%; Pred. No. 7.9e-79;
Matches 348; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 NNVDVFRVTDVFEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKGLVTGDKG 60
:|||||
Db 234 DNVDVFRVTDVFEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKGLVTGDKG 293
:|||||
Qy 61 ENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSGTNVTTFASGK 120
|||
Db 294 ENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSGTNVTTFASGK 353
|||||
Qy 121 TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK 180
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Db 354 TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK 413
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Qy 181 MDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKK 239
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Db 414 MDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKD 473
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|||||

RESULT 12
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AC Q93QY4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Nhha outer membrane protein.
```

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GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62297 MW; 9DD448B04B3A8EA2 CRC64;

Query Match 96.7%; Score 1753.5; DB 2; Length 594;
Best Local Similarity 97.2%; Pred. No. 1.1e-78;
Matches 347; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 NNVDVFRVTDVFEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKGLVTGDKG 60
:|||||
Db 238 DNVDVFRVTDVFEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDKGLVTGDKG 297
:|||||
Qy 61 ENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSGTNVTTFASGK 120
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Db 298 ENDSSTDKGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETVTSGTNVTTFASGK 357
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Db 358 TTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGK 417
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Qy 181 MDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSKK 239
|||||
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|||||
Qy 240 DNKPVRTITNAPVKGEGDVTNVAQLKGVAQNLRNIDNVGNRAGIAQAIAATAGLVQAY 299
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Db 478 ANKPVRTITNAPVKGEGDVTNVAQLKGVAQNLRNIDNVGNRAGIAQAIAATAGLVQAY 537
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Qy 300 LPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 356
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Db 538 LPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 594
|||||

RESULT 13
Q9JQW4 PRELIMINARY; PRT; 592 AA.
AC Q9JQW4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Putative surface fibril protein (Outer membrane protein GNA992).
GN NMA1200 OR GNA992.
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699, 487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491.";
RL Nature 404:502-506(2000).
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Query Match      96.6%; Score 1750.5; DB 2; Length 594;
Best Local Similarity 97.2%; Pred. No. 1.6e-78;
Matches 347; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

Qy 1 NNVDVFRTYDTVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVIKEKDKGLVTGKDKG 60
Db :|||||
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Db :|||||
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Db :|||||
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Qy 121 TTATVSKDDQGNITVYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 180
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Db :|||||
Qy 418 MDETNNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDEGALNVGSKD 477
Db :|||||
Qy 240 DNKPVRITNVAPGVKEGDTNVAQLKGVAQNLRNIDNVDCNARAGIAQAIAITAGLVQAY 299
Db :|||||
Qy 478 ANKPVRITNVAPGVKEGDTNVAQLKGVAQNLRNIDNVDCNARAGIAQAIAITAGLVQAY 537
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Qy 300 LPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGHFGASASVGYOW 356
Db :|||||
Qy 538 LPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGHFGASASVGYOW 594
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Search completed: October 6, 2003, 09:30:53
Job time : 28.1469 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 ; Search time 32.8045 Seconds
(without alignments)
1848.329 Million cell updates/sec

Title: US-09-771-382-38

Perfect score: 1947

Sequence: 1 NRAASVKDVLNAGWNKGVK.....TASGNSRCHFGASASGVQW 382

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1947	100.0	433	22	AAU06185 N. meningitidis PM
2	1941	99.7	512	22	AAU06182 N. meningitidis PM
3	1941	99.7	591	20	AAAY27202 Amino acid sequenc
4	1941	99.7	591	20	AAAY23741 A surface protein
5	1941	99.7	591	20	AAAY23746 A surface protein
6	1941	99.7	591	22	AAU06171 N. meningitidis PM
7	1941	99.7	591	22	AAU06175 N. meningitidis EG
8	1938	99.5	591	21	AAAY57045 BASB029 amino acid
9	1937	99.5	592	20	AAAY23737 A surface protein

10	1891.5	97.1	502	22	AAU06186 N. meningitidis PM
11	1886.5	96.9	594	20	AAAY23740 A surface protein
12	1886.5	96.9	594	21	AAAY57044 BASB029 amino acid
13	1886.5	96.9	594	22	AAU06174 N. meningitidis EG
14	1881.5	96.6	599	20	AAAY23743 A surface protein
15	1881.5	96.6	599	22	AAU06176 N. meningitidis H3
16	1874.5	96.3	594	20	AAAY23739 A surface protein
17	1874.5	96.3	594	22	AAU06179 N. meningitidis B2
18	1861.5	95.6	513	22	AAU06183 N. meningitidis H4
19	1861.5	95.6	592	20	AAAY23744 A surface protein
20	1861.5	95.6	592	22	AAU06172 N. meningitidis H4
21	1861.5	95.6	598	20	AAAY23738 A surface protein
22	1861.5	95.6	598	20	AAAY23742 A surface protein
23	1861.5	95.6	598	22	AAU06177 N. meningitidis H1
24	1861.5	95.6	598	22	AAU06178 N. meningitidis B2
25	1854.5	95.2	592	22	AAU06180 N. meningitidis Z2
26	1837.5	94.4	592	20	AAAY27203 Amino acid sequenc
27	1817.5	93.3	589	20	AAAY23745 A surface protein
28	1817.5	93.3	589	22	AAU06173 N. meningitidis P2
29	1810	93.0	407	22	AAU06184 N. meningitidis PM
30	1736.5	89.2	604	22	AAU06181 N. meningitidis su
31	710	36.5	1098	17	AAAR9392 Haemophilus adhesi
32	690.5	35.5	1094	21	AAAB23858 Haemophilus influe
33	660	33.9	2353	17	AAAR9393 Haemophilus influe
34	660	33.9	2411	21	AAAB23860 Haemophilus influe
35	600	30.8	116	21	AAAB37832 Neisserial adhesi
36	470.5	24.2	679	17	AAAR9394 Haemophilus influe
37	470.5	24.2	679	21	AAAB23855 Haemophilus influe
38	414.5	21.3	1002	21	AAAB23854 Haemophilus influe
39	406	20.9	1004	21	AAAB23857 Haemophilus influe
40	392	20.1	1104	21	AAAB23856 Haemophilus influe
41	392	20.1	1104	21	AAAB23859 Haemophilus influe
42	378	19.4	245	20	AAAY27201 Amino acid sequenc
43	366	18.8	72	21	AAAB37830 Neisserial conserv
44	356	18.3	2139	24	ABP71294 M. catarrhalis sur
45	354.5	18.2	2314	22	AAAB69136 M. catarrhalis les

ALIGNMENTS

RESULT 1
AAU06185
ID AAU06185 standard; Protein; 433 AA.

XX AAU06185;

XX 24-OCT-2001 (first entry)

XX N. meningitidis PMC21 Nhha deletion mutant #3.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine;
mutant; mutcin.

OS Neisseria meningitidis strain PMC21.
Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..51

FT Protein /label= signal_peptide

FT /label= 52..433

FT /note= Mature_Nhha_deletion_mutant_#3

FT claimed in claim 12"

XX WO200155182-A1.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

PA (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI: 2001-488774/53.
DR N-PSDB; AAS09175.
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX Claim 12; Fig 8; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #3.
XX
SQ Sequence 433 AA;

Query Match 100.0%; Score 1947; DB 22; Length 433;
Best Local Similarity 100.0%; Pred. No. 6.5e-122;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NRAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDKGK 60
DB 52 NRAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDKGK 111
QY 61 TEVKIGAKTSVIEKDGKLVTKGDKGSGSTDEGELVTAKEVIDAVNKAGWRMKTSTA 120
DB 112 TEVKIGAKTSVIEKDGKLVTKGDKGSGSTDEGELVTAKEVIDAVNKAGWRMKTSTA 171
QY 121 NGOTGQADKFTVTSGTNVTFASGKGTATVSKDDGNTVMYDNNVGDALNVLQNSG 180
DB 172 NGOTGQADKFTVTSGTNVTFASGKGTATVSKDDGNTVMYDNNVGDALNVLQNSG 231
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DB 232 WNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKGNIDTATSWTPQFSS 291
QY 241 VSLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVAPGVKEGDTNVVAQLKGVAQNLR 300
DB 292 VSLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVAPGVKEGDTNVVAQLKGVAQNLR 351
QY 301 IDNVGDNARAGIAQAATAGLVQAYLPKGSMAIGGTYRGEAGYAGYSSISDGGNWII 360
DB 352 IDNVGDNARAGIAQAATAGLVQAYLPKGSMAIGGTYRGEAGYAGYSSISDGGNWII 411
QY 361 KGTASNSRGHFGCASASGVQW 382
DB 412 KGTASNSRGHFGCASASGVQW 433

RESULT 2
AAU06182
ID AAU06182 standard; Protein; 512 AA.
XX
AC AAU06182;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 Nhha deletion mutant #1.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutein.

XX Neisseria meningitidis strain PMC21.
OS Synthetic.
XX
FH Location/Qualifiers
FT Peptide 1..51
FT /label= Signal_peptide
FT Protein 52..512
FT /label= Mature_Nhha_deletion_mutant.#1
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12."
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU000069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
XX N-PSDB; AAS09172.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 5; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #1.
XX
SQ Sequence 512 AA;

Query Match 99.7%; Score 1941; DB 22; Length 512;
Best Local Similarity 100.0%; Pred. No. 2e-121;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDKGK 61
DB 132 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDKGK 191
QY 62 EVKIGAKTSVIEKDGKLVTKGDKGSGSTDEGELVTAKEVIDAVNKAGWRMKTSTA 121
DB 192 EVKIGAKTSVIEKDGKLVTKGDKGSGSTDEGELVTAKEVIDAVNKAGWRMKTSTA 251
QY 122 GQTGQADKFTVTSGTNVTFASGKGTATVSKDDGNTVMYDNNVGDALNVLQNSGW 181
DB 252 GQTGQADKFTVTSGTNVTFASGKGTATVSKDDGNTVMYDNNVGDALNVLQNSGW 311
QY 182 NLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKGNIDTATSWTPQFSS 241
DB 312 NLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKGNIDTATSWTPQFSS 371
QY 242 SLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVAPGVKEGDTNVVAQLKGVAQNLR 301
DB 372 SLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVAPGVKEGDTNVVAQLKGVAQNLR 431
QY 302 DNVGDNARAGIAQAATAGLVQAYLPKGSMAIGGTYRGEAGYAGYSSISDGGNWII 361


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Db 432 DNVGNGRAGIAQAIATAGLVQAYLPKGSMAITGGTYRGEAGYATGYSISDGGNWIIL 491
QY 362 GTASGNSRGHFGASASVGYQW 382
Db 492 GTASGNSRGHFGASASVGYQW 512

RESULT 3
ID AAY27202 standard; Protein; 591 AA.
XX
AC AAY27202;
XX
DT 24-SEP-1999 (first entry)
DE Amino acid sequence of N. meningitidis protein ORF40-1.
XX
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW bacterial infection; treatment.
XX
OS Neisseria meningitidis.
XX
PN WO9936544-A2.
XX
PD 22-JUL-1999.
XX
PF 14-JAN-1999; 99WO-IB00103.
XX
PR 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
XX
DR N-PSDB; AAX99124.
XX
PT New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
PS Claim 1; Page 62; 123pp; English.
XX
CC The invention provides proteins (AAY27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisseria
CC bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 591 AA;
Query Match 99.7%; Score 1941; DB 20; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.4e-121;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RAASVKDVLNAGWNIGKVGKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVEKDKNGKKT 61
|||||
Db 211 RAASVKDVLNAGWNIGKVGKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVEKDKNGKKT 270
QY 62 EVKIGAKTSVIKEKDKGLVTGKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTAN 121
|||||
Db 271 EVKIGAKTSVIKEKDKGLVTGKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTAN 330
QY 122 GQTGQADKFTVTSGTNVTFASGKGTATATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 181
|||||
Db 331 GQTGQADKFTVTSGTNVTFASGKGTATATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 390
QY 182 NLDSKAVAGSSGKVIISGNVSPSKGKMDVTNINAGNNIETRNKNIDIATSMTPQFSSV 241
|||||
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|||||
Db 391 NLDSKAVAGSSGKVIISGNVSPSKGKMDVTNINAGNNIETRNKNIDIATSMTPQFSSV 450
QY 242 SLGAGADAPTLSDVDGALNVGSKKDNKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 301
|||||
Db 451 SLGAGADAPTLSDVDGALNVGSKKDNKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 510
QY 302 DNVGNGRAGIAQAIATAGLVQAYLPKGSMAITGGTYRGEAGYATGYSISDGGNWIIL 361
|||||
Db 511 DNVGNGRAGIAQAIATAGLVQAYLPKGSMAITGGTYRGEAGYATGYSISDGGNWIIL 570
QY 362 GTASGNSRGHFGASASVGYQW 382
Db 571 GTASGNSRGHFGASASVGYQW 591

RESULT 4
AAY23741
ID AAY23741 standard; Protein; 591 AA.
XX
AC AAY23741;
XX
DT 08-SEP-1999 (first entry)
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU ) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI; 1999-418754/35.
XX
DR N-PSDB; AAX85793.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 104-106; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 591 AA;
Query Match 99.7%; Score 1941; DB 20; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.4e-121;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RAASVKDVLNAGWNIGKVGKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVEKDKNGKKT 61
|||||
Db 211 RAASVKDVLNAGWNIGKVGKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVEKDKNGKKT 270
QY 62 EVKIGAKTSVIKEKDKGLVTGKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTAN 121
|||||
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|||||
271 EVKIGAKTSVKEKDKGLVTKGDKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 330
122 GQTQADKFEFVTSGTNVTFASGKGTATATVSKDDQGNITVMDVNVGDALNVNQLNSGW 181
331 GQTQADKFEFVTSGTNVTFASGKGTATATVSKDDQGNITVMDVNVGDALNVNQLNSGW 390
182 NLDKAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRNKKNIDIAISMTPOFSSV 241
391 NLDKAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRNKKNIDIAISMTPOFSSV 450
242 SLGAGADAPTLISVDGDALNVGSKKDNKPVRTTNVAPGVKEGDVTNVAQLKGVAQNLNRI 301
451 SLGAGADAPTLISVDGDALNVGSKKDNKPVRTTNVAPGVKEGDVTNVAQLKGVAQNLNRI 510
302 DNVDGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGAGYAGYSSISDGGNWI 361
511 DNVDGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGAGYAGYSSISDGGNWI 570
362 GTASGNSRGHFGASASVGYOW 382
571 GTASGNSRGHFGASASVGYOW 591

RESULT 5

AA023746
ID AAY23746 standard; Protein; 591 AA.

XX AC AAY23746;

XX DT 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX KW Surface protein; surface glycoprotein; infection; vaccine;

XX KW immunoreactive peptide.

XX OS Neisseria meningitidis.

XX PN WO9931132-A1.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-AU01031.

XX PR 12-DEC-1997; 97GB-0026398.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Jennings MP, Moxon ER, Peak IRA;

XX DR WPI; 1999-418754/35.

XX DR N-PSDB; RAX85798.

XX PT Neisseria meningitidis surface proteins useful for treating N.

XX PT meningitidis infections

XX PS Claim 1; Page 127-128; 132pp; English.

XX CC The present sequence represents a surface protein of Neisseria

XX CC meningitidis which is approximately 62 kDa. The N. meningitidis

XX CC surface glycoproteins, nucleic acids, the primers and optionally

XX CC a thermostable polymerase, or antibodies are useful in a kit for

XX CC the detection or diagnosis of N. meningitidis infection in humans.

XX CC The N. meningitidis surface glycoproteins can also be used to

XX CC prevent or treat N. meningitidis infection in humans, especially

XX CC in the form of vaccines. The proteins and antibodies can also

XX CC be used to identify immunoreactive peptides.

XX SQ Sequence 591 AA;

Query Match 99.78; Score 1941; DB 20; Length 591;

Best Local Similarity 100.0%; Pred. No. 2.4e-121;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RAASVKDVLNAGWIKGVKPGTTASDNVDVFRVTDYTFEFLSADTKTTTVNVESKDKGKT 61
Db 211 RAASVKDVLNAGWIKGVKPGTTASDNVDVFRVTDYTFEFLSADTKTTTVNVESKDKGKT 270
Qy 62 EVKIGAKTSVKEKDKGLVTKGDKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
Db 271 EVKIGAKTSVKEKDKGLVTKGDKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 330
Qy 122 GQTQADKFEFVTSGTNVTFASGKGTATATVSKDDQGNITVMDVNVGDALNVNQLNSGW 181
Db 331 GQTQADKFEFVTSGTNVTFASGKGTATATVSKDDQGNITVMDVNVGDALNVNQLNSGW 390
Qy 182 NLDKAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRNKKNIDIAISMTPOFSSV 241
Db 391 NLDKAVAGSSGKVISGNVSPSKGMDTVNINAGNIEITRNKKNIDIAISMTPOFSSV 450
Qy 242 SLGAGADAPTLISVDGDALNVGSKKDNKPVRTTNVAPGVKEGDVTNVAQLKGVAQNLNRI 301
Db 451 SLGAGADAPTLISVDGDALNVGSKKDNKPVRTTNVAPGVKEGDVTNVAQLKGVAQNLNRI 510
Qy 302 DNVDGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGAGYAGYSSISDGGNWI 361
Db 511 DNVDGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGAGYAGYSSISDGGNWI 570
Qy 362 GTASGNSRGHFGASASVGYOW 382
Db 571 GTASGNSRGHFGASASVGYOW 591

RESULT 6

AA006171

ID AA006171 standard; Protein; 591 AA.

XX AC AA006171;

XX DT 24-OCT-2001 (first entry)

XX DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.

XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain PMC21.

XX FH Key Location/Qualifiers

FT Peptide 1..51 /label= Signal_peptide

FT Region 1..50 /label= C1

FT /note= "Conserved region 1"

FT Region 51..108 /label= V1

FT /note= "Variable region 1"

FT Protein 52..591 /label= Mature_Nhha

FT /note= "Predicted mature protein, specifically

FT /label= C2

FT Region 109..120 /label= C2

FT /note= "Conserved region 2"

FT Region 121..124 /label= V2

FT /note= "Variable region 2"

FT Region 125..188 /label= C3

FT /note= "Conserved region 3"

FT Region 189..210 /label= V3

FT /note= "Variable region 3"

FT Region 211..229 /label= C4

FT Region /note= "Conserved region 4"
230..236
/label= V4
FT FT
FT Region /note= "Variable region 4"
237..591
/label= C5
FT FT
FT /note= "Conserved region 5"

XX W0200155182-A1.

PN 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

XX (UYQU) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;

PI WPI; 2001-488774/53.

DR N-PSDB; AAS09161.

XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -

XX Claim 9; Fig 1; 91pp; English.

XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.

SQ Sequence 591 AA;

Query Match 99.7%; Score 1941; DB 22; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.4e-121;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGNINIKVPGTASDNVDFVRTYDFEFLSADTKTTTVNVEKDKGKKT 61
DB 211 RAASVKDVLNAGNINIKVPGTASDNVDFVRTYDFEFLSADTKTTTVNVEKDKGKKT 270
QY 62 EVKIGAKTSVIREKDKGLVTGDKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITAN 121
DB 271 EVKIGAKTSVIREKDKGLVTGDKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITAN 330
QY 122 GQTQADKFTVTSCTNVTTFASGKGTATVSKDDQGNITVMYDVNVDALNVNQLNSGW 181
DB 331 GQTQADKFTVTSCTNVTTFASGKGTATVSKDDQGNITVMYDVNVDALNVNQLNSGW 390
QY 182 NLDSKAVAGSSGKVISGNVSPSKGKMDVTNINAGNIEITRNKNIDITATMTPOFSSV 241
DB 391 NLDSKAVAGSSGKVISGNVSPSKGKMDVTNINAGNIEITRNKNIDITATMTPOFSSV 450
QY 242 SLGAGADAPTLSDGDLNAGVSKDKNKPVRITNVPAGVKEGDVTNVAQLKGVAQNLNRI 301
DB 451 SLGAGADAPTLSDGDLNAGVSKDKNKPVRITNVPAGVKEGDVTNVAQLKGVAQNLNRI 510
QY 302 DNVVDGNARAGIAQAATAGLVQAYLPKGSMAIGGTYRGEAGYATGYSISDGGNWIK 361
DB 511 DNVVDGNARAGIAQAATAGLVQAYLPKGSMAIGGTYRGEAGYATGYSISDGGNWIK 570

QY 362 GTASGNSRGHFGASASVGYQW 382
DB 571 GTASGNSRGHFGASASVGYQW 591
RESULT 7
AAU06175
ID AAU06175 standard; Protein; 591 AA.
XX
AC AAU06175;
XX 24-OCT-2001 (first entry)
XX N. meningitidis EG329 surface antigen Nhha polypeptide sequence.
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX Neisseria meningitidis strain EG329.
XX Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..108
FT /label= V1
FT /note= "Variable region 1"
FT Region 109..120
FT /label= C2
FT /note= "Conserved region 2"
FT Region 121..124
FT /label= V2
FT /note= "Variable region 2"
FT Region 125..188
FT /label= C3
FT /note= "Conserved region 3"
FT Region 189..210
FT /label= V3
FT /note= "Variable region 3"
FT Region 211..229
FT /label= C4
FT /note= "Conserved region 4"
FT Region 230..236
FT /label= V4
FT /note= "Variable region 4"
FT Region 237..591
FT /label= C5
FT /note= "Conserved region 5"
PN W0200155182-A1.
XX
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
PI WPI; 2001-488774/53.
DR N-PSDB; AAS09165.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.

CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of *N. meningitidis*, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of *N. meningitidis* strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen NhhA
CC from *N. meningitidis* strain EG329 is 1 of 10 NhhA polypeptide sequences
CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in
CC the present invention.

XX SQ Sequence 591 AA;

Query Match 99.7%; Score 1941; DB 22; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.4e-121;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGNWKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNCKKT 61
DB 211 RAASVKDVLNAGNWKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNCKKT 270
QY 62 EVKIGAKTSYVKEKDKGLVTGKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
DB 271 EVKIGAKTSYVKEKDKGLVTGKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 330
QY 122 GQTQADKFFETVTSNVTASGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGW 181
DB 331 GQTQADKFFETVTSNVTASGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGW 390
QY 182 NLDSKAVAGSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDTATMTPOFSSV 241
DB 391 NLDSKAVAGSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDTATMTPOFSSV 450
QY 242 SLGAGADAPTLSDVDGALNVGSKKDNKPVRTTNVAPGVKEGDTNVAQLKGVAQNLNRI 301
DB 451 SLGAGADAPTLSDVDGALNVGSKKDNKPVRTTNVAPGVKEGDTNVAQLKGVAQNLNRI 510
QY 302 DNVDGNARAGIAQAIAATAGLVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI 361
DB 511 DNVDGNARAGIAQAIAATAGLVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI 570
QY 362 GTASGNSRHFHGASASVGYQW 382
DB 571 GTASGNSRHFHGASASVGYQW 591

RESULT 8

AA57045

ID - AA57045 standard; Protein: 591 AA.

XX AC

AA57045;

XX XX

21-FEB-2000 (first entry)

XX XX

BASB029 amino acid sequence from *N. meningitidis* strain H44/76.

XX KW BASB029; *Neisseria meningitidis*; surface fibril protein; HSF; diagnosis;
XX KW infection; treatment; prevent; antibacterial drug.

XX OS *Neisseria meningitidis*.

XX FH

Key Location/Qualifiers

FH Misc-difference 90

FT /note= "Encoded by AAT"

FT Misc-difference 92

FT /note= "Encoded by GAT"

FT Misc-difference 98

FT /note= "Encoded by AAC"

FT Misc-difference 108

FT /note= "Encoded by AATC"

FT Misc-difference 123

FT /note= "Encoded by ACA"

FT

FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGT"
XX XX
XX WO9958683-A2.
XX XX
XX 18-NOV-1999.
XX XX
XX 07-MAY-1999; 99WO-EP03255.
XX XX
XX 13-MAY-1998; 98GB-0010276.
XX XX

(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

Ruelle J;

WPI; 2000-053103/04.

DR N-PSDB; AA239865.

XX XX

New polypeptide from *Neisseria meningitidis* useful for diagnosis,

PT treatment or prevention of bacterial infections in mammal

XX XX

Claim 4; Fig 2; 74pp; English.

XX XX

This is the *Neisseria meningitidis* BASB029 amino acid sequence from

CC serogroup B strain H44/76. The BASB029 protein is homologous to the

CC Haemophilus influenzae surface fibril (HSF) protein. The invention

CC relates to BASB029 polynucleotide sequences (AA239864-239865) and

CC polypeptide sequences (AA57044-57045) and their immunogenic fragments.

CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*

CC meningitidis infection in a mammal. Compositions containing BASB029

CC polynucleotides and polypeptides are useful for generating an immune

CC response in an animal. A therapeutic composition comprising an antibody

CC directed against BASB029 is useful in treating humans with *Neisseria*

CC meningitidis disease. The polynucleotide is useful in the diagnosis of

CC infection which results from increased or decreased expression of the

CC polynucleotide, and for therapeutic or prophylactic purposes,

CC particularly genetic immunisation. Antibodies against BASB029

CC polynucleotides and polypeptides are also useful for treating infections

CC particularly bacterial infections. The protein is useful in the

CC screening and development of antibacterial drugs. Fused recombinant

CC protein is useful for the stimulation of the immune system of an organism

XX receiving the protein.

XX SQ

Sequence 591 AA;

Query Match 99.5%; Score 1938; DB 21; Length 591;

Best Local Similarity 99.7%; Pred. No. 3.8e-121;

Matches 380; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGNWKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNCKKT 61

DB 211 RAASVKDVLNAGNWKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNCKKT 270

QY 62 EVKIGAKTSYVKEKDKGLVTGKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121

DB 271 EVKIGAKTSYVKEKDKGLVTGKDKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 330

QY 122 GQTQADKFFETVTSNVTASGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGW 181

DB 331 GQTQADKFFETVTSNVTASGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGW 390

QY 182 NLDSKAVAGSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDTATMTPOFSSV 241

DB 391 NLDSKAVAGSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDTATMTPOFSSV 450

QY 242 SLGAGADAPTLSDVDGALNVGSKKDNKPVRTTNVAPGVKEGDTNVAQLKGVAQNLNRI 301

DB 451 SLGAGADAPTLSDVDGALNVGSKKDNKPVRTTNVAPGVKEGDTNVAQLKGVAQNLNRI 510

QY 302 DNVDGNARAGIAQAIAATAGLVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI 361

FT

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|||||
Db 511 DNVGNGRAGIAQAIAATAGLVQAYLPKSMMAITGGTYRGEAGYAIYSSISDGGNWI 570
|||||
QY 362 GTASGNSRGHFGASASVGYQW 382
|||||
Db 571 GTASGNSRGHFGASASVGYQW 591
|||||

RESULT 9
ID AAY23737 standard; Protein; 592 AA.
XX
AC AAY23737;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
PD
PE 14-DEC-1998; 98WO-AU01031.
PF
PR 12-DEC-1997; 97GB-0026398.
PX
PA (ISIS-) ISIS INNOVATION LTD.
XX (UYQU ) UNIV QUEENSLAND.
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI; 1999-418754/35.
DR N-PSDB; AAX85788.
PT
PT Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections
PS
PS Claim 1; Page 86-87; 132pp; English.
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 592 AA;
Query Match 99.5%; Score 1937; DB 20; Length 592;
Best Local Similarity 99.7%; Pred. No. 4.4e-121;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 RAASVKDVLNAGNINIKVPGTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKGKKT 61
|||||
Db 212 RAASVKDVLNAGNINIKVPGTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKGKKT 271
|||||
QY 62 EVKIGAKTSVIKEKDKGLVTGDKGNGSSTDBEGGLVTAKEVIDAVNKGWRMKT 121
|||||
Db 272 EVKIGAKTSVIKEKDKGLVTGDKGNGSSTDBEGGLVTAKEVIDAVNKGWRMKT 331
|||||
QY 122 GQTQADKFTVTSCTNVTNFASCKGTATVSKDQGNITVMYDNYGDALNVNQLNSGW 181
|||||
Db 332 GQTQADKFTVTSCTNVTNFASCKGTATVSKDQGNITVMYDNYGDALNVNQLNSGW 391
|||||
QY 182 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIETTRNGKNIDIATSTPQFSSV 241
|||||

|||||
Db 392 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIETTRNGKNIDIATSTPQFSSV 451
|||||
QY 242 SLGAGADAPTLSVDGDALNVGSKKDNKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 301
|||||
Db 452 SLGAGADAPTLSVDGDALNVGSKKDNKPVRIITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 511
|||||
QY 302 DNVGNGRAGIAQAIAATAGLVQAYLPKSMMAITGGTYRGEAGYAIYSSISDGGNWI 361
|||||
Db 512 DNVGNGRAGIAQAIAATAGLVQAYLPKSMMAITGGTYRGEAGYAIYSSISDGGNWI 571
|||||
QY 362 GTASGNSRGHFGASASVGYQW 382
|||||
Db 572 GTASGNSRGHFGASASVGYQW 592
|||||

RESULT 10
AAU06186
ID AAU06186 standard; Protein; 502 AA.
XX
AC AAU06186;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 Nhha deletion mutant #4.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine;
mutant; mutein.
XX
OS Neisseria meningitidis strain PMC21.
XX
XX Synthetic.
XX
XX Key
XX Peptide 1..49 Location/Qualifiers
XX Protein 50..502 /label= Signal_peptide
XX /label= Mature_Nhha_deletion_mutant_#4
XX /note= "Predicted mature protein, specifically
XX claimed in claim 12"
PN WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
DR
DR N-PSDB; AAS09176.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 12; Fig 9; 91pp; English.
PS
PS The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence represents N. meningitidis strain PMC21 surface
CC antigen Nhha deletion mutant #4.
```

XX SQ Sequence 502 AA;
Query Match 97.1%; Score 1891.5; DB 22; Length 502;
Best Local Similarity 97.9%; Pred. No. 3.9e-118;
Matches 374; Conservative 1; Mismatches 0; Indels 7; Gaps 1;
QY 1 NRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKK 60
DB DRAASVKDVLNAGWNIKGVK-----NVDFVRYDTVEFLSADTKTTTVNVESKDNGKK 180
QY 61 TEVKIGAKTSVKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKGWPKMTT 120
DB 181 TEVKIGAKTSVKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKGWPKMTT 240
QY 121 NGQTGOADKFFETVTSCTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSG 180
DB 241 NGQTGOADKFFETVTSCTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSG 300
QY 181 WNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDTATSMTPQFSS 240
DB 301 WNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDTATSMTPQFSS 360
QY 241 VSLGAGADAPTLSDGDLNAGVSKKDNKPVRIITNVAPGVKEGDTNVAQLKGVAQNLLNR 300
DB 361 VSLGAGADAPTLSDGDLNAGVSKKDNKPVRIITNVAPGVKEGDTNVAQLKGVAQNLLNR 420
QY 301 IDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYATGYSSISDGGNWII 360
DB 421 IDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYATGYSSISDGGNWII 480
QY 361 KGTASGNSRGHFGASASVGQW 382
DB 481 KGTASGNSRGHFGASASVGQW 502

RESULT 11
AAV57044
ID AAV57044 standard; Protein: 594 AA.

AC AAV57044;

DT 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

DE Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.

XX Neisseria meningitidis.

OS WO9931132-A1.

PN 24-JUN-1999.

PD 14-DEC-1998; 98WO-AU01031.

PF 12-DEC-1997; 97GB-0026398.

PR (ISIS-) ISIS INNOVATION LTD.

PA (UQU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

DR N-PSDB; AAX85792.

XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections

PS Claim 1; Page 100-101; 132pp; English.

XX The present sequence represents a surface protein of Neisseria

CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

XX Sequence 594 AA;

Query Match 96.9%; Score 1886.5; DB 20; Length 594;
Best Local Similarity 97.6%; Pred. No. 1e-117;
Matches 373; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 2 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKK 61
DB 213 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKK 272

QY 62 EVKIGAKTSVKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKGWPKMTTAN 121
DB 273 EVKIGAKTSVKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKGWPKMTTAN 332

QY 122 GQTGOADKFFETVTSCTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 181
DB 333 GQTGOADKFFETVTSCTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 392

QY 182 NLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDTATSMTPQFSSV 241
DB 393 NLDKAVAGSSGKVISGNVSPSKGMDETVNIAGNNIETRNKKNIDTATSMTPQFSSV 452

QY 242 SLGAGADAPTLSDGDLNAGVSKKDNKPVRIITNVAPGVKEGDTNVAQLKGVAQNLLNR 300
DB 453 SLGAGADAPTLSDGDLNAGVSKKDNKPVRIITNVAPGVKEGDTNVAQLKGVAQNLLNR 512

QY 301 IDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYATGYSSISDGGNWII 360
DB 513 IDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYATGYSSISDGGNWII 572

QY 361 KGTASGNSRGHFGASASVGQW 382
DB 573 KGTASGNSRGHFGASASVGQW 594

RESULT 12

AAV57044
ID AAV57044 standard; Protein: 594 AA.

AC AAV57044;

DT 21-FEB-2000 (first entry)

DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.

KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.

OS Neisseria meningitidis.

XX Key Location/Qualifiers

FT Misc-difference 104 /note= "Encoded by AATC"

XX WO9958683-A2.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-EP03255.

XX 13-MAY-1998; 98GB-0010276.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Ruelle J;
XX WPI; 2000-053103/04.
DR N-PSDB; AA239864.
XX
XX
PT New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal -
XX
XX
PS Claim 4; Fig 2; 74pp; English.
XX
XX This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AA239864-239865) and
CC polypeptide sequences (AA239864-239865) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing a Neisseria
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX
SQ Sequence 594 AA;

Query Match 96.9%; Score 1886.5; DB 21; Length 594;
Best Local Similarity 97.6%; Pred. No. 1e-117; 5; Gaps 1;
Matches 373; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 2 RAASVKDLNAGNINIKGKPGTASDNVDFVRYDTPVEFLSADTKTTTVNVEKDKGKRT 61
DB 213 RAASVKDLNAGNINIKGKPGTASDNVDFVRYDTPVEFLSADTKTTTVNVEKDKGKRT 272
QY 62 EVKIGAKTSVIREKDKLVTGDKDENGSSSTDEGEGLVTAKEVIDAVNAGWRMKTITAN 121
DB 273 EVKIGAKTSVIREKDKLVTGDKDENGSSSTDEGEGLVTAKEVIDAVNAGWRMKTITAN 332
QY 122 GQTQADKFTVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVDALNVLNOLNSGW 181
DB 333 GQTQADKFTVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVDALNVLNOLNSGW 392
QY 182 NLDSKAVAGSSGKVISGNSVSPSKGMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSV 241
DB 393 NLDSKAVAGSSGKVISGNSVSPSKGMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSV 452
QY 242 SLGAGADAPTLSDVGD-ALNVGSKDKNKPVRTITNAPGVKEDVTNVAQLKGVAQNLNHR 300
DB 453 SLGAGADAPTLSDVGD-ALNVGSKDKNKPVRTITNAPGVKEDVTNVAQLKGVAQNLNHR 512
QY 301 IDNVDCNARAGTAQATATAGLQVAYLPKGSMAIGGTYRGEAGYAGYSSTSDGNNWII 360
DB 513 IDNVDCNARAGTAQATATAGLQVAYLPKGSMAIGGTYRGEAGYAGYSSTSDGNNWII 572
QY 361 KGATASGNSRGHFGASASVGYQW 382
DB 573 KGATASGNSRGHFGASASVGYQW 594

RESULT 13
AAU06174
ID AAU06174 standard; Protein; 594 AA.
XX
AC AAU06174;
XX
DT 24-OCT-2001 (first entry)

XX N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
XX Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX
XX Neisseria meningitidis strain EG327.
XX
XX Key Location/Qualifiers
XX Region 1..50 /label= C1
XX /note= "Conserved region 1"
XX Region 51..104 /label= V1
XX /note= "Variable region 1"
XX Region 105..116 /label= C2
XX /note= "Conserved region 2"
XX Region 117..126 /label= V2
XX /note= "Variable region 2"
XX Region 127..190 /label= C3
XX /note= "Conserved region 3"
XX Region 191..212 /label= V3
XX /note= "Variable region 3"
XX Region 213..231 /label= C4
XX /note= "Conserved region 4"
XX Region 232..238 /label= V4
XX /note= "Variable region 4"
XX Region 239..594 /label= C5
XX /note= "Conserved region 5"
XX
XX WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU000069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09164.
XX New NhhA surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen NhhA
XX (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen NhhA
XX from N. meningitidis strain EG327 is 1 of 10 NhhA polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX Sequence 594 AA;

Query Match 96.9%; Score 1886.5; DB 22; Length 594;
Best Local Similarity 97.6%; Pred. No. 1e-117;
Matches 373; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 2 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 61
DB 213 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKRT 272

QY 62 EVKIGAKTSVIKEDKGLVTKDGKGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTAN 121
DB 273 EVKIGAKTSVIKEDKGLVTKDGKGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTAN 332

QY 122 GQTQADKPFETVTSCTNVTFAASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 181
DB 333 GQTQADKPFETVTSCTNVTFAASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 392

QY 182 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIETIRNGKNIIDIAATSMTPQFSSV 241
DB 393 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIETIRNGKNIIDIAATSMTPQFSSV 452

QY 242 SLGAGADAPTLSDVGD-ALNVGSKDKNKPVRITNVAPGVKEGDTNVNVAOLKGVQAQNLNNH 300
DB 453 SLGAGADAPTLSDVGDALNVGSKDKNKPVRITNVAPGVKEGDTNVNVAOLKGVQAQNLNNH 512

QY 301 IDNVGDNARAGIAQAATATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 360
DB 513 IDNVGDNARAGIAQAATATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 572

QY 361 KGTSAGNSRGHFGASASVGYQW 382
DB 573 KGTSAGNSRGHFGASASVGYQW 594

RESULT 14

AAY23743
ID AAY23743 standard; Protein; 599 AA.

AC AAY23743;

DT 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

KW Surface protein; surface glycoprotein; infection; vaccine;
immunoreactive peptide.

OS Neisseria meningitidis.

PN W09931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

DR N-PSDB; AAX85795.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

PS Claim 1; Page 114-115; 132pp; English.

XX The present sequence represents a surface protein of Neisseria

CC meningitidis which is approximately 62 kDa. The N. meningitidis

CC surface glycoproteins, nucleic acids, the primers and optionally

CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

XX SQ Sequence 599 AA;

Query Match 96.6%; Score 1881.5; DB 20; Length 599;
Best Local Similarity 97.6%; Pred. No. 2.3e-117;
Matches 373; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 2 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 61
DB 218 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKRT 277

QY 62 EVKIGAKTSVIKEDKGLVTKDGKGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTAN 121
DB 278 EVKIGAKTSVIKEDKGLVTKDGKGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTAN 337

QY 122 GQTQADKPFETVTSCTNVTFAASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 181
DB 338 GQTQADKPFETVTSCTNVTFAASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 397

QY 182 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIETIRNGKNIIDIAATSMTPQFSSV 241
DB 398 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIETIRNGKNIIDIAATSMTPQFSSV 457

QY 242 SLGAGADAPTLSDVGD-DALNVGSKDKNKPVRITNVAPGVKEGDTNVNVAOLKGVQAQNLNNR 300
DB 458 SLGAGADAPTLSDVDDKALNVGSKDKNKPVRITNVAPGVKEGDTNVNVAOLKGVQAQNLNNR 517

QY 301 IDNVGDNARAGIAQAATATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 360
DB 518 IDNVGDNARAGIAQAATATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 577

QY 361 KGTSAGNSRGHFGASASVGYQW 382

DB 578 KGTSAGNSRGHFGASASVGYQW 599

RESULT 15

AAU06176
ID AAU06176 standard; Protein; 599 AA.

AC AAU06176;

XX 24-OCT-2001 (first entry)

XX N. meningitidis H38 surface antigen Nhha polypeptide sequence.

DE Surface antigen Nhha; meningococcal disease; meningitis vaccine.

KW Neisseria meningitidis strain H38.

XX Key Location/Qualifiers

FT Region 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT Region 51..105

FT /label= V1

FT /note= "Variable region 1"

FT Region 106..117

FT /label= C2

FT /note= "Conserved region 2"

FT Region 118..131

FT /label= V2

FT /note= "Variable region 2"

FT Region 132..195

FT /label= C3

FT /note= "Conserved region 3"

FT Region 196..217

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Scoring table: BLOSUM62
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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1941	99.7	591	3	US-09-377-155-11
2	1941	99.7	591	3	US-09-377-155-21
3	1941	99.7	591	4	US-09-669-974-11
4	1941	99.7	591	4	US-09-669-974-21
5	1937	99.5	592	3	US-09-377-155-2
6	1937	99.5	592	4	US-09-669-974-2
7	1886.5	96.9	594	3	US-09-377-155-9
8	1886.5	96.9	594	4	US-09-669-974-9
9	1881.5	96.6	599	3	US-09-377-155-15
10	1881.5	96.6	599	4	US-09-669-974-15
11	1874.5	96.3	594	3	US-09-377-155-7
12	1874.5	96.3	594	4	US-09-669-974-7
13	1861.5	95.6	592	3	US-09-377-155-17
14	1861.5	95.6	592	4	US-09-669-974-17
15	1861.5	95.6	598	3	US-09-377-155-5
16	1861.5	95.6	598	4	US-09-669-974-5
17	1861.5	95.6	598	3	US-09-377-155-13
18	1861.5	95.6	598	4	US-09-669-974-13
19	1817.5	93.3	589	3	US-09-377-155-19
20	1817.5	93.3	589	4	US-09-669-974-19
21	710	36.5	1098	1	US-08-409-995-2
22	710	36.5	1098	3	US-08-685-467-2
23	710	36.5	1098	3	US-09-377-155-32
24	710	36.5	1098	3	US-08-913-942-2
25	710	36.5	1098	4	US-09-669-974-32
26	710	36.5	1098	4	US-09-268-347-44
27	692	33.5	658	1	US-08-409-995-5

28	692	35.5	658	3	US-08-685-467-5	Sequence 5, Appli
29	692	35.5	658	3	US-08-913-942-5	Sequence 5, Appli
30	690.5	35.5	1094	4	US-09-268-347-32	Sequence 32, Appl
31	660	33.9	2353	3	US-09-377-155-33	Sequence 33, Appl
32	660	33.9	2353	3	US-08-913-942-4	Sequence 4, Appli
33	660	33.9	2353	4	US-09-669-974-33	Sequence 33, Appl
34	660	33.9	2411	4	US-09-268-347-36	Sequence 36, Appl
35	659.5	33.9	2354	4	US-09-268-347-47	Sequence 47, Appl
36	635	32.6	1912	1	US-08-409-995-4	Sequence 4, Appli
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40	612.5	31.5	607	3	US-08-913-942-6	Sequence 6, Appli
41	470.5	24.2	679	3	US-08-913-942-15	Sequence 15, Appl
42	470.5	24.2	679	4	US-09-268-347-26	Sequence 26, Appl
43	414.5	21.3	1002	4	US-09-268-347-24	Sequence 24, Appl
44	406	20.9	1004	4	US-09-268-347-30	Sequence 30, Appl
45	392	20.1	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1						
US-09-377-155-11						
; Sequence 11, Application US/09377155						
; Patent No. 6197312						
; GENERAL INFORMATION:						
; APPLICANT: PEAK, Ian Richard Anselm						
; APPLICANT: JENNINGS, Michael Paul						
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN						
; FILE REFERENCE: 065064/0128						
; CURRENT APPLICATION NUMBER: US/09/377,155						
; CURRENT FILING DATE: 1999-08-19						
; PRIOR APPLICATION NUMBER: PCT/AU98/01031						
; PRIOR FILING DATE: 1998-12-14						
; PRIOR APPLICATION NUMBER: GB 9726398.2						
; PRIOR FILING DATE: 1997-12-12						
; NUMBER OF SEQ ID NOS: 33						
; SOFTWARE: PatentIn ver. 2.0						
; SEQ ID NO 11						
; LENGTH: 591						
; TYPE: PRT						
; ORGANISM: Neisseria meningitidis						
US-09-377-155-11						
Query Match 99.7%; Score 1941; DB 3; Length 591;						
Best Local Similarity 100.0%; Pred. No. 1.8e-150;						
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	2	RAASVKDVLNAGWNKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKKT	61			
Db	211	RAASVKDVLNAGWNKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKKT	270			
Qy	62	EVKIGAKTSVKEKDKGLVTKDKGKNGSSTDEGEGLVTAKEVIDAVNKAGRMKTTTAN	121			
Db	271	EVKIGAKTSVKEKDKGLVTKDKGKNGSSTDEGEGLVTAKEVIDAVNKAGRMKTTTAN	330			
Qy	122	GQTGAQDFEFTVTSNTVTFASGKGTATTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGW	181			
Db	331	GQTGAQDFEFTVTSNTVTFASGKGTATTATVSKDDQGNITVMYDVNVGDALNVQNLQNSGW	390			
Qy	182	NLDSKAVAGSSGKVLGNNVSPSKGMDKDETVNINAGNNIEITRNGKNIDTATSMTPQFSSV	241			
Db	391	NLDSKAVAGSSGKVLGNNVSPSKGMDKDETVNINAGNNIEITRNGKNIDTATSMTPQFSSV	450			
Qy	242	SILGAGADAPTLSDGDLNVGSKDKNPKVRITNVPAGVKEGDVTNVAOLKGVQANLNRI	301			
Db	451	SILGAGADAPTLSDGDLNVGSKDKNPKVRITNVPAGVKEGDVTNVAOLKGVQANLNRI	510			
Qy	302	DNVGDNARAGIAQAATATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI	361			

; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 99.7%; Score 1941; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.8e-150;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKNGKKT 61
DB 211 RAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKNGKKT 270
QY 62 EVKIGAKTSVIREKDGKLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITAN 121
DB 271 EVKIGAKTSVIREKDGKLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITAN 330
QY 122 GOTGQADKFETVTSCTNVTTFASGKGTATVSKDDQGNITVMYDVNVGDLNVLNQLNSGW 181
DB 331 GOTGQADKFETVTSCTNVTTFASGKGTATVSKDDQGNITVMYDVNVGDLNVLNQLNSGW 390
QY 182 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNIDIATSMTPQFSSV 241
DB 391 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNIDIATSMTPQFSSV 450
QY 242 SLGAGADAPTLSDGDALNVGSKDNKPKVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 301
DB 451 SLGAGADAPTLSDGDALNVGSKDNKPKVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 510
QY 302 DNVDGNARAGIAQAIAATAGLVQAYLPKSKMMAIGGTYRGEAGYAIYSSISDGGNWIIL 361
DB 511 DNVDGNARAGIAQAIAATAGLVQAYLPKSKMMAIGGTYRGEAGYAIYSSISDGGNWIIL 570
QY 362 GTASGNSRHHFGASASVGYOW 382
DB 571 GTASGNSRHHFGASASVGYOW 591

RESULT 5

US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312

; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT

; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 99.5%; Score 1937; DB 3; Length 592;
Best Local Similarity 99.7%; Pred. No. 3.8e-150;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKNGKKT 61
DB 212 RAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKNGKKT 271
QY 62 EVKIGAKTSVIREKDGKLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITAN 121
DB 272 EVKIGAKTSVIREKDGKLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITAN 331
QY 122 GOTGQADKFETVTSCTNVTTFASGKGTATVSKDDQGNITVMYDVNVGDLNVLNQLNSGW 181

DB 332 GOTGQADKFETVTSCTNVTTFASGKGTATVSKDDQGNITVMYDVNVGDLNVLNQLNSGW 391
QY 182 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNIDIATSMTPQFSSV 241
DB 392 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNIDIATSMTPQFSSV 451
QY 242 SLGAGADAPTLSDGDALNVGSKDNKPKVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 301
DB 452 SLGAGADAPTLSDGDALNVGSKDNKPKVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 511
QY 302 DNVDGNARAGIAQAIAATAGLVQAYLPKSKMMAIGGTYRGEAGYAIYSSISDGGNWIIL 361
DB 512 DNVDGNARAGIAQAIAATAGLVQAYLPKSKMMAIGGTYRGEAGYAIYSSISDGGNWIIL 571
QY 362 GTASGNSRHHFGASASVGYOW 382
DB 572 GTASGNSRHHFGASASVGYOW 592

RESULT 6

US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 6333173

; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT

; ORGANISM: Neisseria meningitidis
US-09-669-974-2

Query Match 99.5%; Score 1937; DB 4; Length 592;
Best Local Similarity 99.7%; Pred. No. 3.8e-150;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKNGKKT 61
DB 212 RAASVKDVLNAGWNKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKNGKKT 271
QY 62 EVKIGAKTSVIREKDGKLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITAN 121
DB 272 EVKIGAKTSVIREKDGKLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITAN 331
QY 122 GOTGQADKFETVTSCTNVTTFASGKGTATVSKDDQGNITVMYDVNVGDLNVLNQLNSGW 181
DB 332 GOTGQADKFETVTSCTNVTTFASGKGTATVSKDDQGNITVMYDVNVGDLNVLNQLNSGW 391
QY 182 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNIDIATSMTPQFSSV 241
DB 392 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNNIEITRNGKNIDIATSMTPQFSSV 451
QY 242 SLGAGADAPTLSDGDALNVGSKDNKPKVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 301
DB 452 SLGAGADAPTLSDGDALNVGSKDNKPKVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRI 511
QY 302 DNVDGNARAGIAQAIAATAGLVQAYLPKSKMMAIGGTYRGEAGYAIYSSISDGGNWIIL 361
DB 512 DNVDGNARAGIAQAIAATAGLVQAYLPKSKMMAIGGTYRGEAGYAIYSSISDGGNWIIL 571

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Qy 362 GTASGNSRGHFGASASVGYQW 382
Db 572 GTASGNSRGHFGASASVGYQW 594

RESULT 7
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9
Query Match 96.9%; Score 1886.5; DB 3; Length 594;
Best local Similarity 97.6%; Pred. No. 5.1e-146;
Matches 373; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 2 RAASVKDVLNAGWNIKGKPGCTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKT 61
Db 213 RAASVKDVLNAGWNIKGKPGCTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRT 272

Qy 62 EVKIGAKTSVIKEKDGKLVTKDKGNGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
Db 273 EVKIGAKTSVIKEKDGKLVTKDKGNGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 332

Qy 122 GQTQADKFFETVSGTNVTFASGKGTATVSKDDQGNITVYDYNVGDALNVQLQNSGW 181
Db 333 GQTQADKFFETVSGTNVTFASGKGTATVSKDDQGNITVYDYNVGDALNVQLQNSGW 392

Qy 182 NLDSKAVAGSGGKVISGNVSPSKGMDETVNIAGNNIETTRGNKNDIATSMTPQFSSV 241
Db 393 NLDSKAVAGSGGKVISGNVSPSKGMDETVNIAGNNIETTRGNKNDIATSMTPQFSSV 452

Qy 242 SLGAGADAPTLSDVDG-ALNVGSKDKNPKVRITNVAPGVKEGDTNVVAQLKGVAQNLNHR 300
Db 453 SLGAGADAPTLSDVDGALNVGSKDKNPKVRITNVAPGVKEGDTNVVAQLKGVAQNLNHR 512

Qy 301 IDNVGNARAGIAQAATAGLVOAYLPKSKMMAIGGTYRGEAGYAGYSSISDGGNWII 360
Db 513 IDNVGNARAGIAQAATAGLVOAYLPKSKMMAIGGTYRGEAGYAGYSSISDGGNWII 572

Qy 361 KGTSAGNSRGHFGASASVGYQW 382
Db 573 KGTSAGNSRGHFGASASVGYQW 594

RESULT 9
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15
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Query Match 96.6%; Score 1881.5; DB 3; Length 599;
Best Local Similarity 97.6%; Pred. No. 1.3e-145;
Matches 373; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 2 RAASVDVNLNAGNWKVPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 61
|||||
DB 218 RAASVDVNLNAGNWKVPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 277
|||||
QY 62 EVKIGAKTSVIKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTITAN 121
|||||
DB 278 EVKIGAKTSVIKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTITAN 337
|||||
QY 122 GQTQADKFFVTSGTNVTFASGKGTATVSKDDQGNITVYDVNVDGALNVNQLNSGW 181
|||||
DB 338 GQTQADKFFVTSGTNVTFASGKGTATVSKDDQGNITVYDVNVDGALNVNQLNSGW 397
|||||
QY 182 NLDSKAVAGSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDDIATSMTPQFSSV 241
|||||
DB 398 NLDSKAVAGSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDDIATSMTPQFSSV 457
|||||
QY 242 SLGAGADAPTLSDVDG-DALNVGSKKDKNPKVRIITNVAPGVKEGDTNVNVAQLKGVAQNLNRR 300
|||||
DB 458 SLGAGADAPTLSDVDGKALNVGSKDANKPVRIITNVAPGVKEGDTNVNVAQLKGVAQNLNRR 517
|||||
QY 301 IDNVGDNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 360
|||||
DB 518 IDNVGDNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 577
|||||
QY 361 KGTASGNSRHFSGASASVGYQW 382
|||||
DB 578 KGTASGNSRHFSGASASVGYQW 599
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RESULT 10
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match 96.6%; Score 1881.5; DB 4; Length 599;
Best Local Similarity 97.6%; Pred. No. 1.3e-145;
Matches 373; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 2 RAASVDVNLNAGNWKVPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 61
|||||
DB 218 RAASVDVNLNAGNWKVPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 277
|||||
QY 62 EVKIGAKTSVIKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTITAN 121
|||||
DB 278 EVKIGAKTSVIKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTITAN 337
|||||
QY 122 GQTQADKFFVTSGTNVTFASGKGTATVSKDDQGNITVYDVNVDGALNVNQLNSGW 181
|||||

DB 338 GQTQADKFFVTSGTNVTFASGKGTATVSKDDQGNITVYDVNVDGALNVNQLNSGW 397
QY 182 NLDSKAVAGSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDDIATSMTPQFSSV 241
|||||
DB 398 NLDSKAVAGSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDDIATSMTPQFSSV 457
|||||
QY 242 SLGAGADAPTLSDVDG-DALNVGSKKDKNPKVRIITNVAPGVKEGDTNVNVAQLKGVAQNLNRR 300
|||||
DB 458 SLGAGADAPTLSDVDGKALNVGSKDANKPVRIITNVAPGVKEGDTNVNVAQLKGVAQNLNRR 517
|||||
QY 301 IDNVGDNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 360
|||||
DB 518 IDNVGDNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 577
|||||
QY 361 KGTASGNSRHFSGASASVGYQW 382
|||||
DB 578 KGTASGNSRHFSGASASVGYQW 599
|||||

RESULT 11
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match 96.3%; Score 1874.5; DB 3; Length 594;
Best Local Similarity 97.4%; Pred. No. 4.9e-145;
Matches 372; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 2 RAASVDVNLNAGNWKVPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 61
|||||
DB 213 RAASVDVNLNAGNWKVPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 272
|||||
QY 62 EVKIGAKTSVIKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTITAN 121
|||||
DB 273 EVKIGAKTSVIKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTITAN 332
|||||
QY 122 GQTQADKFFVTSGTNVTFASGKGTATVSKDDQGNITVYDVNVDGALNVNQLNSGW 181
|||||
DB 333 GQTQADKFFVTSGTNVTFASGKGTATVSKDDQGNITVYDVNVDGALNVNQLNSGW 392
|||||
QY 182 NLDSKAVAGSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDDIATSMTPQFSSV 241
|||||
DB 393 NLDSKAVAGSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDDIATSMAPQFSSV 452
|||||
QY 242 SLGAGADAPTLSDVDG-DALNVGSKKDKNPKVRIITNVAPGVKEGDTNVNVAQLKGVAQNLNRR 300
|||||
DB 453 SLGAGADAPTLSDVDGKALNVGSKDANKPVRIITNVAPGVKEGDTNVNVAQLKGVAQNLNRR 512
|||||
QY 301 IDNVGDNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 360
|||||
DB 513 IDNVGDNARAGIAQAIAATAGLVQAYLPKGSMAIGGTYRGEAGYAIYSSISDGGNWII 572
|||||
QY 361 KGTASGNSRHFSGASASVGYQW 382
|||||

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Db      573 KGTASGNSRGHFGASASVGYQW 594

RESULT 12
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match      96.3%; Score 1874.5; DB 4; Length 594;
Best Local Similarity 97.4%; Pred. No. 4.9e-145;
Matches 372; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy      2 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 61
Db      213 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 272
Qy      62 EVKIGAKTSVIKEDGKLVTKGKDGKENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
Db      273 EVKIGAKTSVIKEDGKLVTKGKDGKENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTITAN 332
Qy      122 GOTQADKFEFVTSCTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 181
Db      333 GOTQADKFEFVTSCTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 392
Qy      182 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKKNIDIAATSMTPQFSSV 241
Db      393 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKKNIDIAATSMTPQFSSV 452
Qy      242 SLGAGADAPTLSDVGD-ALNVGSKDNKPVKITNVAPGVKEGDTNVNAQLKGVAQNLLNR 300
Db      453 SLGAGADAPTLSDVDEGALNVGSKDNTNKPVRITNVAPGVKEGDTNVNAQLKGVAQNLLNR 512
Qy      301 IDNVGDNARAGIAQAIATAGLVQAYLPKSKMMAIGGGTYRGEAGYATGYSISDGGNWII 360
Db      513 IDNVGDNARAGIAQAIATAGLVQAYLPKSKMMAIGGGTYRGEAGYATGYSISDGGNWII 572
Qy      361 KGTASGNSRGHFGASASVGYQW 382
Db      573 KGTASGNSRGHFGASASVGYQW 594

RESULT 13
US-09-377-155-17
; Sequence 17, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
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; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17

Query Match      95.6%; Score 1861.5; DB 3; Length 592;
Best Local Similarity 96.9%; Pred. No. 5.6e-144;
Matches 370; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

Qy      2 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 61
Db      211 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 270
Qy      62 EVKIGAKTSVIKEDGKLVTKGKDGKENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
Db      271 EVKIGAKTSVIKEDGKLVTKGKDGKENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTITAN 330
Qy      122 GOTQADKFEFVTSCTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 181
Db      331 GOTQADKFEFVTSCTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 390
Qy      182 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKKNIDIAATSMTPQFSSV 241
Db      391 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNKKNIDIAATSMTPQFSSV 450
Qy      242 SLGAGADAPTLSDVGD-ALNVGSKDNKPVKITNVAPGVKEGDTNVNAQLKGVAQNLLNR 300
Db      451 SLGAGADAPTLSDVDEGALNVGSKDANKPVKITNVAPGVKEGDTNVNAQLKGVAQNLLNR 510
Qy      301 IDNVGDNARAGIAQAIATAGLVQAYLPKSKMMAIGGGTYRGEAGYATGYSISDGGNWII 360
Db      511 IDNVGDNARAGIAQAIATAGLVQAYLPKSKMMAIGGGTYRGEAGYATGYSISDGGNWII 570
Qy      361 KGTASGNSRGHFGASASVGYQW 382
Db      571 KGTASGNSRGHFGASASVGYQW 592

RESULT 14
US-09-669-974-17
; Sequence 17, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-17

Query Match      95.6%; Score 1861.5; DB 4; Length 592;
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Best Local Similarity 96.9%; Pred. No. 5.6e-144; Matches 370; Conservative 2; Mismatches 9; Indels 1; Gaps 1;	
QY	2 RAASKVDVLNAGNINIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDKGKKT 61
Db	211 RAASKVDVLNAGNINIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDKGKKT 270
QY	62 EVKIGAKTSVIEKDGKLVGTGDKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
Db	271 EVKIGAKTSVIEKDGKLVGTGDKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 330
QY	122 GOTGADKFETVTSCTNTVFASGKGTATVSKDDQGNITVYDVNVDALNVLQNSGW 181
Db	331 GOTGADKFETVTSCTNTVFASGKGTATVSKDDQGNITVYDVNVDALNVLQNSGW 390
QY	182 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNGKNIDIATSWTPOFSSV 241
Db	391 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNGKNIDIATSWTPOFSSV 450
QY	242 SLGAGADAPTLSDVDG-ALNVGSKDKNKPVRITNVPAGVKEGDTVNNVAQLKGVAQNLNRR 300
Db	451 SLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVPAGVKEGDTVNNVAQLKGVAQNLNRR 510
QY	301 IDNVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWII 360
Db	511 IDNVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISAGGNWII 570
QY	361 KGTASGNSRGHFGASASVGYQW 382
Db	571 KGTASGNSRGHFGASASVGYQW 592

RESULT 15

US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis

US-09-377-155-5

Query Match 95.6%; Score 1861.5; DB 3; Length 598;	
Best Local Similarity 96.3%; Pred. No. 5.7e-144;	
Matches 368; Conservative 3; Mismatches 10; Indels 1; Gaps 1;	
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QY	62 EVKIGAKTSVIEKDGKLVGTGDKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
Db	277 EVKIGAKTSVIEKDGKLVGTGDKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 336
QY	122 GOTGADKFETVTSCTNTVFASGKGTATVSKDDQGNITVYDVNVDALNVLQNSGW 181
Db	337 GOTGADKFETVTSCTNTVFASGKGTATVSKDDQGNITVYDVNVDALNVLQNSGW 396
QY	182 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNGKNIDIATSWTPOFSSV 241

Db	397 NLDKAVAGSSGKVISGNVSPSKGMDETVNNAGNIEITRNGKNIDIATSWTPOFSSV 456
QY	242 SLGAGADAPTLSDVDG-ALNVGSKDKNKPVRITNVPAGVKEGDTVNNVAQLKGVAQNLNRR 300
Db	457 SLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVPAGVKEGDTVNNVAQLKGVAQNLNRR 516
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Db	517 IDNVGNARAGIAQAIAATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTCNWVI 576
QY	361 KGTASGNSRGHFGASASVGYQW 382
Db	577 KGTASGNSRGHFGTSASVGYQW 598

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Job time : 11.2154 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2003, 09:31:05 : Search time 19.136 Seconds
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3158.312 Million cell updates/sec

Title: US-09-771-382-38
Perfect score: 1947
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1947	100.0	382	10	US-09-771-382-38	Sequence 38, Appl
2	1947	100.0	433	10	US-09-771-382-26	Sequence 26, Appl
3	1941	99.7	461	10	US-09-771-382-35	Sequence 35, Appl
4	1941	99.7	512	10	US-09-771-382-23	Sequence 23, Appl
5	1941	99.7	540	10	US-09-771-382-33	Sequence 33, Appl
6	1941	99.7	591	10	US-09-797-862-11	Sequence 11, Appl
7	1941	99.7	591	10	US-09-797-862-21	Sequence 21, Appl
8	1941	99.7	591	10	US-09-771-382-1	Sequence 1, Appl
9	1941	99.5	592	10	US-09-771-382-5	Sequence 5, Appl
10	1937	97.1	592	10	US-09-797-862-2	Sequence 2, Appl
11	1891.5	97.1	502	10	US-09-771-382-27	Sequence 27, Appl
12	1886.5	96.9	594	10	US-09-797-862-9	Sequence 9, Appl
13	1886.5	96.9	594	10	US-09-771-382-4	Sequence 4, Appl
14	1881.5	96.6	599	10	US-09-797-862-15	Sequence 15, Appl
15	1881.5	96.6	599	10	US-09-771-382-6	Sequence 6, Appl

16	1874.5	96.3	594	10	US-09-797-862-7	Sequence 7, Appl
17	1874.5	96.3	594	10	US-09-771-382-9	Sequence 9, Appl
18	1861.5	95.6	462	10	US-09-771-382-36	Sequence 36, Appl
19	1861.5	95.6	513	10	US-09-771-382-24	Sequence 24, Appl
20	1861.5	95.6	541	10	US-09-771-382-34	Sequence 34, Appl
21	1861.5	95.6	592	10	US-09-797-862-17	Sequence 17, Appl
22	1861.5	95.6	592	10	US-09-771-382-2	Sequence 2, Appl
23	1861.5	95.6	598	10	US-09-797-862-5	Sequence 5, Appl
24	1861.5	95.6	598	10	US-09-797-862-13	Sequence 13, Appl
25	1861.5	95.6	598	10	US-09-771-382-7	Sequence 7, Appl
26	1861.5	95.6	598	10	US-09-771-382-8	Sequence 8, Appl
27	1854.5	95.2	592	10	US-09-771-382-10	Sequence 10, Appl
28	1817.5	93.3	589	10	US-09-797-862-19	Sequence 19, Appl
29	1817.5	93.3	589	10	US-09-771-382-3	Sequence 3, Appl
30	1810	93.0	407	10	US-09-771-382-25	Sequence 25, Appl
31	1808	92.9	356	10	US-09-771-382-37	Sequence 37, Appl
32	1736.5	89.2	604	10	US-09-771-382-11	Sequence 11, Appl
33	710	36.5	1098	10	US-09-797-862-32	Sequence 32, Appl
34	660	33.9	2353	10	US-09-797-862-33	Sequence 33, Appl
35	607.5	31.2	201	10	US-09-771-382-39	Sequence 39, Appl
36	318.5	16.4	1778	12	US-10-238-075-749	Sequence 749, App
37	298	15.3	2122	10	US-09-813-214A-9	Sequence 9, Appl
38	297	15.3	1833	12	US-10-175-275-4	Sequence 4, Appl
39	297	15.3	1833	12	US-10-175-282-4	Sequence 4, Appl
40	297	15.3	1992	12	US-10-175-275-3	Sequence 3, Appl
41	297	15.3	1992	12	US-10-175-282-3	Sequence 3, Appl
42	234.5	12.0	2039	15	US-10-192-584-7	Sequence 7, Appl
43	227.5	11.7	2042	15	US-10-192-584-6	Sequence 6, Appl
44	186.5	9.6	915	12	US-10-193-764-35	Sequence 35, Appl
45	186.5	9.6	1222	12	US-10-193-764-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-771-382-38
Sequence 38, Application US/09771382
Patent No. US20020160016A1
GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-24U1
CURRENT APPLICATION NUMBER: US/09/771.382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 38
LENGTH: 382
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-771-382-38

Query Match	100.0%	Score 1947	DB 10	Length 382
Best Local Similarity	100.0%	Pred. No. 1.1e-149		
Matches 382	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	1	NRAASVQDVLNAGWNKGVKPGTTASDNVFEVRYDTVEFLSADTKTTTVNVESSKDKGK 60		
DB	1	NRAASVQDVLNAGWNKGVKPGTTASDNVFEVRYDTVEFLSADTKTTTVNVESSKDKGK 60		
OY	61	TEVKIGAKTSVIREKDKGLVTKDKGENSSJDEBGLVTAKEVIDAVNRKAGRMKTTTA 120		
DB	61	TEVKIGAKTSVIREKDKGLVTKDKGENSSJDEBGLVTAKEVIDAVNRKAGRMKTTTA 120		
OY	121	NGGTGADKREYTSNGTVTFASGKGTATVNSDDOCNTIVMYDVNNGDALNNQNLNSG 180		
DB	121	NGGTGADKREYTSNGTVTFASGKGTATVNSDDOCNTIVMYDVNNGDALNNQNLNSG 180		
OY	181	WNDSKAVAGSSGKVISGNVSPSKGMDFTVINAGNNIEITRGNKIDIAISWTPQFSS 240		

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Db 181 WNLDSKAVAGSSGKVTSGNSVPSKGMDETVNINAGNNIETTRNKNIDIAISMTPORSS 240
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; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-2401
; CURRENT APPLICATION NUMBER: US/09/771.382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
us-09-771-382-26

RESULT 2
us-09-771-382-26
; Sequence 26, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-2401
; CURRENT APPLICATION NUMBER: US/09/771.382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
us-09-771-382-26

Query Match 100.0%; Score 1947; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.3e-149;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|
Db 52 NRAASVKDVLNAGNNIKGKPGTTASDNVDFVRYDYVEFLSADTKTTVNVESKDNKK 111
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|
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OY 61 TEVIGAKTSYIKERDGLVTGKDKGENGSTDEEGGLVTAKEVIDAVNKKAGMRKTTTA 120
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|
|
Db 112 TEVIGAKTSYIKERDGLVTGKDKGENSGSTDEEGGLVTAKEVIDAVNKKAGMRKTTTA 171
|
|
|
OY 121 NGGTGQADKFEVTSGTNVTFASGKGTATVSKDDGNTIYWDVNVGDALNVNOLNSG 180
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|
|
Db 172 NGGTGQADKFEVTSGTNVTFASGKGTATVSKDDGNTIYWDVNVGDALNVNOLNSG 231
|
|
|
OY 181 WNLDSKAVAGSSGKVTSGNSVPSKGMDETVNINAGNNIETTRNKNIDIAISMTPORSS 240
|
|
|
Db 232 WNLDSKAVAGSSGKVTSGNSVPSKGMDETVNINAGNNIETTRNKNIDIAISMTPORSS 291
|
|
|
OY 241 VSLGAGADAPTLSDVDGALNVGSKKDNKPVRIITNVAPEVKEGDDYTNVAQLKGVAQNLNRR 300
|
|
|
Db 292 VSLGAGADAPTLSDVDGALNVGSKKDNKPVRIITNVAPEVKEGDDYTNVAQLKGVAQNLNRR 351
|
|
|
OY 301 IDNVGNARAGIAOAIATAGLVQAYLPKSKMAIGGGTYRGEAGYAIGYSSISDGNMII 360
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|
|
Db 352 IDNVGNARAGIAOAIATAGLVQAYLPKSKMAIGGGTYRGEAGYAIGYSSISDGNMII 411
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OY 361 KGASGNSRGHFGASASVGYQW 382
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Db 412 KGASGNSRGHFGASASVGYQW 433
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RESULT 3
us-09-771-382-35
; Sequence 35, Application US/09771382
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; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-2401
; CURRENT APPLICATION NUMBER: US/09/771.382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
us-09-771-382-35

Query Match 99.7%; Score 1941; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|
|
Db 81 RAASVKDVLNAGNNIKGKPGTTASDNVDFVRYDYVEFLSADTKTTVNVESKDNKK 140
|
|
|
OY 62 EVKIGAKTSYIKERDGLVTGKDKGENSGSTDEEGGLVTAKEVIDAVNKKAGMRKTTTA 121
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|
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Db 141 EVKIGAKTSYIKERDGLVTGKDKGENSGSTDEEGGLVTAKEVIDAVNKKAGMRKTTTA 200
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OY 122 GGTGQADKFEVTSGTNVTFASGKGTATVSKDDGNTIYWDVNVGDALNVNOLNSG 181
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Db 201 GGTGQADKFEVTSGTNVTFASGKGTATVSKDDGNTIYWDVNVGDALNVNOLNSG 260
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|
|
OY 182 NLDKAVAGSSGKVTSGNSVPSKGMDETVNINAGNNIETTRNKNIDIAISMTPORSS 241
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Db 261 NLDKAVAGSSGKVTSGNSVPSKGMDETVNINAGNNIETTRNKNIDIAISMTPORSS 320
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|
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OY 242 SLGAGADAPTLSDVDGALNVGSKKDNKPVRIITNVAPEVKEGDDYTNVAQLKGVAQNLNRR 301
|
|
|
Db 321 SLGAGADAPTLSDVDGALNVGSKKDNKPVRIITNVAPEVKEGDDYTNVAQLKGVAQNLNRR 380
|
|
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OY 302 DNVGNARAGIAOAIATAGLVQAYLPKSKMAIGGGTYRGEAGYAIGYSSISDGNMII 361
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|
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Db 381 DNVGNARAGIAOAIATAGLVQAYLPKSKMAIGGGTYRGEAGYAIGYSSISDGNMII 440
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|
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OY 362 GTASGNSRGHFGASASVGYQW 382
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Db 441 GTASGNSRGHFGASASVGYQW 461
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RESULT 4
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; Sequence 23, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-2401
; CURRENT APPLICATION NUMBER: US/09/771.382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
us-09-771-382-23

Query Match 99.7%; Score 1941; DB 10; Length 512;
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Best Local Similarity 100.0%; Pred. No. 5e-149;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 192 EVKIGAKTSYIKKEDGLVTKGDKGENGSSTDEEGELVTAKEVIDAVNKGWRKMTTAN 251
OY 122 GGTGQADKFEFTVSGTNVTFASGKGTATVSKDDQGNITVWYDVNVDALNVNOLNSGW 181
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OY 242 SLGAGADAPLTVSDGDLNVGSKKDNKPVRTTNVAPGVKBDVTNNVQKGVAAQNLNRI 301
Db 372 SLGAGADAPLTVSDGDLNVGSKKDNKPVRTTNVAPGVKBDVTNNVQKGVAAQNLNRI 431
OY 302 DNVGNNRAGIAQAIAATAGLVQAYLPKSKMAIGGTYRGEAGTAIGYSSISDGNMIIK 361
Db 432 DNVGNNRAGIAQAIAATAGLVQAYLPKSKMAIGGTYRGEAGTAIGYSSISDGNMIIK 491
OY 362 GTASGNSRGHFGASASVGYOM 382
Db 492 GTASGNSRGHFGASASVGYOM 512
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RESULT 5

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US-09-771-382-33
; Sequence 33, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; APPLICANT: Jennings, Michael
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-24U1
; CURRENT APPLICATION NUMBER: US/09/771,382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-771-382-33
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Query Match 99.7%; Score 1941; DB 10; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.4e-149;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2 RAASVVDVNLNAGNNIKGKPGTTASDVNDVFRITDYVEFLSADTKTTTVNESKDNGKKT 61
Db 160 RAASVVDVNLNAGNNIKGKPGTTASDVNDVFRITDYVEFLSADTKTTTVNESKDNGKKT 219
OY 62 EVKIGAKTSYIKKEDGLVTKGDKGENGSSTDEEGELVTAKEVIDAVNKGWRKMTTAN 121
Db 220 EVKIGAKTSYIKKEDGLVTKGDKGENGSSTDEEGELVTAKEVIDAVNKGWRKMTTAN 279
OY 122 GGTGQADKFEFTVSGTNVTFASGKGTATVSKDDQGNITVWYDVNVDALNVNOLNSGW 181
Db 280 GGTGQADKFEFTVSGTNVTFASGKGTATVSKDDQGNITVWYDVNVDALNVNOLNSGW 339
OY 182 NLDSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIETTRNGKNIDIAATSMTPQSSV 241
Db 340 NLDSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIETTRNGKNIDIAATSMTPQSSV 399
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OY 242 SLGAGADAPLTVSDGDLNVGSKKDNKPVRTTNVAPGVKBDVTNNVQKGVAAQNLNRI 301
Db 400 SLGAGADAPLTVSDGDLNVGSKKDNKPVRTTNVAPGVKBDVTNNVQKGVAAQNLNRI 459

OY 302 DNVGNNRAGIAQAIAATAGLVQAYLPKSKMAIGGTYRGEAGTAIGYSSISDGNMIIK 361
Db 460 DNVGNNRAGIAQAIAATAGLVQAYLPKSKMAIGGTYRGEAGTAIGYSSISDGNMIIK 519

OY 362 GTASGNSRGHFGASASVGYOM 382
Db 520 GTASGNSRGHFGASASVGYOM 540

RESULT 6

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US-09-797-862-11
; Sequence 11, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-797-862-11
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Query Match 99.7%; Score 1941; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.1e-149;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 211 RAASVVDVNLNAGNNIKGKPGTTASDVNDVFRITDYVEFLSADTKTTTVNESKDNGKKT 270
OY 62 EVKIGAKTSYIKKEDGLVTKGDKGENGSSTDEEGELVTAKEVIDAVNKGWRKMTTAN 121
Db 271 EVKIGAKTSYIKKEDGLVTKGDKGENGSSTDEEGELVTAKEVIDAVNKGWRKMTTAN 330
OY 122 GGTGQADKFEFTVSGTNVTFASGKGTATVSKDDQGNITVWYDVNVDALNVNOLNSGW 181
Db 331 GGTGQADKFEFTVSGTNVTFASGKGTATVSKDDQGNITVWYDVNVDALNVNOLNSGW 390
OY 182 NLDSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIETTRNGKNIDIAATSMTPQSSV 241
Db 391 NLDSKAVAGSSGKVIISGNVSPSKGKMDETVINAGNNIETTRNGKNIDIAATSMTPQSSV 450
OY 242 SLGAGADAPLTVSDGDLNVGSKKDNKPVRTTNVAPGVKBDVTNNVQKGVAAQNLNRI 301
Db 451 SLGAGADAPLTVSDGDLNVGSKKDNKPVRTTNVAPGVKBDVTNNVQKGVAAQNLNRI 510
OY 302 DNVGNNRAGIAQAIAATAGLVQAYLPKSKMAIGGTYRGEAGTAIGYSSISDGNMIIK 361
Db 511 DNVGNNRAGIAQAIAATAGLVQAYLPKSKMAIGGTYRGEAGTAIGYSSISDGNMIIK 570
OY 362 GTASGNSRGHFGASASVGYOM 382
Db 571 GTASGNSRGHFGASASVGYOM 591
```

RESULT 7

US-09-797-862-21
; Sequence 21, Application US/09797862

Patent No. US20020102276A1
GENERAL INFORMATION:
APPLICANT: PEAK, IAN RICHARD ANSELM
APPLICANT: JENNINGS, MICHAEL PAUL
APPLICANT: MOXON, E. RICHARD
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0134
CURRENT APPLICATION NUMBER: US/09/797,862
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 591
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-797-862-21

Query Match 99.7%; Score 1941; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6,1e-149;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGWNKIGVKGPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESSKDKNGKKT 61
DB 211 RAASVKDVLNAGWNKIGVKGPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESSKDKNGKKT 270
QY 62 EVKIGAKTSVIREKKGKLVTKGDKGENSSSTDEGGGLVTAKEVIDAVNKAAGRMKTTTAN 121
DB 271 EVKIGAKTSVIREKKGKLVTKGDKGENSSSTDEGGGLVTAKEVIDAVNKAAGRMKTTTAN 330
QY 122 GOTGADKFEFVTSNTNTPFASGKGTTFATVSKDDGNTTVMVDVNGDALVNOQNSGW 181
DB 331 GOTGADKFEFVTSNTNTPFASGKGTTFATVSKDDGNTTVMVDVNGDALVNOQNSGW 390
QY 182 NIDSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEITRNGKNIDIATSMTPQFSSV 241
DB 391 NIDSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEITRNGKNIDIATSMTPQFSSV 450
QY 242 SLGAGADAPTLSDVDGDLNVGSKDKNKPVRITNVAPEGEGVTVNAQLKGYAQMNLNRI 301
DB 451 SLGAGADAPTLSDVDGDLNVGSKDKNKPVRITNVAPEGEGVTVNAQLKGYAQMNLNRI 510
QY 302 DNVDGNARAGIAQAATATAGLVQAYLPKGSMAIIGGTYRGEAGYALGYSSISDGGNWIIR 361
DB 511 DNVDGNARAGIAQAATATAGLVQAYLPKGSMAIIGGTYRGEAGYALGYSSISDGGNWIIR 570
QY 362 GTASGNSRGRHFGASASVGYQW 382
DB 571 GTASGNSRGRHFGASASVGYQW 591

RESULT 8
US-09-771-382-1
Sequence 1, Application US/09771382
Patent No. US20020160016A1
GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-24U1
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 591
TYPE: PRT
ORGANISM: Neisseria meningitidis

US-09-771-382-1
Query Match 99.7%; Score 1941; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6,1e-149;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGWNKIGVKGPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESSKDKNGKKT 61
DB 211 RAASVKDVLNAGWNKIGVKGPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESSKDKNGKKT 270
QY 62 EVKIGAKTSVIREKKGKLVTKGDKGENSSSTDEGGGLVTAKEVIDAVNKAAGRMKTTTAN 121
DB 271 EVKIGAKTSVIREKKGKLVTKGDKGENSSSTDEGGGLVTAKEVIDAVNKAAGRMKTTTAN 330
QY 122 GOTGADKFEFVTSNTNTPFASGKGTTFATVSKDDGNTTVMVDVNGDALVNOQNSGW 181
DB 331 GOTGADKFEFVTSNTNTPFASGKGTTFATVSKDDGNTTVMVDVNGDALVNOQNSGW 390
QY 182 NIDSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEITRNGKNIDIATSMTPQFSSV 241
DB 391 NIDSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEITRNGKNIDIATSMTPQFSSV 450
QY 242 SLGAGADAPTLSDVDGDLNVGSKDKNKPVRITNVAPEGEGVTVNAQLKGYAQMNLNRI 301
DB 451 SLGAGADAPTLSDVDGDLNVGSKDKNKPVRITNVAPEGEGVTVNAQLKGYAQMNLNRI 510
QY 302 DNVDGNARAGIAQAATATAGLVQAYLPKGSMAIIGGTYRGEAGYALGYSSISDGGNWIIR 361
DB 511 DNVDGNARAGIAQAATATAGLVQAYLPKGSMAIIGGTYRGEAGYALGYSSISDGGNWIIR 570
QY 362 GTASGNSRGRHFGASASVGYQW 382
DB 571 GTASGNSRGRHFGASASVGYQW 591

RESULT 9
US-09-771-382-5
Sequence 5, Application US/09771382
Patent No. US20020160016A1
GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-24U1
CURRENT APPLICATION NUMBER: US/09/771,382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 591
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-771-382-5

Query Match 99.7%; Score 1941; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 6,1e-149;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGWNKIGVKGPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESSKDKNGKKT 61
DB 211 RAASVKDVLNAGWNKIGVKGPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESSKDKNGKKT 270
QY 62 EVKIGAKTSVIREKKGKLVTKGDKGENSSSTDEGGGLVTAKEVIDAVNKAAGRMKTTTAN 121
DB 271 EVKIGAKTSVIREKKGKLVTKGDKGENSSSTDEGGGLVTAKEVIDAVNKAAGRMKTTTAN 330
QY 122 GOTGADKFEFVTSNTNTPFASGKGTTFATVSKDDGNTTVMVDVNGDALVNOQNSGW 181
DB 331 GOTGADKFEFVTSNTNTPFASGKGTTFATVSKDDGNTTVMVDVNGDALVNOQNSGW 390
QY 182 NIDSKAVAGSSGKVIISGNVSPSKGMDFTVINAGNNIEITRNGKNIDIATSMTPQFSSV 241

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|||||
Db 391 NIDSKAVAGSSGVISGNVSPSKGKMDVFNINAGNNIETTRNGKNIDIAITSMTPQSSV 450
QY 242 SLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVAAGVEGDTVNAOLKGYAQNINNR 301
Db 451 SLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVAAGVEGDTVNAOLKGYAQNINNR 510
QY 302 DNVGNAARAGIAQAIATAGLVQAYLPKGSMAIIGGTYRGEAGYAIYSSISDGNWIIK 361
Db 511 DNVGNAARAGIAQAIATAGLVQAYLPKGSMAIIGGTYRGEAGYAIYSSISDGNWIIK 570
QY 362 GTASGNSRGHFGASASVGYOW 382
Db 571 GTASGNSRGHFGASASVGYOW 591
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RESULT 10
US-09-797-862-2

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; Sequence 2, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-797-862-2
```

Query Match 99.5%; Score 1937; DB 10; Length 592;
Best Local Similarity 99.7%; Pred. No. 1.3e-148;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 RAASVADVNLNAGNINIGVKGPGTTASDNVDFVRYDVEFLSADTKTTTVNVESSKDNK 61
Db 212 RAASVADVNLNAGNINIGVKGPGTTASDNVDFVRYDVEFLSADTKTTTVNVESSKDNK 271
QY 62 EVKIGAKTSVIREKDKGLVTGKDKGENSGSTDEGEGLYTAKVEYIDAVNKAQRMKTTTAN 121
Db 272 EVKIGAKTSVIREKDKGLVTGKDKGENSGSTDEGEGLYTAKVEYIDAVNKAQRMKTTTAN 331
QY 122 GGTGQADKFEYVTSNTVFASGKGTATVYSKDDGNTVYMYVNVGDALNVQOLONGSW 181
Db 332 GGTGQADKFEYVTSNTVFASGKGTATVYSKDDGNTVYMYVNVGDALNVQOLONGSW 391
QY 182 NIDSKAVAGSSGVISGNVSPSKGKMDVFNINAGNNIETTRNGKNIDIAITSMTPQSSV 241
Db 392 NIDSKAVAGSSGVISGNVSPSKGKMDVFNINAGNNIETTRNGKNIDIAITSMTPQSSV 451
QY 242 SLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVAAGVEGDTVNAOLKGYAQNINNR 301
Db 452 SLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVAAGVEGDTVNAOLKGYAQNINNR 511
QY 302 DNVGNAARAGIAQAIATAGLVQAYLPKGSMAIIGGTYRGEAGYAIYSSISDGNWIIK 361
Db 512 DNVGNAARAGIAQAIATAGLVQAYLPKGSMAIIGGTYRGEAGYAIYSSISDGNWIIK 571
QY 362 GTASGNSRGHFGASASVGYOW 382
Db 572 GTASGNSRGHFGASASVGYOW 592
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RESULT 11
US-09-771-382-27
; Sequence 27, Application US/09771382
; Patent No. US20020160016A1
; GENERAL INFORMATION:
; APPLICANT: Peak, Ian
; APPLICANT: Jennings, Michael
; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
; FILE REFERENCE: 8795-24U1
; CURRENT APPLICATION NUMBER: US/09/771,382
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/177,917
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-771-382-27
```

Query Match 97.1%; Score 1891.5; DB 10; Length 502;
Best Local Similarity 97.9%; Pred. No. 5e-145; 0; Indels 7; Gaps 1;
Matches 374; Conservative 1; Mismatches 0;

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QY 1 NRAASVADVNLNAGNINIGVKGPGTTASDNVDFVRYDVEFLSADTKTTTVNVESSKDNK 60
Db 128 NRAASVADVNLNAGNINIGVKGPGTTASDNVDFVRYDVEFLSADTKTTTVNVESSKDNK 180
QY 61 TEVKIGAKTSVIREKDKGLVTGKDKGENSGSTDEGEGLYTAKVEYIDAVNKAQRMKTTTAN 120
Db 181 TEVKIGAKTSVIREKDKGLVTGKDKGENSGSTDEGEGLYTAKVEYIDAVNKAQRMKTTTAN 240
QY 121 NGGTGQADKFEYVTSNTVFASGKGTATVYSKDDGNTVYMYVNVGDALNVQOLONGSW 180
Db 241 NGGTGQADKFEYVTSNTVFASGKGTATVYSKDDGNTVYMYVNVGDALNVQOLONGSW 300
QY 181 WNDLSKAVAGSSGVISGNVSPSKGKMDVFNINAGNNIETTRNGKNIDIAITSMTPQSS 240
Db 301 WNDLSKAVAGSSGVISGNVSPSKGKMDVFNINAGNNIETTRNGKNIDIAITSMTPQSS 360
QY 241 VSLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVAAGVEGDTVNAOLKGYAQNINNR 480
Db 361 VSLGAGADAPTLSDVDGALNVGSKKDNKPVRTNVAAGVEGDTVNAOLKGYAQNINNR 420
QY 301 IDNVGNAARAGIAQAIATAGLVQAYLPKGSMAIIGGTYRGEAGYAIYSSISDGNWIIK 360
Db 421 IDNVGNAARAGIAQAIATAGLVQAYLPKGSMAIIGGTYRGEAGYAIYSSISDGNWIIK 480
QY 361 KGTASGNSRGHFGASASVGYOW 382
Db 481 KGTASGNSRGHFGASASVGYOW 502
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RESULT 12
US-09-797-862-9
; Sequence 9, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: MOXON, E. RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

LENGTH: 594
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-797-862-9

Query Match 96.9%; Score 1886.5; DB 10; Length 594;
Best Local Similarity 97.6%; Pred. No. 1.6e-144;
Matches 373; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

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OY 2 RAASVKDVLNAGWNKIKGVPKPTTASDNVDVFRITDYVEFLSADTKTTTVNESKDNCKKT 61
DB 213 RAASVKDVLNAGWNKIKGVPKPTTASDNVDVFRITDYVEFLSADTKTTTVNESKDNCKRT 272
OY 62 EVKIGAKTSVKEKDKGLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTAN 121
DB 273 EVKIGAKTSVKEKDKGLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTAN 332
OY 122 GGTGQADKFEETVTSCTVNTFASGKGTATVSKDDOGNTVYDVNVGDALNVNOLQNSGW 181
DB 333 GGTGQADKFEETVTSCTVNTFASGKGTATVSKDDOGNTVYDVNVGDALNVNOLQNSGW 392
OY 182 NLDSKAAVAGSSGKVIYSGNVSPSKGMDETVINAGNNIEITRNCKNIDIASMTPOFSSV 241
DB 393 NLDSKAAVAGSSGKVIYSGNVSPSKGMDETVINAGNNIEITRNCKNIDIASMTPOFSSV 452
OY 242 SLGAGADAPTLISVDGD-ALNVGSKRDKNPVRITVAPGVEGDTVNAQLKGVAQNLNNR 300
DB 453 SLGAGADAPTLISVDDEGALNVGSKDKANKPVRITVAPGVEGDTVNAQLKGVAQNLNNH 512
OY 301 IDNVGNARAGIAAIAITAGLVQAYLPKGSMAAIGGTYRGEAGYAIGYSSISDGGMWII 360
DB 513 IDNVGNARAGIAAIAITAGLVQAYLPKGSMAAIGGTYRGEAGYAIGYSSISDGGMWII 572
OY 361 KGTAAGNSRGHFGASASVGYQW 382
DB 573 KGTAAGNSRGHFGASASVGYQW 594
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RESULT 13
US-09-771-382-4
Sequence 4, Application US/09771382
Patent No. US20020160016A1
GENERAL INFORMATION:
APPLICANT: Peak, Ian
APPLICANT: Jennings, Michael
TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
FILE REFERENCE: 8795-2401
CURRENT APPLICATION NUMBER: US/09/771.382
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/177,917
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 594
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-771-382-4

Query Match 96.9%; Score 1886.5; DB 10; Length 594;
Best Local Similarity 97.6%; Pred. No. 1.6e-144;
Matches 373; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

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OY 2 RAASVKDVLNAGWNKIKGVPKPTTASDNVDVFRITDYVEFLSADTKTTTVNESKDNCKKT 61
DB 213 RAASVKDVLNAGWNKIKGVPKPTTASDNVDVFRITDYVEFLSADTKTTTVNESKDNCKRT 272
OY 62 EVKIGAKTSVKEKDKGLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTAN 121
DB 273 EVKIGAKTSVKEKDKGLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTAN 332
OY 122 GGTGQADKFEETVTSCTVNTFASGKGTATVSKDDOGNTVYDVNVGDALNVNOLQNSGW 181
DB 333 GGTGQADKFEETVTSCTVNTFASGKGTATVSKDDOGNTVYDVNVGDALNVNOLQNSGW 392
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DB 333 GGTGQADKFEETVTSCTVNTFASGKGTATVSKDDOGNTVYDVNVGDALNVNOLQNSGW 392
OY 182 NLDSKAAVAGSSGKVIYSGNVSPSKGMDETVINAGNNIEITRNCKNIDIASMTPOFSSV 241
DB 393 NLDSKAAVAGSSGKVIYSGNVSPSKGMDETVINAGNNIEITRNCKNIDIASMTPOFSSV 452
OY 242 SLGAGADAPTLISVDGD-ALNVGSKRDKNPVRITVAPGVEGDTVNAQLKGVAQNLNNR 300
DB 453 SLGAGADAPTLISVDDEGALNVGSKDKANKPVRITVAPGVEGDTVNAQLKGVAQNLNNH 512
OY 301 IDNVGNARAGIAAIAITAGLVQAYLPKGSMAAIGGTYRGEAGYAIGYSSISDGGMWII 360
DB 513 IDNVGNARAGIAAIAITAGLVQAYLPKGSMAAIGGTYRGEAGYAIGYSSISDGGMWII 572
OY 361 KGTAAGNSRGHFGASASVGYQW 382
DB 573 KGTAAGNSRGHFGASASVGYQW 594
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RESULT 14
US-09-797-862-15
Sequence 15, Application US/09797862
Patent No. US20020102276A1
GENERAL INFORMATION:
APPLICANT: PEAK, IAN RICHARD ANSELM
APPLICANT: JENNINGS, MICHAEL PAUL
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0134
CURRENT APPLICATION NUMBER: US/09/797,862
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 599
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-797-862-15

Query Match 96.6%; Score 1881.5; DB 10; Length 599;
Best Local Similarity 97.6%; Pred. No. 4.1e-144;
Matches 373; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

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OY 2 RAASVKDVLNAGWNKIKGVPKPTTASDNVDVFRITDYVEFLSADTKTTTVNESKDNCKKT 61
DB 218 RAASVKDVLNAGWNKIKGVPKPTTASDNVDVFRITDYVEFLSADTKTTTVNESKDNCKRT 277
OY 62 EVKIGAKTSVKEKDKGLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTAN 121
DB 278 EVKIGAKTSVKEKDKGLVTKGDKGENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTAN 337
OY 122 GGTGQADKFEETVTSCTVNTFASGKGTATVSKDDOGNTVYDVNVGDALNVNOLQNSGW 181
DB 338 GGTGQADKFEETVTSCTVNTFASGKGTATVSKDDOGNTVYDVNVGDALNVNOLQNSGW 397
OY 182 NLDSKAAVAGSSGKVIYSGNVSPSKGMDETVINAGNNIEITRNCKNIDIASMTPOFSSV 241
DB 398 NLDSKAAVAGSSGKVIYSGNVSPSKGMDETVINAGNNIEITRNCKNIDIASMTPOFSSV 457
OY 242 SLGAGADAPTLISVDGD-ALNVGSKRDKNPVRITVAPGVEGDTVNAQLKGVAQNLNNR 300
DB 458 SLGAGADAPTLISVDKALNVGSKDKANKPVRITVAPGVEGDTVNAQLKGVAQNLNNR 517
OY 301 IDNVGNARAGIAAIAITAGLVQAYLPKGSMAAIGGTYRGEAGYAIGYSSISDGGMWII 360
DB 518 IDNVGNARAGIAAIAITAGLVQAYLPKGSMAAIGGTYRGEAGYAIGYSSISDGGMWII 577
OY 361 KGTAAGNSRGHFGASASVGYQW 382
DB 573 KGTAAGNSRGHFGASASVGYQW 594
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DB 578 KGTASGNSRGHFGASASVGYQW 599

RESULT 15

US-09-771-382-6
 ; Sequence 6, Application US/09771382
 ; Patent No. US20020160016A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Peak, Ian
 ; APPLICANT: Jennings, Michael
 ; TITLE OF INVENTION: MODIFIED SURFACE ANTIGEN
 ; FILE REFERENCE: 8795-2401
 ; CURRENT APPLICATION NUMBER: US/09/771,382
 ; CURRENT FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: US 60/177,917
 ; PRIOR FILING DATE: 2000-01-25
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 599
 ; TYPE: PRT
 ; ORGANISM: Neisseria meningitidis
 US-09-771-382-6

Query Match 96.6%; Score 1881.5; DB 10; Length 599;
 Best Local Similarity 97.6%; Pred. No. 4,1e-144;
 Matches 373; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

OY 2 RAASYVDVINAAGMNIKGVPKGTASDNDVFVRTYDVEFLSADTKTTVNVESKONGKKT 61
 DB 218 RAASYVDVINAAGMNIKGVPKGTASDNDVFVRTYDVEFLSADTKTTVNVESKONGKKT 277
 OY 62 EYKIGAKTSVIEKEKGKLVTKGDKGENGSTDEGBGLYTAKEVIDAVNKAQWRMKTITAN 121
 DB 278 EYKIGAKTSVIEKEKGKLVTKGDKGENGSTDEGBGLYTAKEVIDAVNKAQWRMKTITAN 337
 OY 122 GGTGQADKEEYVTSNTVFASGKGTATATVSKDDGNTITMYDVNVGDALNVNQLONGSM 181
 DB 338 GGTGQADKEEYVTSNTVFASGKGTATATVSKDDGNTITMYDVNVGDALNVNQLONGSM 397
 OY 182 NIDSKAVAGSSGKVIISGNVSPSKKMDDEVINAGNNIETTRNGKNIDIAISMTPOESSV*241
 DB 398 NIDSKAVAGSSGKVIISGNVSPSKKMDDEVINAGNNIETTRNGKNIDIAISMTPOESSV 457
 OY 242 SLGAGADAPTLISVDG-DALNVGSKKDNKPVRTITNVAAGVKEGDDVTNVAQLKGVAQNLNMR 300
 DB 458 SLGAGADAPTLISVDG-DALNVGSKKDNKPVRTITNVAAGVKEGDDVTNVAQLKGVAQNLNMR 517
 OY 301 IDNVGDNARAGIAQAIATAGLVQAVLPKSKMMAIGGTYRGEAGYAIGYSSISDGGNWI 360
 DB 518 IDNVGDNARAGIAQAIATAGLVQAVLPKSKMMAIGGTYRGEAGYAIGYSSISDGGNWI 577
 OY 361 KGTASGNSRGHFGASASVGYQW 382
 DB 578 KGTASGNSRGHFGASASVGYQW 599

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 Job time : 20.136 secs

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 10.9348 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-38
Perfect score: 1947
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1941	99.7	591	G81133	adhesin NMB0992 [i
2	1854.5	95.2	592	A81888	probable surface f
3	336.5	17.3	2059	D82671	surface protein XF
4	335	17.2	1190	A82615	surface protein XF
5	325.5	16.7	1588	A86036	probable adhesin z
6	325.5	16.7	1588	H91188	probable adhesin E
7	318	16.3	1107	AC0976	probable autotrans
8	312	16.0	658	AH0110	probable surface p
9	247	12.7	298	H64138	adhesin homolog HI
10	185	9.5	365	AB3486	cell surface prote
11	176.5	9.1	1004	C82672	surface-exposed ou
12	175	9.0	585	F90961	flagellin [importe
13	175	9.0	585	F85809	hypothetical prote
14	163.5	8.4	584	C48658	flagellin - Escher
15	163	8.4	364	A81019	adhesin/invasin, p
16	159	8.2	1336	A43855	high-molecular-we
17	159	8.2	1910	AF0394	probable adhesin h
18	158.5	8.1	1477	B43855	high-molecular-we
19	156.5	8.0	933	S41539	fibrinogen-binding
20	156	8.0	4919	T31105	hypothetical prote
21	155.5	8.0	989	D89852	fibrinogen-binding
22	155	8.0	1335	T17508	glycoprotein Vp260
23	154.5	7.9	2249	A41477	190K surface anti
24	154	7.9	364	AE0169	probable exported
25	152.5	7.8	595	A48658	flagellin - Escher
26	152.5	7.8	1091	G64964	hypothetical prote
27	152.5	7.8	1635	A10452	hemolysin [impor
28	152.5	7.8	1655	E97835	hypothetical prote
29	152	7.8	2020	C48399	ABC-type transpor

30	152	7.8	2273	2	T09083	hemagglutinin/hemo
31	151	7.8	980	2	H90681	probable flagellin
32	151	7.8	980	2	D85532	probable structural
33	150.5	7.7	1461	2	E90696	hypothetical prote
34	150	7.7	1300	2	S07575	outer membrane pro
35	150	7.7	5188	2	B85547	probable RTX fami
36	150	7.7	5291	2	F90696	hypothetical prote
37	148.5	7.6	595	2	B48658	hypothetical prote
38	148.5	7.6	2551	2	B98047	flagellin - Escher
39	148	7.6	1651	2	JC1340	outer membrane pro
40	147.5	7.6	338	2	D90697	adhesin/invasin-li
41	147.5	7.6	338	2	G85547	adhesin/invasin-li
42	147	7.6	936	2	I40711	sapB protein - Cam
43	147	7.6	1361	2	T03415	S-layer protein -
44	146.5	7.5	906	2	C85739	hypothetical prote
45	146.5	7.5	1011	2	F90879	probable BigA-like

ALIGNMENTS

RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: G81133

R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: G81133

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <FET>

A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match 99.7%; Score 1941; DB 2; Length 591;

Best Local Similarity 100.0%; Pred. No. 3.7e-103;

Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDTVEFLSADTKTTTVNVEKDKGKKT 61

DB 211 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRYTDTVEFLSADTKTTTVNVEKDKGKKT 270

QY 62 EVKIGAKTSVIREKDKGLVTGDKDGENSGSTDEGLVTAKEVIDAVNKGAWRMKTTAN 121

DB 271 EVKIGAKTSVIREKDKGLVTGDKDGENSGSTDEGLVTAKEVIDAVNKGAWRMKTTAN 330

QY 122 GGTGQADKFEETVTSNTVFASGKGTATVSKDDQGNITVMYDVNVDALNVQLNSGW 181

DB 331 GGTGQADKFEETVTSNTVFASGKGTATVSKDDQGNITVMYDVNVDALNVQLNSGW 390

QY 182 NLDSKAVAGSSGKVISGNVSPSKGKMDETVINAGNIEITRNKKNIDTATSTPQFSSV 241

DB 391 NLDSKAVAGSSGKVISGNVSPSKGKMDETVINAGNIEITRNKKNIDTATSTPQFSSV 450

QY 242 SLGAGADAPTLSDGDLNAGSKKDKNKPVRITNVPKVEGDVTNVAOLKGVQNLNRI 301

DB 451 SLGAGADAPTLSDGDLNAGSKKDKNKPVRITNVPKVEGDVTNVAOLKGVQNLNRI 510

QY 302 DNVDGNARAGIAQAIATAGLVQAYLPCKSNMAITGGTYRGEAGYAIYSSISDGGNWIK 361

DB 511 DNVDGNARAGIAQAIATAGLVQAYLPCKSNMAITGGTYRGEAGYAIYSSISDGGNWIK 570

QY 362 GTASGNSRGHFGASASVGQW 382

|||||

Db 571 GTASGNSRGHFGASASVGYQW 591

RESULT 2

A81888

probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 22491)

C:Species: Neisseria meningitidis

C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: A81888

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jagels, K.; Leather, S.; Moulé, S.; Mungall, K.; Quail, M.A.; Rajandream, P.

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.

A:Reference number: A81775; MUID:2022556; PMID:10761919

A:Accession: A81888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-592 <PAR>

A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989

A:Experimental source: serogroup A, strain 22491

C:Genetics:

A:Gene: NMA1200

Query Match 95.2%; Score 1854.5; DB 2; Length 592;

Best Local Similarity 95.8%; Pred. No. 3.1e-98;

Matches 368; Conservative 6; Mismatches 7; Indels 3; Gaps 2;

Qy 2 RAASVKDVLNAGNIKGVKPGTTA--SDNVDFVRYDTVEFLSADTKTTTNNVESKNGK 59

Db 209 RAASIKDVLNAGNIKGVKPGTTGQSENVDFVRYDTVEFLSADTKTTTNNVESKNGK 268

Qy 60 KTEVKGAKTSVIEKDGKLVTKGKGGSSSTDEGEGLVTAKEVIDAVNKGAGRMKTTT 119

Db 269 RTEVKGAKTSVIEKDGKLVTKGKGGSSSTDEGEGLVTAKEVIDAVNKGAGRMKTTT 328

Qy 120 ANGOTGQADKPEVTSNTNFTASGKGTATVSKDDGNTVYDVVNGDALNVNQLNS 179

Db 329 ANGOTGQADKPEVTSNTNFTASGKGTATVSKDDGNTVYDVVNGDALNVNQLNS 388

Qy 180 GWNLDSKAVAGSSGKVSIGNVSPSKGMDVETVNNAGNNTIETRNKNIDTATSWTPOFS 239

Db 389 GWNLDSKAVAGSSGKVSIGNVSPSKGMDVETVNNAGNNTIETRNKNIDTATSWTPOFS 448

Qy 240 SVSLGAGADAPTLSDVDG-ALNVGSKKDKNPVRIITNVPAGVKEGDTNVAQLKGVAQNLN 298

Db 449 SVSLGAGADAPTLSDVDGEGALNVGSKDKANKPVRIITNVPAGVKEGDTNVAQLKGVAQNLN 508

Qy 299 NRIDNVGNARAGTAQAIAATAGLVQAYLPKSKMMAIGGTYRGEAGYAIGYSSISDGGNW 358

Db 509 NRIDNVGNARAGTAQAIAATAGLVQAYLPKSKMMAIGGTYRGEAGYAIGYSSISDGGNW 568

Qy 359 IIKGTASGNSRGHFGASASVGYQW 382

Db 569 IIKGTASGNSRGHFGASASVGYQW 592

RESULT 3

D82671

surface protein Xf1529 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: D82671

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82671

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2059 <SIM>

A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier as-Neto, E.; Docena, C.; El-Doiry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferrio, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovskij-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1529

Query Match 17.3%; Score 336.5; DB 2; Length 2059;

Best Local Similarity 25.1%; Pred. No. 2.7e-11;

Matches 128; Conservative 63; Mismatches 154; Indels 165; Gaps 19;

Qy 5 SVKDVNLNAGNI-----KGVKPGTTASDNVD-----FVRYDTVEFLSADTK--- 46

Db 1583 SVSEAVDKGWTFTASGANGSKVVSOGTVDLKNTDGNLAISKSGDSNDVFNLSKDFKVE 1642

Qy 47 ----TTTNNVESKDNKKTEYKIGAKTSVIEKDGKLVTKGDKGEN-----GSSTDEG 95

Db 1643 VTAGNTVNTDGVKVG--SDVSLGAMGLFIANGPVSATSGFNAGDKVISHVAVGMAADTDA 1700

Qy 96 EGLVTAKEVIDAVNKGAGRMKTTT-----ANGOTGQ---ADKPEVTSNTN--- 139

Db 1701 VNVSQLKQAVOSVTVKATRYYSTNDGGTGGNYDGDGATGSKATAAGVGTQASGEAAV 1760

Qy 140 ----TFASGKGTTA-----TVS-- 152

Db 1761 GSGAASGKSTALGRNAIASADSGVALGDGAKDGGRGASYSYTKYSGVQNTVGTVSVG 1820

Qy 153 ---KDDGNTVYDVNVG-DALNVNL-----QNSGNWLDs----- 185

Db 1821 DAAKETRSINVADEAKEMDAVNLRQLDVAQKSNLQTDMDRHEINNIEDVFKITKGDs 1880

Qy 186 -----KAVAGSSGKVSIGNVSPSKGMDVETVNNAGNNTIETRNKNIDTATSWTP 236

Db 1881 ASSVKGMGVNAMATGTNAVSGTSEVALGK---NTNVSADNAVAI-GNG-----SVAD 1929

Qy 237 QFSSVSLGAGADAPTLSDVDGDALNVGSKKDKNPVRIITNVPAGVKEGDTNVAQLKGVAQN 296

Db 1930 RANSVSVSG-----GSEr-----QVTNVAAGTADTDVAVNVSQLNQGLIT 1969

Qy 297 LNNRIDNVGNAR-----AGIAQAIAATAGLVQAYLPKSKMMAIGGTYRGEAGYAIGYSSI 352

Db 1970 AKQYTDGMVGNLRRETSGGVAALATANLPQAYVQGRGRTSVGVSSYQGSIAVGVSAV 2029

Qy 353 SDGNGNWIKGTASGNSRGHFGASASVGYQW 382

Db 2030 SESGHVWFKFGSANTSRSHVGVGAGVGYQW 2059

RESULT 4

A82615

surface protein Xf1981 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: A82615

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82615

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1190 <SIM>

C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: F90961
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036085.1; PID:g13362130; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:
A:Gene: ECs2662
C:Superfamily: flagellin

Query Match 9.08; Score 175; DB 2; Length 585;
Best Local Similarity 22.7%; Pred. No. 0.0091;
Matches 88; Conservative 59; Mismatches 167; Indels 74; Gaps 17;
Qy 22 GTTASDNVDFR-----TYDTVEPLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKD 76
Db 102 GTNSDSLDLSIQDEIKSRLEIDRVSGQTQFNGVNLAKDGSMAK--IQVGANDGETITID 159
Qy 77 GLKVTGDKDGENSGSTDEGEGLVTAK-EVIDAVNKAGWRMKTTFITANGOTGOAD-KFETVT 134
Db 160 LKKIDSDTLGLNGFNVN-GKGTITNKAAATVSDLTSAKALNTT-----TGLYDLKTENTL 213
Qy 135 SGNVTFAS-GKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSS- 192
Db 214 LTTDAADFPLKNGDKVTV-----GGVDYTYNAKSGDFTTK--STAGTGVDAAQAADSA 266
Qy 193 -----GKVISGNVSPSKGMDETVNIAGNNIEITRNKNIDTATSMTPQF 238
Db 267 SKRDALAATLHADVGKSVNGSYTTKDGTV--SFETDSAGNITIGGSAQYVDDAGNLTTNN 324
Qy 239 SSVSLGA-----GADAPTLVSDGDALNVGSKKDNKPVRIITVAPGVKEGDVTNV 287
Db 325 AGSAKADKALKALKAASEGSDGASLTFTNGTEYTIKA--TPATTTVPAPLIPGGITYQA 381
Qy 288 AOLKGVAQNLNRRIDNVGNARAGIAQIATAGLVQ---AYLPCKSMMAI-----GGG 337
Db 382 TVSKDVVVLS-----ETKAAATSTITFNSGVLSKTIGTAGESSDAAKSYVDDKGGI 433
Qy 338 TYRGEAGYAIYSSISDGNWIKGTAS 365
Db 434 T--NVADYTVSYSVNKGDSVTVAGYAS 459

RESULT 13
F85809
hypothetical protein flic [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: F85809
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <SPO>
A:Cross-references: GB:AE005174; MID:g12516024; PIDN:AAG56938.1; GSPDB:GN00145; UWGP:Z30
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: flic
C:Superfamily: flagellin

Query Match 9.08; Score 175; DB 2; Length 585;

Best Local Similarity 22.7%; Pred. No. 0.0091;
Matches 88; Conservative 59; Mismatches 167; Indels 74; Gaps 17;
Qy 22 GTTASDNVDFR-----TYDTVEPLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKD 76
Db 102 GTNSDSLDLSIQDEIKSRLEIDRVSGQTQFNGVNLAKDGSMAK--IQVGANDGETITID 159
Qy 77 GLKVTGDKDGENSGSTDEGEGLVTAK-EVIDAVNKAGWRMKTTFITANGOTGOAD-KFETVT 134
Db 160 LKKIDSDTLGLNGFNVN-GKGTITNKAAATVSDLTSAKALNTT-----TGLYDLKTENTL 213
Qy 135 SGNVTFAS-GKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSS- 192
Db 214 LTTDAADFPLKNGDKVTV-----GGVDYTYNAKSGDFTTK--STAGTGVDAAQAADSA 266
Qy 193 -----GKVISGNVSPSKGMDETVNIAGNNIEITRNKNIDTATSMTPQF 238
Db 267 SKRDALAATLHADVGKSVNGSYTTKDGTV--SFETDSAGNITIGGSAQYVDDAGNLTTNN 324
Qy 239 SSVSLGA-----GADAPTLVSDGDALNVGSKKDNKPVRIITVAPGVKEGDVTNV 287
Db 325 AGSAKADKALKALKAASEGSDGASLTFTNGTEYTIKA--TPATTTVPAPLIPGGITYQA 381
Qy 288 AOLKGVAQNLNRRIDNVGNARAGIAQIATAGLVQ---AYLPCKSMMAI-----GGG 337
Db 382 TVSKDVVVLS-----ETKAAATSTITFNSGVLSKTIGTAGESSDAAKSYVDDKGGI 433
Qy 338 TYRGEAGYAIYSSISDGNWIKGTAS 365
Db 434 T--NVADYTVSYSVNKGDSVTVAGYAS 459

RESULT 14
C48658
flagellin - Escherichia coli (strain U5-41)
C:Species: Escherichia coli
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 26-Aug-1999
C:Accession: C48658
R:Schoenhals, G.; Whitfield, C.
J. Bacteriol. 175, 5395-5402, 1993
A:Title: Comparative analysis of flagellin sequences from Escherichia coli strains po
A:Reference number: A48658; MUID:93374833; PMID:8366026
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-584 <SCH>
A:Cross-references: GB:L07388; MID:g290438; PIDN:AAA23798.1; PID:g290439
C:Superfamily: flagellin

Query Match 8.4%; Score 163.5; DB 2; Length 584;
Best Local Similarity 23.4%; Pred. No. 0.041;
Matches 91; Conservative 57; Mismatches 164; Indels 77; Gaps 19;
Qy 22 GTTASDNVDFR-----TYDTVEPLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKD 76
Db 102 GTNSDSLDLSIQDEIKSRLEIDRVSGQTQFNGVNLAKDGSMAK--IQVGANDGETITID 159
Qy 77 GLKVTGDKDGENSGSTDEGEGLVTAK-EVIDAVNKAGWRMKTTFITANGOTGOADKFETVTS 135
Db 160 LKKIDSDTLGLNGFNVN-GKGTITNKAAATVSDLTSAKALNTT--GLYGL--KTENTLL 214
Qy 136 GTNVTFAS-GKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSS-- 192
Db 215 TTTDAADFPLKNGDKVTVGGVD-----IYNKSGDFTTK--STAGTGVDAAQAADTSK 266
Qy 193 -----GKVISGNVSPSKGMDETVNIAGNNIEITRNKNIDTATSMTPQ 237
Db 267 KRDALAATLHADVGKSVNGSYTTKDGTV--SFVTDAGN--ITIGGSAQYVDDAGNLTTN 322
Qy 238 FSSVSLGA-----GADAPTLVSDGDALNVGSKKDNKPVRIITVAPGVKEGDVTN 286
Db 323 NAGSARKADKALKALKAASEGSDGASLTFTNGTEYTIKA--TPATTTVPAPLIPGGITYQ 379

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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:06:20 ; Search time 5.89906 Seconds
(without alignments)
3045.266 Million cell updates/sec

Title: US-09-771-382-38

Perfect score: 1947

Sequence: 1 NRAASVKDVLNAGNIKVK.....TASGNSRGHGASASVGQW 382

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	154.5	7.9	2249	1 OMPA_RICRI	P15921 rickettsia
2	152.5	7.8	1039	1 AG43_ECOLI	P39180 escherichia
3	152.5	7.8	1655	1 OMPB_RICCN	Q9kka3 r outer mem
4	152	7.8	2003	1 YDBA_ECOLI	P33666 escherichia
5	150	7.7	1300	1 120K_RICRI	P14914 rickettsia
6	150	7.7	1654	1 OMPB_RICRI	Q53047 r outer mem
7	144	7.4	550	1 FLIC_SHIFL	Q08860 shigella fl
8	142	7.3	1953	1 BIGA_SALTY	P25927 salmonella
9	139.5	7.2	737	1 ALYS_ENTFA	P37710 enterococcu
10	139	7.1	1608	1 HLXA_SERMA	P15320 serratia ma
11	137.5	7.1	1007	1 Y741_CHLMU	Q9pit6 chlamydia m
12	137	7.0	497	1 FLIC_ECOLI	P04949 escherichia
13	137	7.0	1567	1 ICEN_XANCT	P18127 xanthomonas
14	136.5	7.0	930	1 PMPB_CHLPN	Q92393 chlamydia p
15	136	7.0	1577	1 HLXA_PROMI	P16466 proteus mir
16	136	7.0	1656	1 OMPB_RICJA	Q06653 r outer mem
17	134.5	6.9	1286	1 AIDA_ECOLI	Q03155 escherichia
18	134.5	6.9	1569	1 YPJA_ECOLI	P52143 escherichia
19	133	6.8	928	1 PM10_CHLPN	Q9rb65 chlamydia p
20	133	6.8	1645	1 OMPB_RICTY	P96989 r outer mem
21	133	6.8	2021	1 OMPA_RICCN	Q52657 rickettsia
22	131	6.7	434	1 YADA_YERPS	P10858 yersinia ps
23	131	6.7	917	1 HXA3_HAEIN	P45355 haemophilus
24	131	6.7	1148	1 ICEK_PSEEX	Q30611 pseudomonas
25	131	6.7	1153	1 PVDB_PLAKN	P50493 plasmodium
26	131	6.7	1398	1 TOF2_PLAFK	P41001 escherichia
27	130	6.7	2660	1 YEEJ_ECO57	Q8x8v7 escherichia
28	129.5	6.7	716	1 CX80_EUPOC	Q9n9x3 euplotes oc
29	129	6.6	1196	1 ICEV_PSEEX	Q33479 pseudomonas
30	129	6.6	3178	1 YS89_CAEEL	Q09624 caenorhabdi
31	128	6.6	575	1 FLA2_CAMJE	P22251 campylobact
32	128	6.6	933	1 SLAP_CAMFE	P35827 campylobact
33	128	6.6	1025	1 SLAP_CAUCR	P35828 caulobacter

RESULT 1

ID	OMPA_RICRI	STANDARD;	PRT;	2249 AA.
AC	P15921;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).			
GN	OMPA			
OS	Rickettsia rickettsii.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;			
OC	Rickettsiaceae; Rickettsiaseae; Rickettsia.			
OX	NCBI_TaxID=783;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-R;			
RX	MEDLINE=90354033; PubMed=2117568;			
RA	Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;			
RT	"A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";			
RL	Infect. Immun. 58:2760-2769(1990).			
CC	-!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.			
CC	-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.			
CC	-!- PTM: GLYCOSYLATED (PROBABLE).			
CC	-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.			
CC	-----			
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CC	-----			
DR	EMBL; M31227; AAA36380.1; -			
DR	PIR; A41477; A41477.			
DR	InterPro; IPR006315; Autotransport.			
DR	InterPro; IPR005546; Autotransporter.			
DR	Pfam; PF03797; Autotransporter; 1			
DR	TIGRFAMS; TIGR01414; autotrans_Darl; 3.			
KW	Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.			
FT	SIGNAL 1 28 POTENTIAL.			
FT	CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.			
FT	DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.			
FT	REPEAT 212 286 A (TYPE I).			
FT	REPEAT 287 358 B (TYPE I).			
FT	REPEAT 359 430 C (TYPE II).			
FT	REPEAT 431 505 D (TYPE I).			
FT	REPEAT 506 577 E (TYPE II).			
FT	REPEAT 578 652 F (TYPE I).			
FT	REPEAT 653 724 G (TYPE II).			
FT	REPEAT 725 799 H (TYPE I).			
FT	REPEAT 800 874 I (TYPE I).			
FT	REPEAT 875 949 J (TYPE I).			

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FT REPEAT      950 1021      K (TYPE II).
FT REPEAT      1022 1093      L (TYPE II).
FT REPEAT      1094 1165      M (TYPE II).
FT REPEAT      1166 1180      TYPE I (INCOMPLETE).
SQ SEQUENCE      2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match      7.9%; Score 154.5; DB 1; Length 2249;
Best Local Similarity 24.8%; Pred. No. 0.44;
Matches 119; Conservative 41; Mismatches 171; Indels 149; Gaps 25;

Qy 3 AASVGLVNLGNWIKGVKPGTASDNVDVFRVYDTEFLSADTKTTVNVESKDNGKKE 62
Db 833 AASVLTITNANAVLTGAVDNTGDNVGNLNGALSQVTDIGNT-----NSLAT- 883
Qy 63 VKIGAKT-----SVIKRDKGL----- 79
Db 884 ISVGAGTATLGGAVIKATTTKLTNAASVLTITNANAVLTGAIDNTTGGDNVGNLNGAL 943
Qy 80 --VTGKDKGNGST-DEGEGLVT-----AKEVIDAVNKAGWRMKTITTAQTGQADKFE 131
Db 944 SQVTGDIQNTSLATISVGAGTATLGGAVIKATTTKLTDAASAVKFTNPVVVTGAIDNTG 1003
Qy 132 TVTSGTNTVTSAGSGTATVSKDQGNITVMYDGVNVDALNVGNLQNSGNLDSKAVAGS 191
Db 1004 NANNGI-VTFTGNTSVTGNV-----GVTNALATVNVGAGL--LQVGGVVKANITNTDN 1055
Qy 192 SGKVISGNVSPSKGMDETVNNAG-----NNIEITRNGKNIDIATSMTPQFSSVSLGAG 246
Db 1056 ASAVFTNPVVVTGAIDNTGNANNGIVTFTGNSVTGTVGN-----TNALATVNVGAG 1108
Qy 247 ADAPTLVSDGAL--NVGSKKDN-KPVRIINVPKVEGDVTNVVAQLKVAQNLNLRIDN 303
Db 1109 ----LLQVGGVVKANITNTDNASAVFTFN--PVVVTGAIDNTG-----NANNGIVT 1155
Qy 304 VDGNA-----GIAQAIAT----AGL-VQAVLPCKSMMA-----IGSGT 338
Db 1156 FTGNSTVTGIDNTGNALATVNVGAGITLQA---GGSLAANNIDPGARSTLEFNGPLDGG- 1211
Qy 339 YRGAGYAIYG---SSISDGGNWIK-----GTASNSRGH---FGASAVG 379
Db 1212 ----GKAIPYFKGAIANGNAILNVNTKLLTASHLTIGTVAEINIGAGNLTIDASVG 1266

RESULT 2
AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT; 1039 AA.
AC P39180; P75614; P76360; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=K12;
RC MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
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RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=ML 308-225;
RC Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[4]
RN PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
[5]
RN SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
[6]
RN GENE NAME.
RP MEDLINE=97257509; PubMed=9103983;
RX Henderson I.R., Meehan M., Owen P.;
RT "Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
K-12.";
RL FEMS Microbiol. Lett. 149:115-120(1997).
CC -1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
CC FUNCTION AS AN ADHESIN.
CC -1- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
CC CHAIN).
CC -1- SUBCELLULAR LOCATION: Outer membrane-associated.
CC -1- SIMILARITY: TO ADHESIN ALDI-I AND TO BORDETELLA PERTACTIN.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE000291; AAC75061.1; ALT_INIT.
CC EMBL; D90838; BAA15825.1; ALT_INIT.
CC EMBL; D90839; BAA15832.1; ALT_INIT.
CC EMBL; U24429; AAB47869.1; -.
CC HSSP; P07505; ISRD.
CC EcoGene; EG12686; flu.
CC InterPro; IPR006315; Autotransport.
CC InterPro; IPR005546; Autotransporter.
CC InterPro; IPR004899; Pertactin.
CC Pfam; PF03797; Autotransporter; 1.
CC Pfam; PF03212; Pertactin; 1.
CC TIGRFAMs; TIGR01414; autotrans_barl; 1.
CC Outer membrane; Signal; Complete proteome.
FT SIGNAL 1 52
FT CHAIN 53 551 ANTIGEN 43 ALPHA CHAIN.
FT CHAIN 552 1039 ANTIGEN 43 BETA CHAIN.
FT VARIANT 2 2 K -> N (IN STRAIN ML 308-225).
FT VARIANT 41 42 SL -> FF (IN STRAIN ML 308-225).
FT VARIANT 46 46 T -> K (IN STRAIN ML 308-225).
FT VARIANT 157 157 W -> L (IN STRAIN ML 308-225).
FT VARIANT 188 188 V -> F (IN STRAIN ML 308-225).
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FT VARIANT 303 305 ATN -> STI (IN STRAIN ML 308-225).
FT VARIANT 320 320 A -> T (IN STRAIN ML 308-225).
FT VARIANT 372 372 N -> Q (IN STRAIN ML 308-225).
FT VARIANT 493 493 E -> V (IN STRAIN ML 308-225).
FT VARIANT 497 497 S -> N (IN STRAIN ML 308-225).
FT VARIANT 585 585 H -> Y (IN STRAIN ML 308-225).
FT VARIANT 709 709 E -> K (IN STRAIN ML 308-225).
FT VARIANT 721 721 M -> T (IN STRAIN ML 308-225).
FT VARIANT 751 753 GHL -> SHF (IN STRAIN ML 308-225).
FT VARIANT 803 803 S -> P (IN STRAIN ML 308-225).
FT VARIANT 815 815 A -> V (IN STRAIN ML 308-225).
FT VARIANT 824 824 C -> S (IN STRAIN ML 308-225).
FT VARIANT 829 835 LNLVHVS -> MNLITNA (IN STRAIN ML 308-225).
FT VARIANT 845 847 QGT -> LGA (IN STRAIN ML 308-225).
FT VARIANT 855 855 S -> T (IN STRAIN ML 308-225).
FT VARIANT 888 888 Q -> L (IN STRAIN ML 308-225).
FT VARIANT 1025 1025 S -> I (IN STRAIN ML 308-225).
FT CONFLICT 61 63 ETV -> TTT (IN REF. 5).
SQ SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEBE0 CRC64;

Query Match 7.8%; Score 152.5; DB 1; Length 1039;
Best Local Similarity 25.2%; Pred. No. 0.23;
Matches 100; Conservative 50; Mismatches 126; Indels 121; Gaps 27;

QY 3 AASVKDVLN-AGNWKGVKPGTASDNVDFVRT-----YDVFELSDTKTTVN 51
Db 162 AIATGTIVNDKQWQV--VKPGTVATDTV--VNTGAEGGPDAGNDGTQFVRGDAVRTIN 217
QY 52 VESKDNGKRTVEKIG-AKTSVIEKDGKLVTKDGENGSSTDE---GGLV-----TAK 102
Db 218 -----KNGRQIVRAEGTANTTV-----YAGGDQTVGHALDTTLNGGYVHNGGTAS 266
QY 103 EVIDAVNKAQWRM-----KTTTANGQTQADKEFTVSTGNTVTFASG----KGTATV 151
Db 267 DTV--VNSDQWQIVKNGVAGNTTVN-QKRL-QVDAGGTATNTVLKQGGALVTSTAATV 322
QY 152 SKDDQG-NITVMYDVNVGDALYNQLONGSNWLDKAVAGSSGKVISGNNVSPSKGRMDET 210
Db 323 T-----GINRLGAFSVVEGRADNV-VLENGG-RLD-----VLTGHTATN----- 359
QY 211 VNINAGNNIITNKGKNDIATSMTPQFSSVSIGAGADAPTLVSDGALNVGSKDNKPV 270
Db 360 TRVDDGGLTDV-RNG-----GTATP-----VSMNGG---VLLADSGAAVSGTRSDGK-- 403
QY 271 RITNAPGVKEGDTVNTVAQLKGVQNLNINRDNVDGNARAGIAQAATATAGLVQAYLPKGS 330
Db 404 -----AFSIGGGQADALMLEKGSFTLN-----AGDTATDTT----- 435
QY 331 MMAIGGTYRGEAGYAGISYSSIDGGNWIKGTASGN 367
Db 436 ---VNGGLETFARGGTLAGTTLNNGAILTLGSKTVNN 469

RESULT 3
OMPE_RICCN STANDARD; PRT; 1655 AA.
ID AC O9KKA3; Q9KKA98; Q9XC45;
DE 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scs5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
```

```
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=2033643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein ompB (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
RT australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -I- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
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CC -----
DR EMBL; AE008659; AAL03623.1; -
DR EMBL; AF123721; AAF34124.1; -
DR EMBL; AF123726; AAF34129.1; -
DR EMBL; AF149110; AAD39533.1; -
DR PIR; E97835; E97835.
DR InterPro; IPR006315; Autotransport.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRfams; TIGR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.
FT CHAIN 1335 1655 32 kDa BETA PEPTIDE.
FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).
FT CONFLICT 353 354 KD -> GH (IN REF. 3).
FT CONFLICT 776 776 F -> S (IN REF. 3).
FT CONFLICT 1159 1159 E -> D (IN REF. 3).
FT CONFLICT 1177 1177 G -> S (IN REF. 3).
FT CONFLICT 1492 1492 H -> R (IN REF. 3).
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;
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Query Match 7.8%; Score 152.5; DB 1; Length 1655;
Best Local Similarity 24.4%; Pred. No. 0.39;
Matches 103; Conservative 49; Mismatches 183; Indels 87; Gaps 21;

QY 10 LNAGWIKGVKPGTASDNVDFVRTYD---TVFELSADTKTTVN-----VESKNG----- 58
Db 417 LKNGFTGDASNPGNTAG-----VITFDANGTLASADANVAVTNNITAEASGAYVQL 471
```


OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS
CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES
CC CONFERRING ANTIGENICITY TO THE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC
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CC -----
DR EMBL; X16353; CAA34402.1; .
DR PIR; S07575; S07575.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter; 1.
DR TIGRFAMs; TIGR01414; autotrans_bar1; 2.
KW Antigen; Glycoprotein; Cell wall; S-layer.
FT CARBOHYD 7 7 N-LINKED (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (POTENTIAL).
FT CARBOHYD 424 424 N-LINKED (POTENTIAL).
FT CARBOHYD 430 430 N-LINKED (POTENTIAL).
FT CARBOHYD 436 436 N-LINKED (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (POTENTIAL).
FT CARBOHYD 547 547 N-LINKED (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (POTENTIAL).
FT CARBOHYD 655 655 N-LINKED (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (POTENTIAL).
FT CARBOHYD 710 710 N-LINKED (POTENTIAL).
FT CARBOHYD 799 799 N-LINKED (POTENTIAL).
FT CARBOHYD 800 800 N-LINKED (POTENTIAL).
FT CARBOHYD 826 826 N-LINKED (POTENTIAL).
FT CARBOHYD 844 844 N-LINKED (POTENTIAL).
FT CARBOHYD 861 861 N-LINKED (POTENTIAL).
FT CARBOHYD 879 879 N-LINKED (POTENTIAL).
FT CARBOHYD 920 920 N-LINKED (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (POTENTIAL).
FT CARBOHYD 1116 1116 N-LINKED (POTENTIAL).
FT CARBOHYD 1128 1128 N-LINKED (POTENTIAL).
FT CARBOHYD 1140 1140 N-LINKED (POTENTIAL).
FT CARBOHYD 1146 1146 N-LINKED (POTENTIAL).
FT CARBOHYD 1211 1211 N-LINKED (POTENTIAL).
SQ SEQUENCE 1300 AA; 132801 MW; E0952C3F647243D CRC64;
Query Match 7.7%; Score 150; DB 1; Length 1300;
Best Local Similarity 23.0%; Pred. No. 0.41;
Matches 104; Conservative 50; Mismatches 172; Indels 126; Gaps 22;

OY 1 NRAASVK--DVLNAGWNIGK--VKPGTTASDNVDVFRYTD---TVEFLSADTKTTVN-- 51

Db 50 NLAQIKVPNAITLTGNTGDASNPNGTAG-----VITFDANGTLESASADANVAVTNNI 104
QY 52 --VESKDNG-----KKTEVKICAKTSVLIKEDGKLVTKDK-----GENSSSTDEGE 96
Db 105 TATEASGAGVVQLSGTHAAELRLGNAGSIFKLADGTIVNGKVNQTALVGGALAAAGTTLD 164
QY 97 GLVTAREVIDAVNKAGWRMKTITANGQTGOADKFETVT-SCTNVTFASG-----RGTT 148
Db 165 GSATITGIDIGNAGGAALORITLAN-----DAKKTTLTGGANIAGGGGTIDLQANGGT 218
QY 149 ATVSKDDQGNITVYDV-----NVGDALNVQLQNSGN-----LSKAVA-----G 190
Db 219 IKLT-STQNNIVVDFDLAIATDQTGVVDASSLTNAQTLTINGKIGTIGCANNKTLGQFNIG 277
QY 191 SSKGVIS-GNV-----SPSKGKMDETVINAGNNEIT 222
Db 278 SSKTVLSNGVAINELVIGNDGAVQFAHTYTLTRTTNAAAGQGIIFNPVNVNGTTTAA- 336
QY 223 RGNKNDIATSMTPQFSVSLGAGADAPTLSDGDALNVGSKDKDKPVRIT-----NVAPG 278
Db 337 --GTNLGSATNPLAEINFGSKGVNVDI-----VLNVGEGVNLATNTTTDANVGSF 386
QY 279 VKEGDVTNVAQLKGVAQNLANRDNVDGNARAGIAQAIATAGLVQAVLPKSKMAIGGGT 338
Db 387 VFNAGGTNIYS-GTVGQGGQGNKFTV-----ALENGTTVKFLGNAT 426
QY 339 YRGEAGYAGYSSISDGGNWIKGTSAGNSRG 370
Db 427 FNGNTTIAAN-STLIQIGGNTADCVASADGTG 457
RESULT 6
OMP_RICRI
ID OMPB_RICRI STANDARD; PRT; 1654 AA.
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOMP B)
DE (rOMP B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOMP B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor";
RL Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC
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CC -----

DR EMBL; X16353; CAA34403.1; -
DR PIR; S18227; S18227.
DR InterPro; IPR006315; Autotransport.
DR InterPro; IPR005546; Autotransporter.
DR Pfam; PF03797; Autotransporter; 1.
DR TrRfam; TrR01414; autotrans_bar1; 2.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 kDa SURFACE-EXPOSED PROTEIN.
FT DOMAIN 1334 1654 32 kDa BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 7.7%; Score 150; DB 1; Length 1654;
Best Local Similarity 23.0%; Pred. No. 0.54;
Matches 104; Conservative 50; Mismatches 172; Indels 126; Gaps 22;

QY 1 NRAASVK--DVLNAGWIKG--VKPTTASDNVDVFTYD---TVEFLSADTKTTVN-- 51
DB 404 NLAQIKVPNAITLTGNTGDASNPNTAG-----VITFDANGTLESASADANVAVTNNI 458
QY 52 --VESKDG-----KKEVKGIGAKTSVIKEDGKLVTKDK-----GENSGSTDEGE 96
DB 459 TATEASAGVVQLSGTHAEELRGNAGSIFKLADGTVINKVNOTALVGGALAGTITLD 518
QY 97 GLVTAKEDAVNKGWIKMTTANGOTGQADKFETVT--SGTNVTFASG-----KGTT 148
DB 519 GSATITGDIGNAGAAALQRTILAN-----DAKKTLTLCGANIIGAGGTIDLOANGGT 572
QY 149 ATYSKDDGQNTVMYDV-----NVGDALNVQLNSGN-----LDSKAVA-----G 190
DB 573 IKLT-STONNIVVDLAIATDQGVVDVDSLTNAQTLTNGKIGTIGANNKTLGQFNIG 631
QY 191 SSKKVIS--GNV-----SPSKMDETVINAGNNIEIT 222
DB 632 SSKTVLSNGVAINELVIGNDGAVQFAHDYILITRTTNAAGQKIIIPNVVNGTTLAA- 690
QY 223 RGNKIDIAISMTQPFSSVSLGAGADAPTLSDVDGALNVGSKDKNKPVRIT----NVAPG 278
DB 691 --GTNLGASATNPLAEINFGSKGVNDT-----VLNVGEGVNLATNITTTDANVGSF 740
QY 279 VKEDVTNVQALQKVAQNLNRRINDVGNARAGTAQAIAATAGLVQAYLPCKSMMAIGGTT 338
DB 741 VFNAGGTNIVS--GTVGGQGNKNTV-----ALENGTTVKFLGNAT 780
QY 339 YRGEAGYAGYSSISDGNMIIKGTASGNSRG 370
DB 781 FNGNTTAAAN-STLIQNGTADCVASADGTG 811

RESULT 7
FLIC_SHIFL STANDARD; PRT; 550 AA.
AC O0860;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Flagellin.
GN FLIC OR SF1966.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IID642;
RX MEDLINE=94335647; PubMed=8057852;

RA Toninaga A., Mahmoud M.A.-H., Mukaihara T., Enomoto M.;
RT "Molecular characterization of intact, but cryptic, flagellin genes
RT in the genus Shigella."
RL Mol. Microbiol. 12:277-285(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Xu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
CC -----
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CC -----
DR EMBL; D16819; BAA04093.1; -
DR EMBL; AE015215; AAN43516.1; -
DR PIR; S44980; S44980.
DR InterPro; IPR001029; Flagellin_C.
DR InterPro; IPR001492; Flagellin_N.
DR Pfam; PF00700; Flagellin_C; 1.
DR Pfam; PF00669; Flagellin_N; 1.
DR PRINTS; PR00207; FLAGELLIN.
KW Flagella.
SQ SEQUENCE 550 AA; 56636 MW; CC921C9A8EF200B6 CRC64;

Query Match 7.4%; Score 144; DB 1; Length 550;
Best Local Similarity 21.5%; Pred. No. 0.33;
Matches 76; Conservative 55; Mismatches 167; Indels 56; Gaps 14;

QY 22 GTTASDNVDVR-----TYDTVEFLSADTKTTTVNVEKSKDKKTEYKIGAKTSVIREKD 76
DB 102 GTNSDSDLDSIQDEIKSRLEIDRVSGQTQFNGVNLAKDGSMAK--IQVGANDQQTITD 159
QY 77 GLVTKGDKGENSGSTDEGEGL---VTAKEVIDAVNKGWIKMTTANGQTG---QADKFE 131
DB 160 LKKIDSDTLGLNGFNVNGGAVANTAASKADLVAAANATVVGNYTVSAGYDAKASDLA 219
QY 132 TVTSGTNV--TFASGKGTATVS--KDDOGNITVMYDVNVGDALNVQLNSGNLSDSKA 187
DB 220 GVSDDGTIVQATINNGFGTAASATNYKYDSASKSVSFDTTTASAADVOKYLTGP----- 272
QY 188 VAGSSGK---VISGNVSPSKGMDETVINAGNNI-----EITRNGKNIDIAISMTQPF 238
DB 273 -VGDTAKGTTITDGSADVOISSDGKITASNGDKLYIDTTGRLTKNGS----GASLFEAS 327
QY 239 SSVSLGAGADAPTLSDVDGALNVGSKDKNKPVRITNVAPGKEDVTNVQALQKVAQNLN 298
DB 328 LSTLAANNKTTATIDIGGTISIF-TGNSTTPDTITYSVTGAK---VDOAAAFDRAVSTSGN 383
QY 299 N-----RIDNVGDNARAGI-----AQAIATAGLVQAYLPCKSMMAIGGG 337
DB 384 NVDFETAGYSVNGTGTGATKGVDSVYVDNNEALTTSDTVDFYLODDSGSVNGSG 437

RESULT 8
BIGA_SALT
ID BIGA_SALT
AC P25927; P25928; O9XCQ3;
DT 01-MAY-1992 (Rel. 22, Created)


```
QY 265 K--DNKPVRTNVPAGV-----KEGDV-----TNVAQLKGVQNLN-----NRIDNV 304
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 933 KRSSSOAVVSSVQAGSIDINAKGEVRDQGTQOASKG-AVNLTADSHRSEAAANRQDEQ 991
QY 305 DGNARAGIAQIATAGIQAVALPCKSKMAIG---GCTYRGEAGYAGIYSSISDGGNW-- 358
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 992 SRDRF-----GSAG-VRYTTTGGSDLTVDKAGEGQGTQRNSSSASOAVTGSIDAANGIN 1043
QY 359 -----IIRGTASGNSRSHFGASA 376
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1044 VNVKDAIYOGTALNGGRGKTAVNA 1068

RESULT 11
Y741_CHLMU
ID Y741_CHLMU STANDARD; PRT; 1007 AA.
AC Q9PJ76;
RC STRAIN=MoPn / Ni9g;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., deBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AK39.;" 28:1397-1406(2000).
RL Nucleic Acids Res.
CC -1- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0572/CR456/TC0741
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE002342; AAF39550.1; .
DR PIR; H81670; H81670.
DR TIGR; TC0741; .
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 51 POTENTIAL.
FT CHAIN 52 1007 HYPOTHETICAL PROTEIN TC0741.
SQ SEQUENCE 1007 AA; 104006 MW; 842800C087B1518 CRC64;

Query Match
Best Local Similarity 7.1%; Score 137.5; DB 1; Length 1007;
Matches 109; Conservative 52; Mismatches 165; Indels 171; Gaps 26;

QY 9 VLNAGWNKGVK-----PGT-TASDNVDFVRYDTVFLSADTKT---TTVNVE 53
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 VINNVNVGVTNNVIGDNTVNSKSGTPTSSQSDM--STDTSDLDTSIDITNNQTNNGDIN 480
QY 54 SKDNGKTEVKIGAKTSVIEKDG---KLVTGDKD----- 85
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 TNDNSNVGDSLSVDVSRVEDDGVSDTESTNGNSGKTTSTEENGDPSPGDILAAVRKH 540
QY 86 -----GENSSSTDEGGLVTAKE---VIDAVNKAGWRMKTITANGQTGQADKFEVTS 135
D 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 541 LDTVPYENGSGT---EGPLPANQNLGNVHDVEQNSAKETIITPGDTGPTDSSSVDA 597
```

RESULT 12

```
FLIC_ECOLI
ID FLIC_ECOLI STANDARD; PRT; 497 AA.
AC P04949;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Flagellin.
GN FLIC OR FLAF OR HAG OR B1923.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=87057066; PubMed=3536885;
RA Kuwajima G., Asaka J.-I., Fujiwara T., Fujiwara T., Node K., Kondo E.;
RT "Nucleotide sequence of the hag gene encoding flagellin of
RT Escherichia coli.;"
RL J. Bacteriol. 168:1479-1483(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=89281489; PubMed=2659972;
RA Hanafusa T., Sakai A., Tominaga A., Enomoto M.;
RT "Isolation and characterization of Escherichia coli hag operator
RT mutants whose hag48 expression has become repressible by a Salmonella
RT H1 repressor.;"
RL Mol. Gen. Genet. 216:44-50(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97251358; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.;"
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
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```
RESULT 15
HLVA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPWA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN=Isolate 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent
RT hemolysin genes (hpmA and hpmB) reveals sequence similarity with the
RT Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPWA
CC REQUIRES HPMB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
CC MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
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CC -----
EMBL; M30186; AAA25657.1; -
DR PIR; A35140; A35140.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
FT SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;
Query Match 7.0%; Score 136; DB 1; Length 1577;
Best Local Similarity 23.0%; Pred. No. 3;
Matches 97; Conservative 58; Mismatches 141; Indels 126; Gaps 25;
Qy 6 VKDVLNAGWIKGVKPGTTASDNVDFVRYTDTVEFLS--ADTKTTVNVVE----- 53
Db 880 VKKAIEDGVNT--TKPGNN--TDLTKVTARDAIANLANLSNLETPNMGVEVGKGGSQ 936
Qy 54 SKDNGKKTEVKIGAKTSVIREKDKLVTKGDKGNGSGSDDEGEGLVTAKEVIDA-VNKAG 112
Db 937 SQTDSQAVSTISNAGKIDI-DSNNKL---HDQGHYOSTQEGISLTANTHTSEATLDKHQ 992
Qy 113 WRMKTTTANGQTGOADKFEVTSNTVFA-SGKGTTA-----TVSKDDQGNITVMYDV 165
Db 993 TTFHETKGGGIGVSTK-----TGSDDITVAIKGEGQTTDNALMETKAKGSOFTSNGDISI 1047
Qy 166 NVGDALNVQLQNSGWNLDKAVAGSSGKVISGNVSPSKMDETVINAGNIEITR-- 223
Db 1048 NVGE-----NAHYEGAQFDAQ-----RGK---TV-INAGGDLTLAQAT 1081
Qy 224 -----NGK-NIDIATSMTPQFSSVSLGAGADAPTL--SVDGDALNVGSKKKNKP 270
Db 1082 DTHSESOSNVNGSANLKVGT--TPE--SKDYGGGFNAGTTHHSKEQTAKVGTITGSQGI 1137
```

```
Qy 271 RITNVAPGVKEGDVTNVVAQLKGVAQNLNRRID-----NVDGNARAGIAQ--- 314
Db 1138 ELNAGHNLTLQG--THLSSEQDIALNATNKVDLQSSASSEHTEKGNLNSGGVQAGFGKKMT 1195
Qy 315 --AIATAGLVQAYLPGKSMMAIG-----GGTYRGEAGYAIGYSSISDGNWLIKG 362
Db 1196 DDASSVNL-----GSAQFAIGKQDEKSVSREGGT-----INNSNLTLNG 1236
Qy 363 TA 364
Db 1237 NS 1238
Search completed: October 6, 2003, 09:24:20
Job time : 7.89906 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 ; Search time 28.0565 seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-38

Perfect score: 1947

Sequence: 1 NRAASVKDVLNAGWNIRGVK.....TASGNSRGHFAGASVGVQW 382

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_ivirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1941	99.7	591	2 Q93QY3	Q93QY3 neisseria m
2	1941	99.7	591	2 Q9JPS7	Q9JPS7 neisseria m
3	1941	99.7	591	16 Q9JRI8	Q9JRI8 neisseria m
4	1937	99.5	592	2 Q9AQF0	Q9AQF0 neisseria m
5	1920	98.6	526	2 Q9JPS4	Q9JPS4 neisseria m
6	1920	98.6	530	2 Q9JPS1	Q9JPS1 neisseria m
7	1903	97.7	600	2 Q9JPS6	Q9JPS6 neisseria m
8	1895.5	97.4	592	2 Q9JPS9	Q9JPS9 neisseria m
9	1889.5	97.0	590	2 Q9JPS3	Q9JPS3 neisseria m
10	1886.5	96.9	594	2 Q93QY4	Q93QY4 neisseria m
11	1883.5	96.7	594	2 Q9JPI3	Q9JPI3 neisseria m
12	1883.5	96.7	594	2 Q9JPS2	Q9JPS2 neisseria m
13	1881.5	96.6	599	2 Q9JPR8	Q9JPR8 neisseria m
14	1874.5	96.3	594	2 Q9UPH7	Q9UPH7 neisseria m
15	1874.5	96.3	598	2 Q9JPR9	Q9JPR9 neisseria m
16	1861.5	95.6	592	2 Q93QY2	Q93QY2 neisseria m

17	1861.5	95.6	598	2 Q9JPS0	Q9JPS0 neisseria m
18	1861.5	95.6	598	2 Q93QY5	Q93QY5 neisseria m
19	1861.5	95.6	598	2 Q9JPT0	Q9JPT0 neisseria m
20	1860.5	95.6	598	2 Q9JPR7	Q9JPR7 neisseria m
21	1860.5	95.6	599	2 Q9JPS8	Q9JPS8 neisseria m
22	1854.5	95.2	592	16 Q9JQW4	Q9JQW4 neisseria m
23	1852.5	95.1	595	2 Q9UPH0	Q9UPH0 neisseria m
24	1846.5	94.8	600	2 Q9JPS5	Q9JPS5 neisseria m
25	1829.5	94.0	589	2 Q9JPI0	Q9JPI0 neisseria m
26	1817.5	93.3	589	2 Q93QY1	Q93QY1 neisseria m
27	710	36.5	1098	2 Q48152	Q48152 haemophilus
28	708.5	36.4	1096	2 Q8GM79	Q8GM79 haemophilus
29	679.5	34.9	1204	2 Q8GM76	Q8GM76 haemophilus
30	662.5	34.0	1210	2 Q8GM74	Q8GM74 haemophilus
31	660	33.9	2353	2 P71401	P71401 haemophilus
32	653.5	33.6	1210	2 Q8GM75	Q8GM75 haemophilus
33	418.5	21.5	1004	2 Q8GM77	Q8GM77 haemophilus
34	417.5	21.4	1002	2 Q8GM78	Q8GM78 haemophilus
35	374.5	19.2	1299	16 Q9F3X6	Q9F3X6 pasteurella
36	352.5	18.1	2314	2 Q8QK08	Q8QK08 moraxella c
37	336.5	17.3	2059	16 Q9PD50	Q9PD50 xylella fas
38	335	17.2	1190	16 Q9PC04	Q9PC04 xylella fas
39	325.5	16.7	1588	16 Q8XDC4	Q8XDC4 escherichia
40	320	16.4	1461	16 Q8ZL64	Q8ZL64 salmonella
41	318.5	16.4	1778	16 Q8FCB2	Q8FCB2 escherichia
42	318	16.3	1107	16 Q9F2D8	Q9F2D8 salmonella
43	312	16.0	641	16 Q8CKM1	Q8CKM1 versinia pe
44	312	16.0	658	16 Q8ZH30	Q8ZH30 versinia pe
45	300.5	15.4	2712	16 Q9F3X5	Q9F3X5 pasteurella

ALIGNMENTS

RESULT 1

Q93QY3 ID Q93QY3 PRELIMINARY; PRT: 591 AA.
AC Q93QY3;
DC 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE NHa outer membrane protein.
GN NHa.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157606; AAK68867.1;
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 591 AA, 62048 MW; C0DC600798859C65 CRC64;

Query Match 99.7%; Score 1941; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 4.8e-84;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGWNIRGVKPGTTASDNVDFVYTDVFEFLSADTKTTTVNVEKONGKKT 61
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DB 211 RAASVKDVLNAGWNIRGVKPGTTASDNVDFVYTDVFEFLSADTKTTTVNVEKONGKKT 270
QY 62 EVKIGAKTSVKEKDGKLVTKDGKNGSSTDEGGLVTAKEVIDAVNKAQWRMKTITAN 121
|||||
DB 271 EVKIGAKTSVKEKDGKLVTKDGKNGSSTDEGGLVTAKEVIDAVNKAQWRMKTITAN 330
QY 122 GOTGQADKPFVTSGTNVTFASGKGTATVSKDDGNTVYDVNVGVDAALNVQNSGW 181
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Db 331 GQTQADKFFETVTSCTNTWTASGKGTATATVSKDDQGNITVWYDVNVGDALNVNQLNSGW 390
Qy 182 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNIDIAITSMTPQFSSV 241
Db 391 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNIDIAITSMTPQFSSV 450
Qy 242 SLGAGADAPLTSVVDGDALNVGSKDKNKPVRITNVAPGVKGGDVTNVVAGLKGVAQNLNRI 301
Db 451 SLGAGADAPLTSVVDGDALNVGSKDKNKPVRITNVAPGVKGGDVTNVVAGLKGVAQNLNRI 510
Qy 302 DNVDGNARAGIAQAIAATAGLVQVAYLPCKSMMAIGGGTYRGAGYAGYSSISDGGNWI 361
Db 511 DNVDGNARAGIAQAIAATAGLVQVAYLPCKSMMAIGGGTYRGAGYAGYSSISDGGNWI 570
Qy 362 GTASGNSRGHFGASASVGYQW 382
Db 571 GTASGNSRGHFGASASVGYQW 591

RESULT 2
Q9JPS7 PRELIMINARY; PRT; 591 AA.
AC Q9JPS7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2147;
RA MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226366; AAF42515.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 99.7%; Score 1941; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 4.8e-84;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RAASVKDVLNAGNIKGVKPGTTASDNVDVFRYDYVFEFLSADTKTTNVNVEKDKNGKKT 61
Db 211 RAASVKDVLNAGNIKGVKPGTTASDNVDVFRYDYVFEFLSADTKTTNVNVEKDKNGKKT 270
Qy 62 EVKIGAKTSVKEKDKGLVTGKDKGNGSSTDEGEGLVTAKVIDAVNKGAWRMKTTAN 121
Db 271 EVKIGAKTSVKEKDKGLVTGKDKGNGSSTDEGEGLVTAKVIDAVNKGAWRMKTTAN 330
Qy 122 GQTQADKFFETVTSCTNTWTASGKGTATATVSKDDQGNITVWYDVNVGDALNVNQLNSGW 181
Db 331 GQTQADKFFETVTSCTNTWTASGKGTATATVSKDDQGNITVWYDVNVGDALNVNQLNSGW 390
Qy 182 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNIDIAITSMTPQFSSV 241
Db 391 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNIDIAITSMTPQFSSV 450
Qy 242 SLGAGADAPLTSVVDGDALNVGSKDKNKPVRITNVAPGVKGGDVTNVVAGLKGVAQNLNRI 301
Db 511 DNVDGNARAGIAQAIAATAGLVQVAYLPCKSMMAIGGGTYRGAGYAGYSSISDGGNWI 570
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Db 451 SLGAGADAPLTSVVDGDALNVGSKDKNKPVRITNVAPGVKGGDVTNVVAGLKGVAQNLNRI 510
Qy 302 DNVDGNARAGIAQAIAATAGLVQVAYLPCKSMMAIGGGTYRGAGYAGYSSISDGGNWI 361
Db 511 DNVDGNARAGIAQAIAATAGLVQVAYLPCKSMMAIGGGTYRGAGYAGYSSISDGGNWI 570
Qy 362 GTASGNSRGHFGASASVGYQW 382
Db 571 GTASGNSRGHFGASASVGYQW 591

RESULT 3
Q9JRI8 PRELIMINARY; PRT; 591 AA.
AC Q9JRI8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Adhesin) (Nhha outer membrane
DE protein).
GN GNA992 OR NMB0992 OR NHHA.
OS Neisseria meningitidis.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B, BZ169, BZ83, and H44/76;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizzia M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=N. meningitidis; STRAIN=PMC21;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226375; AAF42524.1; -.
DR EMBL; AE002450; AAF41395.1; -.
DR EMBL; AF226367; AAF42516.1; -.
DR EMBL; AF226370; AAF42519.1; -.
DR EMBL; AF226374; AAF42523.1; -.
DR EMBL; AF157611; AAK68872.1; -.
DR TIGR; NMB0992; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
KW Complete proteome.
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAEF7F73EC6 CRC64;
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Query Match          99.7%; Score 1941; DB 16; Length 591;
Best Local Similarity 100.0%; Pred. No. 4.8e-84;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNGKKT 61
DB 211 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNGKKT 270
QY 62 EVKIGAKTSVKEKDKGLVTGDKGKNGSTDEGGLVTAKEVIDAVNKGWRMKTITAN 121
DB 271 EVKIGAKTSVKEKDKGLVTGDKGKNGSTDEGGLVTAKEVIDAVNKGWRMKTITAN 330
QY 122 GQTQADKPFETVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 181
DB 331 GQTQADKPFETVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 390
QY 182 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIIETRNKKNIDTATSTPQSSV 241
DB 391 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIIETRNKKNIDTATSTPQSSV 450
QY 242 SLGAGADAPTLSDVDGALNVGSKKDNKPVKITVAPGVKEGDVTNVAQLKGVAQNLNRI 301
DB 451 SLGAGADAPTLSDVDGALNVGSKKDNKPVKITVAPGVKEGDVTNVAQLKGVAQNLNRI 510
QY 302 DNVGDNARAGIAIAIATAGLVQAYLPCKSMMAIGGTYRGEAGYAIYSSISDGGNWI 361
DB 511 DNVGDNARAGIAIAIATAGLVQAYLPCKSMMAIGGTYRGEAGYAIYSSISDGGNWI 570
QY 362 GTASGNSRHFAGASASGVQW 382
DB 571 GTASGNSRHFAGASASGVQW 591

RESULT 4
Q9AQF0
ID Q9AQF0 PRELIMINARY; PRT; 592 AA.
AC Q9AQF0
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterisation of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match          99.5%; Score 1937; DB 2; Length 592;
Best Local Similarity 99.7%; Pred. No. 7.5e-84;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNGKKT 61
DB 212 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNGKKT 271
QY 62 EVKIGAKTSVKEKDKGLVTGDKGKNGSTDEGGLVTAKEVIDAVNKGWRMKTITAN 121
DB 272 EVKIGAKTSVKEKDKGLVTGDKGKNGSTDEGGLVTAKEVIDAVNKGWRMKTITAN 331
QY 122 GQTQADKPFETVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 181
DB 331 GQTQADKPFETVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 390

Query Match          98.6%; Score 1920; DB 2; Length 526;
Best Local Similarity 99.0%; Pred. No. 4.1e-83;
Matches 377; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNGKKT 61
DB 146 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNGKKT 205
QY 62 EVKIGAKTSVKEKDKGLVTGDKGKNGSTDEGGLVTAKEVIDAVNKGWRMKTITAN 121
DB 206 EVKIGAKTSVKEKDKGLVTGDKGKNGSTDEGGLVTAKEVIDAVNKGWRMKTITAN 265
QY 122 GQTQADKPFETVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 181
DB 266 GQTQADKPFETVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 325
QY 182 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIIETRNKKNIDTATSTPQSSV 241
DB 326 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIIETRNKKNIDTATSTPQSSV 385
QY 242 SLGAGADAPTLSDVDGALNVGSKKDNKPVKITVAPGVKEGDVTNVAQLKGVAQNLNRI 301
DB 385 SLGAGADAPTLSDVDGALNVGSKKDNKPVKITVAPGVKEGDVTNVAQLKGVAQNLNRI 511

Query Match          98.6%; Score 1920; DB 2; Length 526;
Best Local Similarity 99.0%; Pred. No. 4.1e-83;
Matches 377; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNGKKT 61
DB 146 RAASVKDVLNAGNIIKGVKPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNGKKT 205
QY 62 EVKIGAKTSVKEKDKGLVTGDKGKNGSTDEGGLVTAKEVIDAVNKGWRMKTITAN 121
DB 206 EVKIGAKTSVKEKDKGLVTGDKGKNGSTDEGGLVTAKEVIDAVNKGWRMKTITAN 265
QY 122 GQTQADKPFETVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 181
DB 266 GQTQADKPFETVTSCTNVTASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGW 325
QY 182 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIIETRNKKNIDTATSTPQSSV 241
DB 326 NLDKAVAGSSGKVISGNVSPSKGKMDETVNIAGNIIETRNKKNIDTATSTPQSSV 385
QY 242 SLGAGADAPTLSDVDGALNVGSKKDNKPVKITVAPGVKEGDVTNVAQLKGVAQNLNRI 301
DB 385 SLGAGADAPTLSDVDGALNVGSKKDNKPVKITVAPGVKEGDVTNVAQLKGVAQNLNRI 511
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Db 386 SLGAGADAPTLVSVDGALNVGSKDKNPVRTNTNVPAGVKGEDVTNVAQLKGVAQNLNRI 445
Qy 302 DNVGDNARAGIAQAIAATAGLVQVAYLPKGSMMAIGGGTYRGAGYAGYSSISDGGNNIIK 361
Db 446 DNVGDNARAGIAQAIAATAGLVQVAYLPKGSMMAIGGGTYRGAGYAGYSSISDGGNNIIK 505
Qy 362 GTASGNSRGHFGASASVGYOW 382
Db 506 GTASGNSRGHFGASASVGYOW 526

RESULT 6
Q9JPS1 ID Q9JPS1 PRELIMINARY; PRT; 530 AA.
AC Q9JPS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGF26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226380; AAF42529.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 530 AA; 55190 MW; 1F836CA57598515B CRC64;

Query Match 98.6%; Score 1920; DB 2; Length 530;
Best Local Similarity 99.0%; Pred. No. 4.1e-83;
Matches 377; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RAASVKDVLNAGWIKGVKPGTTASDNVDFVRYTDTVEFLSADPTKTTVNVESKDNGKKT 61
Db 150 RAASVKDVLNAGWIKGVKPGTTASDNVDFVRYTDTVEFLSADPTKTTVNVESKDNGKKT 209
Qy 62 EVKIGAKTSVKEKDKGLVTKGDKGENSGSTDEGEGLVTAKEVIDAYNKAGWRMKTITAN 121
Db 210 EVKIGAKTSVKEKDKGLVTKGDKGENSGSTDEGEGLVTAKEVIDAYNKAGWRMKTITAN 269
Qy 122 GQTQADKFEFTVSGTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNOLQNSGW 181
Db 270 GQTQADKFEFTVSGTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNOLQNSGW 329
Qy 182 NLDKAVAGSGKVISGNVSPSKGMDVTNINAGNIEITRNKNIDIAITSMTPQFSSV 241
Db 330 NLDKAVAGSGKVISGNVSPSKGMDVTNINAGNIEITRNKNIDIAITSMTPQFSSV 389
Qy 242 SLGAGADAPTLVSVDGALNVGSKDKNPVRTNTNVPAGVKGEDVTNVAQLKGVAQNLNRI 301
Db 390 SLGAGADAPTLVSVDGALNVGSKDKNPVRTNTNVPAGVKGEDVTNVAQLKGVAQNLNRI 449
Qy 302 DNVGDNARAGIAQAIAATAGLVQVAYLPKGSMMAIGGGTYRGAGYAGYSSISDGGNNIIK 361
Db 450 DNVGDNARAGIAQAIAATAGLVQVAYLPKGSMMAIGGGTYRGAGYAGYSSISDGGNNIIK 509
Qy 362 GTASGNSRGHFGASASVGYOW 382
Db 506 GTASGNSRGHFGASASVGYOW 526
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Db 510 GTASGNSRGHFGASASVGYOW 530

RESULT 7
Q9JPS6 ID Q9JPS6 PRELIMINARY; PRT; 600 AA.
AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226371; AAF42520.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 97.7%; Score 1903; DB 2; Length 600;
Best Local Similarity 98.4%; Pred. No. 3e-82;
Matches 375; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 RAASVKDVLNAGWIKGVKPGTTASDNVDFVRYTDTVEFLSADPTKTTVNVESKDNGKKT 61
Db 220 RAASVKDVLNAGWIKGVKPGTTASDNVDFVRYTDTVEFLSADPTKTTVNVESKDNGKKT 279
Qy 62 EVKIGAKTSVKEKDKGLVTKGDKGENSGSTDEGEGLVTAKEVIDAYNKAGWRMKTITAN 121
Db 280 EVKIGAKTSVKEKDKGLVTKGDKGENSGSTDEGEGLVTAKEVIDAYNKAGWRMKTITAN 339
Qy 122 GQTQADKFEFTVSGTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNOLQNSGW 181
Db 340 GQTQADKFEFTVSGTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVNOLQNSGW 399
Qy 182 NLDKAVAGSGKVISGNVSPSKGMDVTNINAGNIEITRNKNIDIAITSMTPQFSSV 241
Db 400 NLDKAVAGSGKVISGNVSPSKGMDVTNINAGNIEITRNKNIDIAITSMTPQFSSV 459
Qy 242 SLGAGADAPTLVSVDGALNVGSKDKNPVRTNTNVPAGVKGEDVTNVAQLKGVAQNLNRI 301
Db 460 SLGAGADAPTLVSVDGALNVGSKDKNPVRTNTNVPAGVKGEDVTNVAQLKGVAQNLNRI 519
Qy 302 DNVGDNARAGIAQAIAATAGLVQVAYLPKGSMMAIGGGTYRGAGYAGYSSISDGGNNIIK 361
Db 520 DNVGDNARAGIAQAIAATAGLVQVAYLPKGSMMAIGGGTYRGAGYAGYSSISDGGNNIIK 579
Qy 362 GTASGNSRGHFGASASVGYOW 382
Db 580 GTASGNSRGHFGASASVGYOW 600

RESULT 8
Q9JPS9 ID Q9JPS9 PRELIMINARY; PRT; 592 AA.
AC Q9JPS9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.

OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;

[1]

RN SEQUENCE FROM N.A.

RC STRAIN=660800;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226361; AAF42510.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;

Query Match 97.4%; Score 1895.5; DB 2; Length 592;

Best Local Similarity 98.4%; Pred. No. 6.7e-82;

Matches 376; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKGKT 61

DB 211 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKGKT 270

QY 62 EVKIGAKTSVKEKDKGLVTGDKGNGSSSTDEGLVTAKEVIDAVNKGAWRMKTTTAN 121

DB 271 EVKIGAKTSVKEKDKGLVTGDKGNGSSSTDEGLVTAKEVIDAVNKGAWRMKTTTAN 330

QY 122 GQTQADKFTVTSGTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGW 181

DB 331 GQTQADKFTVTSGTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGW 390

QY 182 NLDKAVAGSSGKVISGNVSPSKGMDVTNINAGNIEITRNKKNIDATSMTPQFSSV 241

DB 391 NLDKAVAGSSGKVISGNVSPSKGMDVTNINAGNIEITRNKKNIDATSMTPQFSSV 450

QY 242 SLGAGADAPTLSDVG-DALNVGSKDKPKVRIITNVPAGVKEGDTNVAQLKGVAQNLR 300

DB 451 SLGAGADAPTLSDVDDGALNVGSKDKPKVRIITNVPAGVKEGDTNVAQLKGVAQNLR 510

QY 301 IDNVGDNARAGIAQAATAGLVQAYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWII 360

DB 511 IDNVGDNARAGIAQAATAGLVQAYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWII 570

QY 361 KGTSAGNSRGHFGASASVGQW 382

DB 571 KGTSAGNSRGHFGASASVGQW 592

RESULT 9

Q9JPS3

ID Q9JPS3 PRELIMINARY; PRT; 590 AA.

AC Q9JPS3;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE Outer membrane protein GNA992.

GN GNA992.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;

[1]

RN SEQUENCE FROM N.A.

RC STRAIN=NCE28;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226378; AAF42527.1; -

DR InterPro: IPR005594; Yada.

DR Pfam: PF03895; Yada; 1.

SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 97.0%; Score 1889.5; DB 2; Length 590;

Best Local Similarity 97.9%; Pred. No. 1.3e-81;

Matches 374; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 2 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKGKT 61

DB 209 RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDKGKT 268

QY 62 EVKIGAKTSVKEKDKGLVTGDKGNGSSSTDEGLVTAKEVIDAVNKGAWRMKTTTAN 121

DB 269 EVKIGAKTSVKEKDKGLVTGDKGNGSSSTDEGLVTAKEVIDAVNKGAWRMKTTTAN 328

QY 122 GQTQADKFTVTSGTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGW 181

DB 329 GQTQADKFTVTSGTNVTFASGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGW 388

QY 182 NLDKAVAGSSGKVISGNVSPSKGMDVTNINAGNIEITRNKKNIDATSMTPQFSSV 241

DB 389 NLDKAVAGSSGKVISGNVSPSKGMDVTNINAGNIEITRNKKNIDATSMTPQFSSV 448

QY 242 SLGAGADAPTLSDVG-DALNVGSKDKPKVRIITNVPAGVKEGDTNVAQLKGVAQNLR 300

DB 449 SLGAGADAPTLSDVDDGALNVGSKDKPKVRIITNVPAGVKEGDTNVAQLKGVAQNLR 508

QY 301 IDNVGDNARAGIAQAATAGLVQAYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWII 360

DB 509 IDNVGDNARAGIAQAATAGLVQAYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWII 568

QY 361 KGTSAGNSRGHFGASASVGQW 382

DB 569 KGTSAGNSRGHFGASASVGQW 590

RESULT 10

Q93QY4

ID Q93QY4 PRELIMINARY; PRT; 594 AA.

AC Q93QY4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE Outer membrane protein.

GN NHHA.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EG327;

RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer

membrane protein of Neisseria meningitidis.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF157605; AAK68866.1; -

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DR InterPro: IPR005594; YadaA.
DR Pfam: PF03895; YadaA; 1.
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match          96.9%; Score 1886.5; DB 2; Length 594;
Best Local Similarity 97.6%; Pred. No. 1.8e-81;
Matches 373; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 2 RAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 61
   |||||
DB 213 RAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 272

QY 62 EVKIGAKTSVIKEDGKLVTKDKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
   |||||
DB 273 EVKIGAKTSVIKEDGKLVTKDKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 332

QY 122 GQTQADKFEFTVSGTNTVFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 181
   |||||
DB 333 GQTQADKFEFTVSGTNTVFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 392

QY 182 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNIDIAIATMTPTQFSSV 241
   |||||
DB 393 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNIDIAIATMTPTQFSSV 452

QY 242 SLGAGADAPTLSDVGD-ALNVGSKDNKPVRIITNVAPGVKEGDTNVVAQLKGVAQNLNRR 300
   |||||
DB 453 SLGAGADAPTLSDVGDALNVGSKDNKPVRIITNVAPGVKEGDTNVVAQLKGVAQNLNRR 512

QY 301 IDNVGDNARAGIAQAIATAGLVQAYLPKSNMATTGGCTYRGEAGYATGYSISDGGNWII 360
   |||||
DB 513 IDNVGDNARAGIAQAIATAGLVQAYLPKSNMATTGGCTYRGEAGYATGYSISDGGNWII 572

QY 361 KGTSAGNSRGRHFGASASVGYQW 382
   |||||
DB 573 KGTSAGNSRGRHFGASASVGYQW 594

RESULT 11
Q9JPI3 PRELIMINARY; PRT; 594 AA.
AC Q9JPI3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, and BZ232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -
DR EMBL: AF226369; AAF42518.1; -
DR InterPro: IPR005594; YadaA.
DR Pfam: PF03895; YadaA; 1.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match          96.7%; Score 1883.5; DB 2; Length 594;
Best Local Similarity 97.6%; Pred. No. 2.5e-81;
Matches 373; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 2 RAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 61
   |||||
DB 213 RAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 272

QY 62 EVKIGAKTSVIKEDGKLVTKDKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
   |||||
DB 273 EVKIGAKTSVIKEDGKLVTKDKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 332

QY 122 GQTQADKFEFTVSGTNTVFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 181
   |||||
DB 333 GQTQADKFEFTVSGTNTVFASGKGTATVSKDDQGNITVMYDYNVGDALNVNQLNSGW 392

QY 182 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNIDIAIATMTPTQFSSV 241
   |||||
DB 393 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNIAGNNIEITRNGKNIDIAIATMTPTQFSSV 452

QY 242 SLGAGADAPTLSDVGD-ALNVGSKDNKPVRIITNVAPGVKEGDTNVVAQLKGVAQNLNRR 300
   |||||
DB 453 SLGAGADAPTLSDVGDALNVGSKDNKPVRIITNVAPGVKEGDTNVVAQLKGVAQNLNRR 512

QY 301 IDNVGDNARAGIAQAIATAGLVQAYLPKSNMATTGGCTYRGEAGYATGYSISDGGNWII 360
   |||||
DB 513 IDNVGDNARAGIAQAIATAGLVQAYLPKSNMATTGGCTYRGEAGYATGYSISDGGNWII 572

QY 361 KGTSAGNSRGRHFGASASVGYQW 382
   |||||
DB 573 KGTSAGNSRGRHFGASASVGYQW 594

RESULT 12
Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -
DR InterPro: IPR005594; YadaA.
DR Pfam: PF03895; YadaA; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2AC3A78F53D256 CRC64;

Query Match          96.7%; Score 1883.5; DB 2; Length 594;
Best Local Similarity 97.6%; Pred. No. 2.5e-81;
Matches 373; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 2 RAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 61
   |||||
DB 213 RAASVKDVLNAGWNIKGVPCTTASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNGKKT 272

QY 62 EVKIGAKTSVIKEDGKLVTKDKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
   |||||
DB 273 EVKIGAKTSVIKEDGKLVTKDKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 332
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QY 122 GQTGQADKFEFVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGDALNVQLNSGW 181
|||||
Db 333 GQTGQADKFEFVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGDALNVQLNSGW 392
|||||
QY 182 NLDKSAVAGSGKVIISGNVSPSKGMDVTVINAGNNIEITRNGKNIDIASTMTPOFSSV 241
|||||
Db 393 NLDKSAVAGSGKVIISGNVSPSKGMDVTVINAGNNIEITRNGKNIDIASTMTPOFSSV 452
|||||
QY 242 SLGACADAPTLSVDG-ALNVGSKKDNKPVRTITNVAPGVKGDVTVNAQLKGVAQNLR 300
|||||
Db 453 SLGACADAPTLSVDGEGALNVGSKDANKPVRTITNVAPGVKGDVTVNAQLKGVAQNLR 512
|||||
QY 301 IDNVGNARAGTAQAIATAGLVQAYLPKGSMAIIGGTYRGAGYAGYSSISDGNWII 360
|||||
Db 513 IDNVGNARAGTAQAIATAGLVQAYLPKGSMAIIGGTYRGAGYAGYSSISDGNWII 572
|||||
QY 361 KGTASGNSRGHFGASASVGYQW 382
|||||
Db 573 KGTASGNSRGHFGASASVGYQW 594
|||||

RESULT 13

Q9JPR8 PRELIMINARY; PRT; 599 AA.
ID Q9JPR8
AC Q9JPR8;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -;
DR EMBL: AF157608; AAK68869.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match 96.6%; Score 1881.5; DB 2; Length 599;
Best Local Similarity 97.6%; Pred. No. 3.1e-81;
Matches 373; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 2 RAASKVDLVNAGNNIKGVKPGTASDNVDFVITYDTVEFLSADTKTTTVNVESKNGKKT 61
|||||
Db 218 RAASKVDLVNAGNNIKGVKPGTASDNVDFVITYDTVEFLSADTKTTTVNVESKNGKKT 277
|||||
QY 62 EVKIGAKTSVKEKDGKLVTKGDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTITAN 121
|||||
Db 278 EVKIGAKTSVKEKDGKLVTKGDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTITAN 337
|||||

QY 122 GQTGQADKFEFVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGDALNVQLNSGW 181
|||||
Db 338 GQTGQADKFEFVTSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGDALNVQLNSGW 397
|||||
QY 182 NLDKSAVAGSGKVIISGNVSPSKGMDVTVINAGNNIEITRNGKNIDIASTMTPOFSSV 241
|||||
Db 398 NLDKSAVAGSGKVIISGNVSPSKGMDVTVINAGNNIEITRNGKNIDIASTMTPOFSSV 457
|||||
QY 242 SLGACADAPTLSVDG-DALNVGSKKDNKPVRTITNVAPGVKGDVTVNAQLKGVAQNLR 300
|||||
Db 458 SLGACADAPTLSVDGDKGALNVGSKDANKPVRTITNVAPGVKGDVTVNAQLKGVAQNLR 517
|||||
QY 301 IDNVGNARAGTAQAIATAGLVQAYLPKGSMAIIGGTYRGAGYAGYSSISDGNWII 360
|||||
Db 518 IDNVGNARAGTAQAIATAGLVQAYLPKGSMAIIGGTYRGAGYAGYSSISDGNWII 577
|||||
QY 361 KGTASGNSRGHFGASASVGYQW 382
|||||
Db 578 KGTASGNSRGHFGASASVGYQW 599
|||||

RESULT 14

Q9JPH7 PRELIMINARY; PRT; 594 AA.
ID Q9JPH7
AC Q9JPH7;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (Nhha outer membrane protein).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BZ198;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42517.1; -;
DR EMBL: AF226383; AAF42507.1; -;
DR EMBL: AF157604; AAK68865.1; -;
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62361 MW; 436BDDDED68263C5C CRC64;

Query Match 96.3%; Score 1874.5; DB 2; Length 594;
Best Local Similarity 97.4%; Pred. No. 6.6e-81;
Matches 372; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 2 RAASKVDLVNAGNNIKGVKPGTASDNVDFVITYDTVEFLSADTKTTTVNVESKNGKKT 61
|||||
Db 213 RAASKVDLVNAGNNIKGVKPGTASDNVDFVITYDTVEFLSADTKTTTVNVESKNGKKT 272
|||||
QY 62 EVKIGAKTSVKEKDGKLVTKGDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTITAN 121
|||||

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Db 273 EVKIGAKTSVIKEDGKLVTKGKDENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 332
Qy 122 GQTQADKFFETVSGTNVTFASGKGTATATVSKDQGNITVMYDYNVGDALNVQLNSGW 181
Db 333 GQTQADKFFETVSGTNVTFASGKGTATATVSKDQGNITVKYDYNVGDALNVQLNSGW 392
Qy 182 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDIIATSWTPQFSSV 241
Db 393 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDIIATSWTPQFSSV 452
Qy 242 SLGAGADAPTLISVDGD-ALNVGSKKDNKPVRIITNVAPGVKGDVTVNAQLKGVAQNLNNR 300
Db 453 SLGAGADAPTLISVDDEGALNVGSKDTPVRIITNVAPGVKGDVTVNAQLKGVAQNLNNR 512
Qy 301 IDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAGYAIYSSISDGGNWII 360
Db 513 IDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAGYAIYSSISDGGNWII 572
Qy 361 KGTSAGNSRGHFGASASVGYQW 382
Db 573 KGTSAGNSRGHFGASASVGYQW 594
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RESULT 15

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Q9JPR9 PRELIMINARY; PRT; 598 AA.
AC Q9JPR9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RA MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226382; AAF42531.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
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Query Match 96.3%; Score 1874.5; DB 2; Length 598;
Best Local Similarity 97.4%; Pred. No. 6.6e-81;
Matches 372; Conservative 1; Mismatches 8; Indels 1; Gaps 1;
Qy 2 RAASVKDVLNAGWNKIGKVPKGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 61
Db 217 RAASVKDVLNAGWNKIGKVPKGTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKKT 276
Qy 62 EVKIGAKTSVIKEDGKLVTKGKDENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 121
Db 277 EVKIGAKTSVIKEDGKLVTKGKDENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITAN 336
Qy 122 GQTQADKFFETVSGTNVTFASGKGTATATVSKDQGNITVMYDYNVGDALNVQLNSGW 181
Db 337 GQTQADKFFETVSGTNVTFASGKGTATATVSKDQGNITVKYDYNVGDALNVQLNSGW 396
Qy 182 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDIIATSWTPQFSSV 241
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Db 397 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNNAGNIEITRNKNIDIIATSWTPQFSSV 456
Qy 242 SLGAGADAPTLISVDGD-ALNVGSKKDNKPVRIITNVAPGVKGDVTVNAQLKGVAQNLNNR 300
Db 457 SLGAGADAPTLISVDDEGALNVGSKDTPVRIITNVAPGVKGDVTVNAQLKGVAQNLNNR 516
Qy 301 IDNVGDNARAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAGYAIYSSISDGGNWII 360
Db 517 IDNVGDNALAGIAQAIATAGLVQAYLPGKSMMAIGGTYRGEAGYAIYSSISDGGNWII 576
Qy 361 KGTSAGNSRGHFGASASVGYQW 382
Db 577 KGTSAGNSRGHFGASASVGYQW 598
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Search completed: October 6, 2003, 09:30:54
Job time : 29.0565 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:05:45 ; Search time 17.261 Seconds
(without alignments)
1848.329 Million cell updates/sec

Title: US-09-771-382-39

Perfect score: 1018

Sequence: 1 SANTLKAGNLKIKQFTYSL.....AGWRMKTTFANGQTQADKF 201

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1018	100.0	502	22 AAU06186	N. meningitidis PM
2	957.5	94.1	591	20 AAY27202	Amino acid sequenc
3	957.5	94.1	591	20 AAY23741	A surface protein
4	957.5	94.1	591	20 AAY23746	A surface protein
5	957.5	94.1	591	22 AAU06171	N. meningitidis PM
6	957.5	94.1	591	22 AAU06175	N. meningitidis EG
7	954.5	93.8	591	21 AAY57045	BAS029 amino acid
8	953.5	93.7	592	20 AAY23737	A surface protein
9	925.5	90.9	598	20 AAY23738	A surface protein

10	925.5	90.9	598	22 AAU06178	N. meningitidis BZ
11	925.5	90.9	599	20 AAY23743	A surface protein
12	925.5	90.9	599	22 AAU06176	N. meningitidis H3
13	923.5	90.7	594	20 AAY23739	A surface protein
14	923.5	90.7	594	22 AAU06179	N. meningitidis BZ
15	922.5	90.6	594	20 AAY23740	A surface protein
16	922.5	90.6	594	21 AAY57044	BAS029 amino acid
17	922.5	90.6	594	22 AAU06174	N. meningitidis EG
18	921.5	90.5	598	20 AAY23742	A surface protein
19	921.5	90.5	598	22 AAU06177	N. meningitidis H1
20	918.5	90.2	589	20 AAY23745	A surface protein
21	918.5	90.2	589	22 AAU06173	N. meningitidis P2
22	907.5	89.1	592	20 AAY23744	A surface protein
23	907.5	89.1	592	22 AAU06172	N. meningitidis H4
24	903.5	88.8	592	22 AAU06180	N. meningitidis Z2
25	898.5	88.3	592	20 AAY27203	Amino acid sequenc
26	864.5	84.9	512	22 AAU06182	N. meningitidis PM
27	831.5	81.7	604	22 AAU06181	N. meningitidis su
28	820.5	80.6	513	22 AAU06183	N. meningitidis H4
29	673.5	66.2	245	20 AAY27201	Amino acid sequenc
30	622.5	61.1	2353	17 AAR99393	Haemophilus adhesi
31	622.5	61.1	2411	21 AAB23860	Haemophilus influe
32	618	60.7	1098	17 AAR99392	Haemophilus adhesi
33	608.5	59.8	433	22 AAU06185	N. meningitidis PM
34	555	54.5	1094	21 AAB23858	Haemophilus influe
35	523.5	51.4	407	22 AAU06184	N. meningitidis PM
36	417	41.0	679	17 AAR99394	Haemophilus adhesi
37	417	41.0	679	21 AAB23855	Haemophilus influe
38	374	36.7	298	24 AAB30477	Haemophilus influe
39	327.5	32.2	1004	21 AAB23857	Haemophilus influe
40	320	31.4	1002	21 AAB23854	Haemophilus influe
41	311.5	30.6	1104	21 AAB23856	Haemophilus influe
42	311.5	30.6	1104	21 AAB23859	Haemophilus influe
43	279	27.4	56	21 AAB37827	Neisserial conserv
44	238	23.4	53	21 AAB37828	Neisserial conserv
45	201	19.7	2139	24 ABP71294	M. catarrhalis sur

ALIGNMENTS

RESULT 1
AAU06186
ID AAU06186 standard; Protein: 502 AA.
XX AC AAU06186;
XX AC
XX 24-OCT-2001 (first entry)
XX N. meningitidis PMC21 Nhha deletion mutant #4.
DE Surface antigen Nhha; meningococcal disease; meningitis vaccine;
KW mutant; mutain.
KW Neisseria meningitidis strain PMC21.
XX Synthetic.
OS
OS
FH Key Location/Qualifiers
FT Peptide 1..49
FT Protein /label= Signal_peptide
FT /label= Mature_Nhha_deletion_mutant.#4
FT /note= "Predicted mature protein, specifically claimed in claim 12"

DR WPI: 1999-418754/35.
DR N-PSDB; AAX85793.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 104-106; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 591 AA;

Query Match 94.1%; Score 957.5; DB 20; Length 591;
Best Local Similarity 85.7%; Pred. No. 8.3e-73;
Matches 198; Conservative 0; Mismatches 0; Indels 33; Gaps 3;

QY 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNPAKET 59
DB 109 TLKAGDNLKIKQNGTNTFTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNPAKET 168

QY 60 AGTNGDTTVHLNGIGSTLT-----RAASVKDVLNAGWNKIGV 97
DB 169 AGTNGDTTVHLNGIGSTLTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKIGV 228

QY 98 K-----NVDFVRYDYTVFEFLSADTKTTVNVESKDNGKTEVKIGAKTSVKEKDGKL 150
DB 229 KPGTTASDNVDFVRYDYTVFEFLSADTKTTVNVESKDNGKTEVKIGAKTSVKEKDGKL 288

QY 151 VTGKDKGENSGSTDEGEGLVTAKEVIDAVNKGAGWRMKTITANGQTQADKF 201
DB 289 VTGKDKGENSGSTDEGEGLVTAKEVIDAVNKGAGWRMKTITANGQTQADKF 339

RESULT 4
AAY23746
ID AAY23746 standard; Protein; 591 AA.
XX
AC AAY23746;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYOU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI: 1999-418754/35.
DR N-PSDB; AAX85798.
XX
PT Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections
XX
PS Claim 1; Page 127-128; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 591 AA;

Query Match 94.1%; Score 957.5; DB 20; Length 591;
Best Local Similarity 85.7%; Pred. No. 8.3e-73;
Matches 198; Conservative 0; Mismatches 0; Indels 33; Gaps 3;

QY 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNPAKET 59
DB 109 TLKAGDNLKIKQNGTNTFTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNPAKET 168

QY 60 AGTNGDTTVHLNGIGSTLT-----RAASVKDVLNAGWNKIGV 97
DB 169 AGTNGDTTVHLNGIGSTLTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKIGV 228

QY 98 K-----NVDFVRYDYTVFEFLSADTKTTVNVESKDNGKTEVKIGAKTSVKEKDGKL 150
DB 229 KPGTTASDNVDFVRYDYTVFEFLSADTKTTVNVESKDNGKTEVKIGAKTSVKEKDGKL 288

QY 151 VTGKDKGENSGSTDEGEGLVTAKEVIDAVNKGAGWRMKTITANGQTQADKF 201
DB 289 VTGKDKGENSGSTDEGEGLVTAKEVIDAVNKGAGWRMKTITANGQTQADKF 339

RESULT 5
AAU06171
ID AAU06171 standard; Protein; 591 AA.
XX
AC AAU06171;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
XX
KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain PMC21.
XX
FH Key Location/Qualifiers
FH Peptide 1..51
FH /label= Signal_peptide
FH Region 1..50
FH /label= C1
FH /note= "Conserved region 1"
FH Region 51..108
FH /label= V1
FH /note= "Variable region 1"
FH Protein 52..591
FH /label= Mature_NhhA
FH /note= "Predicted mature protein, specifically
FH claimed in claim 12"
FH Region 109..120
FH /label= C2
FH /note= "Conserved region 2"
FH Region 121..124
FH /label= V2
FH /note= "Variable region 2"
FH Region 125..188
FH /label= C3
FH /note= "Conserved region 3"

FT	Region	189..210 /label= V3 /note= "Variable region 3"
FT	Region	211..229 /label= C4 /note= "Conserved region 4"
FT	Region	230..236 /label= V4 /note= "Variable region 4"
FT	Region	237..591 /label= C5 /note= "Conserved region 5"
XX	W0200155182-A1.	
PN	02-AUG-2001.	
XX	25-JAN-2001; 2001WO-AU00069.	
PF	25-JAN-2000; 2000US-0177917.	
XX	(UYQU) UNIV QUEENSLAND.	
PA	Peak IRA, Jennings MP;	
PI	WPI; 2001-488774/53.	
DR	N-PSDB; AAS09161.	
DR	New Nhha surface antigen polypeptides and polynucleotides from	
PT	Neisseria meningitidis, useful in producing vaccines for treating or	
PT	preventing broad spectrum of Neisseria meningitidis -	
XX	Claim 9; Fig 1; 9lpp; English.	
PS	The present invention relates to the isolation of novel Neisseria	
XX	meningitidis mutant polypeptides of the surface antigen Nhha	
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are	
CC	characterised by deletions of non-conserved amino acids, particularly	
CC	the deletion of variable regions. The deletion mutants are useful in	
CC	diagnostics, therapeutic and prophylactic vaccines against a broader	
CC	spectrum of N. meningitidis, and in designing and/or screening of	
CC	medicaments. The mutant proteins when used as a vaccine can effectively	
CC	immunise against a broader spectrum of N. meningitidis strains than	
CC	would be expected from a corresponding wild-type surface antigen.	
CC	The present sequence representing the wild type surface antigen Nhha	
CC	from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences	
CC	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in	
XX	the present invention.	
XX	Sequence 591 AA;	
SQ	Query Match 94.1%; Score 957.5; DB 22; Length 591; Best Local Similarity 85.7%; Pred. No. 8.3e-73; Matches 199; Conservative 0; Mismatches 33; Gaps 3;	
QY	4 TLKAGDNLKIQTQ-----FTYSLKLDLTDLTSVGTSEKLSFSANGKNVNITSDTKGLNFAKET 59	
Dd	109 TLKAGDNLKIQTGNTFTYSELKKDLTDLTSVGTSEKLSFSANGKNVNITSDTKGLNFAKET 168	
QY	60 AGTNGDTTVHLNGIGSTLTD-----RAASYKDVNLNAGWNIKGV 97	
Dd	169 AGTNGDTTVHLNGIGSTLTDLLNTGATTNVNDNVTDDEKKAASVKVDVLNAGWNIKGV 228	
QY	98 K-----NVDFVRTYDTVEFLSADTKTTTNVESKDNGKKTVEKVIKAKTSVIEKGDKL 150	
Dd	229 KPGETASDNVDYRTYDTVEFLSADTKTTTNVESKDNGKKTVEKVIKAKTSVIEKGDKL 288	
QY	151 VTCKDKGENSGSSDTEGEGLYTAKEVIDAVNKAGWRMKT---TANGOTGOADKF 201	
Dd	289 VTCKDKGENSGSSDTEGEGLYTAKEVIDAVNKAGWRMKT---TANGOTGOADKF 339	

RESULT 6

CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain EG329 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.

XX SQ Sequence 591 AA;

Query Match 94.1%; Score 957.5; DB 22; Length 591;
Best Local Similarity 85.7%; Pred. No. 8.3e-73;
Matches 198; Conservative 0; Mismatches 0; Indels 33; Gaps 3;

Qy 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSGTEKLSFANGKVNITSDTKGLNFAKET 59
||||| 109 TLKAGDNLKIKQNGSNFTYSLKKDLTDLTSGTEKLSFANGKVNITSDTKGLNFAKET 168
Qy 60 AGTNGDTPVHLNGIGSTLTD-----RAASVKDVLNAGWNKIGV 97
||||| 169 AGTNGDTPVHLNGIGSTLTDLLNTGATNTVNDVDEKKRAASVKDVLNAGWNKIGV 228
Qy 98 K-----NVDVFTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKL 150
| 229 KPGTTASDNVDVFTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKL 288
Qy 151 VTGDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKF 201
||||| 289 VTGDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKF 339

RESULT 7
AAV57045
ID AAV57045 standard; Protein; 591 AA.
XX AC AAV57045;
XX 21-FEB-2000 (first entry)
XX BASB029 amino acid sequence from N. meningitidis strain H44/76.
DE BASB029; *Neisseria meningitidis*; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX *Neisseria meningitidis*.

Key	Location/Qualifiers
FT	Misc-difference 90 /note= "Encoded by AAT"
FT	Misc-difference 92 /note= "Encoded by GAT"
FT	Misc-difference 98 /note= "Encoded by AAC"
FT	Misc-difference 108 /note= "Encoded by AATC"
FT	Misc-difference 123 /note= "Encoded by ACA"
FT	Misc-difference 269 /note= "Encoded by AAA"
FT	Misc-difference 389 /note= "Encoded by CGT"

XX WO9958683-A2.
XX 18-NOV-1999.
XX 07-MAY-1999; 99WO-EP03255.
XX 13-MAY-1998; 98GB-0010276.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX Ruelle J;
XX WPI; 2000-053103/04.
DR N-PSDB; AAZ39865.

XX New polypeptide from *Neisseria meningitidis* useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal -
XX Claim 4; Fig 2; 74pp; English.

XX This is the *Neisseria meningitidis* BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC *Haemophilus influenzae* surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
CC polypeptide sequences (AAV57044-57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*
CC meningitidis infection in a mammal. Compositions containing an immune
CC polynucleotides and polypeptides are useful for generating an antibody
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with *Neisseria*
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.

XX SQ Sequence 591 AA;

Query Match 93.8%; Score 954.5; DB 21; Length 591;
Best Local Similarity 85.3%; Pred. No. 1.5e-72;
Matches 197; Conservative 1; Mismatches 0; Indels 33; Gaps 3;

Qy 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSGTEKLSFANGKVNITSDTKGLNFAKET 59
||||| 109 TLKAGDNLKIKQNGSNFTYSLKKDLTDLTSGTEKLSFANGKVNITSDTKGLNFAKET 168
Qy 60 AGTNGDTPVHLNGIGSTLTD-----RAASVKDVLNAGWNKIGV 97
||||| 169 AGTNGDTPVHLNGIGSTLTDLLNTGATNTVNDVDEKKRAASVKDVLNAGWNKIGV 228
Qy 98 K-----NVDVFTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKL 150
| 229 KPGTTASDNVDVFTYDVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIREKDGKL 288
Qy 151 VTGDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKF 201
||||| 289 VTGDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKF 339

RESULT 8
AAV23737
ID AAV23737 standard; Protein; 592 AA.
XX AC AAV23737;
XX 08-SEP-1999 (first entry)
XX A surface protein of *Neisseria meningitidis*.
DE Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX *Neisseria meningitidis*.
XX WO9931132-A1.
XX 24-JUN-1999.
XX 14-DEC-1998; 98WO-AU01031.
XX 12-DEC-1997; 97GB-0026398.
XX

PA (ISIS-) ISIS INNOVATION LTD.
 XX (UYOU) UNIV QUEENSLAND.
 XX Jennings MP, Moxon ER, Peak IRA;
 XX
 DR WPI: 1999-418754/35.
 DR N-PSDB; AAX85788.
 XX
 XX Neisseria meningitidis surface proteins useful for treating N.
 PT meningitidis infections
 XX
 PS Claim 1; Page 86-87; 132pp; English.
 XX
 CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 XX
 SQ Sequence 592 AA;
 Query Match 93.7%; Score 953.5; DB 20; Length 592;
 Best Local Similarity 85.3%; Pred. No. 1.8e-72;
 Matches 197; Conservative 0; Mismatches 1; Indels 33; Gaps 3;
 QY 4 TLKAGDNLKIQ-----FTYSLKKDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKET 59
 DB 110 TLKAGDNLKIQKONGFTYSLKKDLTDLTSVGTSEKLSFANGKNVITSDTKGLNFAKET 169
 QY 60 AGTNGDITVHLNGIGSTLTD-----RAASVKDVLNAGWNIKV 97
 DB 170 AGTNGDITVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKV 229
 QY 98 K-----NVDFVRYDYVFEFLSADTKTTTVNVESKDNKGKTEVKIGARTSVIKEKDGKL 150
 DB 230 KPGTTASDNVDVRYDYVFEFLSADTKTTTVNVESKDNKGKTEVKIGARTSVIKEKDGKL 289
 QY 151 VTGKDKGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKF 201
 DB 290 VTGKDKGENSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKF 340
 RESULT 9
 AAY23738
 ID AAY23738 standard; Protein; 598 AA.
 AC AAY23738;
 XX
 XX 08-SEP-1999 (first entry)
 XX
 DE A surface protein of Neisseria meningitidis.
 XX
 KW Surface protein; surface glycoprotein; infection; vaccine;
 KW immunoreactive peptide.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO9931132-A1.
 XX
 XX 24-JUN-1999.
 PD
 PF 14-DEC-1998; 98WO-AU01031.
 XX
 PR 12-DEC-1997; 97GB-0026398.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA (UYOU) UNIV QUEENSLAND.
 XX
 XX Jennings MP, Moxon ER, Peak IRA;

XX WPI: 1999-418754/35.
 DR N-PSDB; AAX85790.
 XX
 XX Neisseria meningitidis surface proteins useful for treating N.
 PT meningitidis infections
 XX
 PS Claim 1; Page 91-93; 132pp; English.
 XX
 CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 XX
 SQ Sequence 598 AA;
 Query Match 90.9%; Score 925.5; DB 20; Length 598;
 Best Local Similarity 79.8%; Pred. No. 4.3e-70;
 Matches 194; Conservative 1; Mismatches 5; Indels 43; Gaps 3;
 QY 2 ANTLKAGDNLKIQ-----FTYSLKKDLTDLTSVGTSEKLSFANGKNVIT 47
 DB 103 AITLKAGDNLKIQKONTNENTNDSSFTYSLKKDLTDLTSVGTSEKLSFANGKNVIT 162
 QY 48 SDTKGLNFAKETAGTNGDITVHLNGIGSTLTD-----RAASVK 85
 DB 163 SDTKGLNFAKETAGTNGDITVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKRAASVK 222
 QY 86 DVLNAGWNIKV-----NVDFVRYDYVFEFLSADTKTTTVNVESKDNKGKTEVKICA 138
 DB 223 DVLNAGWNIKVGPCTTASDNVDVRYDYVFEFLSADTKTTTVNVESKDNKGKTEVKICA 282
 QY 139 KTSVKEKDGKLVTKGKGENSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQOA 198
 DB 283 KTSVKEKDGKLVTKGKGENSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQOA 342
 QY 199 DKF 201
 DB 343 DKF 345
 RESULT 10
 AAU06178
 ID AAU06178 standard; Protein; 598 AA.
 XX
 AC AAU06178;
 XX
 XX 24-OCT-2001 (first entry)
 XX
 DE N. meningitidis Bz10 surface antigen NhhA polypeptide sequence.
 XX
 KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
 XX
 OS Neisseria meningitidis strain Bz10.
 XX
 FH Key Location/Qualifiers
 FT Region 1..50
 FT /label= C1
 FT /note= "Conserved region 1"
 FT Region 51..104
 FT /label= V1
 FT /note= "Variable region 1"
 FT Region 105..116
 FT /label= C2
 FT /note= "Conserved region 2"
 FT Region 117..130
 FT /label= V2
 FT /note= "Variable region 2"

Qy 201 F 201
Db 346 F 346

RESULT 12
AAU06176
ID AAU06176 standard; Protein: 599 AA.
XX AC AAU06176;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis H38 surface antigen NhhA polypeptide sequence.
XX KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain H38.
XX FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..105
FT /label= V1
FT /note= "Variable region 1"
FT Region 106..117
FT /label= C2
FT /note= "Conserved region 2"
FT Region 118..131
FT /label= V2
FT /note= "Variable region 2"
FT Region 132..195
FT /label= C3
FT /note= "Conserved region 3"
FT Region 196..217
FT /label= V3
FT /note= "Variable region 3"
FT Region 218..236
FT /label= C4
FT /note= "Conserved region 4"
FT Region 237..243
FT /label= V4
FT /note= "Variable region 4"
FT Region 244..599
FT /label= C5
FT /note= "Conserved region 5"
XX WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09166.
XX New NhhA surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 9lpp; English.
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen NhhA
XX (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen NhhA
CC from N. meningitidis strain H38 is 1 of 10 NhhA polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX SQ Sequence 599 AA;
Query Match 90.9%; Score 925.5; DB 22; Length 599;
Best Local Similarity 80.1%; Pred. No. 4.3e-70;
Matches 193; Conservative 1; Mismatches 4; Indels 43; Gaps 3;
Qy 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTKEKLSFSGANGKVNITSD 49
Db 106 TLKAGDNLKIKQNTKNTNNTNDSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSD 165
Qy 50 TKGLNFAKETAGTNGDTTVHLNGIGSTLTD-----RAASVKDV 87
Db 166 TKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTNTNDVDDKKRAASVKDV 225
Qy 88 LNAGWNKIGVK-----NVDFVRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKT 140
Db 226 LNAGWNKIGVKPGTTASDNVDFVHTYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKT 285
Qy 141 SVIKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADK 200
Db 286 SVIKEKDKGLVTGKDKGENSGSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADK 345
Qy 201 F 201
Db 346 F 346
RESULT 13
AAU23739
ID AAU23739 standard; Protein: 594 AA.
XX AC AAU23739;
XX DT 08-SEP-1999 (first entry)
XX DE A surface protein of Neisseria meningitidis.
XX KW Surface protein; surface glycoprotein; infection; vaccine;
XX KW Immunoreactive peptide.
XX OS Neisseria meningitidis.
XX PN WO9931132-A1.
XX PD 24-JUN-1999.
XX PF 14-DEC-1998; 98WO-AU01031.
XX PR 12-DEC-1997; 97GB-0026398.
XX PA (ISIS-) ISIS INNOVATION LTD.
XX PA (UYQU) UNIV QUEENSLAND.
XX PI Jennings MP, Moxon ER, Peak IRA;
XX WPI; 1999-418754/35.
XX N-PSDB; AAX85791.
XX PT Neisseria meningitidis surface proteins useful for treating N.
XX PT meningitidis infections
XX

XX	Surface protein; surface glycoprotein; infection; vaccine;
KW	immunoreactive peptide.
XX	
OS	Neisseria meningitidis.
PN	W05931132-A1.
XX	
PD	24-JUN-1999.
XX	
XX	14-DEC-1998; 98WO-AU01031.
PF	
XX	
XX	12-DEC-1997; 97GB-0026398.
PR	
XX	
XX	(ISIS-) ISIS INNOVATION LTD.
PA	(UYOU) UNIV QUEENSLAND.
PA	
XX	
XX	Jennings MP, Moxon ER, Peak IRA;
PI	
XX	
XX	WPI; 1999-418754/35.
DR	
DR	N-PSDB; AAX85792.
XX	
PT	Neisseria meningitidis surface proteins useful for treating N.
PT	meningitidis infections
XX	
XX	Claim 1; Page 100-101; 132pp; English.
PS	
XX	
CC	The present sequence represents a surface protein of Neisseria
CC	meningitidis which is approximately 62 kDa. The N. meningitidis
CC	surface glycoproteins, nucleic acids, the primers and optional
CC	a thermostable polymerase, or antibodies are useful in a kit f
CC	the detection or diagnosis of N. meningitidis infection in hum
CC	The N. meningitidis surface glycoproteins can also be used to
CC	prevent or treat N. meningitidis infection in humans, especial
CC	in the form of vaccines. The proteins and antibodies can also
CC	be used to identify immunoreactive peptides.
XX	
XX	Sequence 594 AA;
SQ	

; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match 94.1%; Score 957.5; DB 3; Length 591;
Best Local Similarity 85.7%; Pred. No. 2.4e-84;
Matches 198; Conservative 0; Mismatches 0; Indels 33; Gaps 3;

Qy 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKET 59
Db 109 TLKAGDNLKIKQNGTNTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKET 168
Qy 60 AGTNGDITVHLNGIGSLTLD-----RAASVKDVLNAGNKGK 97
Db 169 AGTNGDITVHLNGIGSLTLDLLNTGATNTVNDNVTDDEKRAASVKDVLNAGNKGK 228
Qy 98 K-----NVDVFRTYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDGKL 150
Db 229 KPGTTASDNVDVFRTYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDGKL 288
Qy 151 VTGKDKGENSGSTDEGGLVTAKEVIDAVNKGAGWRMKTITTTANGOTGOADKF 201
Db 289 VTGKDKGENSGSTDEGGLVTAKEVIDAVNKGAGWRMKTITTTANGOTGOADKF 339

RESULT 3
US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11

Query Match 94.1%; Score 957.5; DB 4; Length 591;
Best Local Similarity 85.7%; Pred. No. 2.4e-84;
Matches 198; Conservative 0; Mismatches 0; Indels 33; Gaps 3;

Qy 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKET 59
Db 109 TLKAGDNLKIKQNGTNTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKET 168
Qy 60 AGTNGDITVHLNGIGSLTLD-----RAASVKDVLNAGNKGK 97
Db 169 AGTNGDITVHLNGIGSLTLDLLNTGATNTVNDNVTDDEKRAASVKDVLNAGNKGK 228
Qy 98 K-----NVDVFRTYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDGKL 150
Db 229 KPGTTASDNVDVFRTYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDGKL 288
Qy 151 VTGKDKGENSGSTDEGGLVTAKEVIDAVNKGAGWRMKTITTTANGOTGOADKF 201
Db 289 VTGKDKGENSGSTDEGGLVTAKEVIDAVNKGAGWRMKTITTTANGOTGOADKF 339

Qy 60 AGTNGDITVHLNGIGSLTLD-----RAASVKDVLNAGNKGK 97
Db 169 AGTNGDITVHLNGIGSLTLDLLNTGATNTVNDNVTDDEKRAASVKDVLNAGNKGK 228
Qy 98 K-----NVDVFRTYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDGKL 150
Db 229 KPGTTASDNVDVFRTYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDGKL 288
Qy 151 VTGKDKGENSGSTDEGGLVTAKEVIDAVNKGAGWRMKTITTTANGOTGOADKF 201
Db 289 VTGKDKGENSGSTDEGGLVTAKEVIDAVNKGAGWRMKTITTTANGOTGOADKF 339

RESULT 4
US-09-669-974-21
; Sequence 21, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 94.1%; Score 957.5; DB 4; Length 591;
Best Local Similarity 85.7%; Pred. No. 2.4e-84;
Matches 198; Conservative 0; Mismatches 0; Indels 33; Gaps 3;

Qy 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKET 59
Db 109 TLKAGDNLKIKQNGTNTYSLKKDLTDLTSVGTSEKLSFSAANGKVNITSDTKGLNFAKET 168
Qy 60 AGTNGDITVHLNGIGSLTLD-----RAASVKDVLNAGNKGK 97
Db 169 AGTNGDITVHLNGIGSLTLDLLNTGATNTVNDNVTDDEKRAASVKDVLNAGNKGK 228
Qy 98 K-----NVDVFRTYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDGKL 150
Db 229 KPGTTASDNVDVFRTYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDGKL 288
Qy 151 VTGKDKGENSGSTDEGGLVTAKEVIDAVNKGAGWRMKTITTTANGOTGOADKF 201
Db 289 VTGKDKGENSGSTDEGGLVTAKEVIDAVNKGAGWRMKTITTTANGOTGOADKF 339

RESULT 5
US-09-377-155-2
; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19

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; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRP
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

```

Query Match	93.7%	Score	953.5;	DB	3;	Length	592;	
Best Local Similarity	85.3%;	Pred.	No. 5.8e-84;					
Matches	197; Conservative	0;	Mismatches	1;	Indels	33;	Gaps	3;

QY	4	TLKAGDNLKIKQ-----FTYSLKLDLTLSVGTGTEKLFSANGNKVNITSDTKGLNPAKET	59
Db	110	TLKAGDNLKIQNGTNTFYSLKKDLTDLTLSVGTGTEKLFSANGNKVNITSDTKGLNPAKET	169
QY	60	AGTNGDTTVHLNGIGSTPLD-----RAASVKVDVLNAGWNITKV	97
Db	170	AGTNGDTTVHLNGIGSTPLDTLLNTGATTNTVNDNVTDDEKKRAASVKVDVLNAGWNITKV	229
QY	98	K-----NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKGDKL	150
Db	230	KPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKATEVKIGKTSVIKEKGDKL	289
QY	151	VTCKDKGENSGSSDDEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKF	201
Db	290	VTCKDKGENSGSSDDEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKF	340

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RESULT 6
US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 6331173
; General Information:
; APPLICANT: PEAK, Ian Richard Ansell
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/09/37
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 97263
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO. 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2

```

Query Match	93.7%	Score 953.5	DB 4	Length 592
Best Local Similarity	85.3%	Pred. No. 5.8e-84		
Matches 197	Conservative	0	Mismatches 1	Indels 33
			Gaps	3

QY	4	TLKAGDNLKIKQ----	FTYSLKKDLTDLTSVGTGTEKLSF	SANGNKVNITSDTKGLNFAKET	59
Db	110	TLKAGDNLKIKQNGFT	YSLKKDLTDLTSVGTGTEKLSF	SANGNKVNITSDTKGLNFAKET	169
QY	60	AGTNGDVTVHLNGIG	STLTD-----	RAASYKDVNLNAGWNKGV	97
Db	170	AGTNGDVTVHLNGIG	STLTDLLNTGATTVNTD	NVTDDKKRAASYKDVNLNAGWNKGV	229
QY	98	K-----	NWDFVRTYDVTVEFLS	ADTKTTTVNVESKDNGKKTEVWIGAKTSV	150

Db	230	KPGTTASDNVDVFRVYDTVFELSDTKTTTVNVEKDKNGKKTEVKGKTSVIKEKDGL	289
QY	151	VTGKDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKF	201
Db	290	VTGKDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKF	340

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RESULT 7
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

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Query Match          90.9%; Score 925.5; DB 3; Length 598;
Best Local Similarity 79.8%; Pred. No. 3e-81;
Matches 194; Conservative 1; Mismatches 5; Indels 43; Gaps 3;

QY      2  ANTLLKAGDNLKIQ-----FTYSLKKDLTDLTSVTEKLSFSGANGKVNIT 47
DB      103 AITLLKAGDNLKIQNTNENTNDSSFTYSLKKDLTDLTSVTEKLSFSGANGKVNIT 162

QY      48 SDTKGLNFAKETAGTNGDPTVHNLNGIGSTLTD-----RAASVK 85
DB      163 SDTKGLNFAKETAGTNGDPTVHNLNGIGSTLTDLLNTGATNTVNDNVTDDEKKRAASVK 222

QY      86 DVLNAGWNKIGVK-----NVDFVRTYDFVEFLSADTKTTTVNVESKONGKKTVEVKIGA 138
DB      223 DVLNAGWNKIGVKPGTASNDVDFVRTYDFVEFLSADTKTTTVNVESKONGKKTVEVKIGA 282

QY      139 KTSVIREKDGKLVTKGDKGNGSGSTDEGEGLVTAKEVIDAVNKGWRMKTTTTANGOTGOA 198
DB      283 KTSVIREKDGKLVTKGDKGNGSGSTDEGEGLVTAKEVIDAVNKGWRMKTTTTANGOTGOA 342

QY      199 DKF 201
DB      343 DKF 345

RESULT 8
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2

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RESULT 8
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2

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; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match
Best Local Similarity 90.7%; Score 923.5; DB 3; Length 594;
Matches 194; Conservative 0; Mismatches 6; Indels 39; Gaps 3;

QY 2 ANTLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSGANGKVNITSDTK 51
Db 103 AITLKAGDNLKIKQNTNENTNDSSFTYSLKKDLTDLTSVETSEKLSFGANGKVNITSDTK 162
QY 52 GLNFAKETAGTNGDPTVHLNGIGSTLTD-----RAASVKDVLN 89
Db 163 GLNFAKETAGTNGDPTVHLNGIGSTLTDPLLTNGATTNTVNDVDEKKRAASVKDVLN 222
QY 90 AGWNKGVK-----NVDFVRYDTVEFLSADTKTTTVNVESKONGKKEVKIGAKTSV 142
Db 223 AGWNKGVKPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKKEVKIGAKTSV 282
QY 143 IREKDGKLVTKDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKF 201
Db 283 IREKDGKLVTKDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKF 341

RESULT 12
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1997-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match
Best Local Similarity 90.7%; Score 923.5; DB 4; Length 594;
Matches 194; Conservative 0; Mismatches 6; Indels 39; Gaps 3;

QY 2 ANTLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSGANGKVNITSDTK 51
Db 103 AITLKAGDNLKIKQNTNENTNDSSFTYSLKKDLTDLTSVETSEKLSFGANGKVNITSDTK 162
QY 52 GLNFAKETAGTNGDPTVHLNGIGSTLTD-----RAASVKDVLN 89
Db 163 GLNFAKETAGTNGDPTVHLNGIGSTLTDPLLTNGATTNTVNDVDEKKRAASVKDVLN 222
QY 90 AGWNKGVK-----NVDFVRYDTVEFLSADTKTTTVNVESKONGKKEVKIGAKTSV 142
Db 223 AGWNKGVKPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKKEVKIGAKTSV 142
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match
Best Local Similarity 90.6%; Score 922.5; DB 3; Length 594;
Matches 192; Conservative 3; Mismatches 3; Indels 39; Gaps 3;

QY 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGL 53
Db 105 TLKAGDNLKIKQNTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGL 164
QY 54 NFAKETAGTNGDPTVHLNGIGSTLTD-----RAASVKDVLNAG 91
Db 165 NFAKETAGTNGDPTVHLNGIGSTLTDPLLTNGATTNTVNDVDEKKRAASVKDVLNAG 224
QY 92 WNKGVK-----NVDFVRYDTVEFLSADTKTTTVNVESKONGKKEVKIGAKTSV 144
Db 225 WNKGVKPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKKEVKIGAKTSV 284
QY 145 EKDGLVTKDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKF 201
Db 285 EKDGLVTKDKGSGSSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGOTGQADKF 341

RESULT 14
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1997-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
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Search completed: October 6, 2003, 09:36:01
Job time : 6.37514 secs

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; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match          90.6%; Score 922.5; DB 4; Length 594;
Best Local Similarity 81.0%; Pred. No. 5.8e-81;
Matches 192; Conservative 3; Mismatches 3; Indels 39; Gaps 3;

QY 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSANGNKVNITSDTKGL 53
Db 105 TLKAGDNLKIKQNTNENTNASSFTYSLKKDLTDLTSVGTSEKLSFSANGNKVNITSDTKGL 164
QY 54 NFAKETAGTNGDTPVHLNGIGSTLTD-----RAASVKDVLNAG 91
Db 165 NFAKTAETNGDTPVHLNGIGSTLTDLLNTGATTNVDNNDVDEKKRAASVKDVLNAG 224
QY 92 WNIKGVK-----NVDFVRTYDTVEFLSADTKTTNNVESKDNGKKTEVKIGAKTSVIK 144
Db 225 WNIKGVKPGTTASDNVDVVRTYDTVEFLSADTKTTNNVESKDNGKKRTVEKIGAKTSVIK 284
QY 145 EKDGKLVTKDKGSGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKF 201
Db 285 EKDGKLVTKDKGSDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKF 341
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RESULT 15
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13
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Query Match          90.5%; Score 921.5; DB 3; Length 598;
Best Local Similarity 79.8%; Pred. No. 7.3e-81;
Matches 194; Conservative 0; Mismatches 6; Indels 43; Gaps 3;

QY 2 ANTILKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSANGNKVNIT 47
Db 103 ANTILKAGDNLKIKQNTNENTNDSFTYSLKKDLTDLTSVGTSEKLSFGANGNKVNIT 162
QY 48 SDTKGLNFAKETAGTNGDTPVHLNGIGSTLTD-----RAASVK 85
Db 163 SDTKGLNFAKETAGTNGDTPVHLNGIGSTLTDLLNTGATTNVDNNDVDEKKRAASVK 222
QY 86 DVLNAGWNKIGVK-----NVDFVRTYDTVEFLSADTKTTNNVESKDNGKKTEVKIGA 138
Db 223 DVLNAGWNKIGVKPGTTASDNVDVVRTYDTVEFLSADTKTTNNVESKDNGKKTEVKIGA 282
QY 139 KTSVIKEKDKGLVTKDKGSGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQA 198
Db 283 KTSVIKEKDKGLVTKDKGSGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQA 342
QY 199 DKF 201
Db 343 DKF 345
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:35 ; Search time 5.75367 Seconds
(without alignments)
3359.577 Million cell updates/sec

Title: US-09-771-382-39
Perfect score: 1018
Sequence: 1 SANTLKAGDNLKIKQFTYSL.....AGWRMKTTFANGTGQADKF 201
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	957.5	94.1	591	2 G81133	adhesin NMB0992 [i
2	903.5	88.8	592	2 A81888	probable surface f
3	374	36.7	298	2 I64138	adhesin homolog HI
4	116.5	11.4	507	2 S33192	phase-1 flagellin
5	116.5	11.4	508	2 A53465	phase 1 flagellin
6	113	11.1	585	2 F90961	flagellin [importe
7	113	11.1	585	2 F85809	hypothetical prote
8	112.5	11.1	462	2 S61332	IgA-specific metal
9	112	11.0	1336	2 A43855	high-molecular-we
10	109.5	10.8	584	2 C48658	flagellin - Escher
11	109.5	10.8	920	2 I40614	surface array prot
12	108.5	10.7	569	2 T39577	hypothetical prote
13	105	10.3	621	2 H71713	glucose inhibited
14	105	10.3	1109	2 A56143	surface-array prot
15	105	10.3	1477	2 B43855	high-molecular-we
16	104.5	10.3	462	2 AH1184	wall associated pr
17	104.5	10.3	733	2 T23507	hypothetical prote
18	104.5	10.3	1635	2 AI0452	hemolysin [importe
19	104.5	10.3	2044	2 AB1180	probable peptidogl
20	103	10.1	504	2 S33194	phase-1 flagellin
21	102	10.0	504	2 S33186	phase-1 flagellin
22	102	10.0	595	2 A48658	flagellin - Escher
23	102	10.0	1020	2 B86414	hypothetical prote
24	101.5	10.0	653	2 T03319	gene 112 protein -
25	100.5	9.9	550	2 S44980	flagellin - Shigel
26	100.5	9.9	2551	2 B98047	hypothetical prote
27	100	9.8	441	2 A97000	pectate lyase rela
28	99.5	9.8	1386	2 AC1533	surface protein (L
29	99	9.7	796	2 A90541	hypothetical prote

protein F59B2.12 [conserved hypothet
hypothetical prote
probable lipoprote
polymorphic outer
polymorphic membra
S-layer protein pr
flagellin - Escher
peroxidase (EC 1.1
phase-1 flagellin
S-layer protein -
cell wall-associat
phase-1 flagellin
internalin protein
hypothetical prote

ALIGNMENTS

RESULT 1
G81133
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <TET>
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

Query Match 94.1%; Score 957.5; DB 2; Length 591;
Best Local Similarity 85.7%; Pred. No. 6.4e-60;
Matches 198; Conservative 0; Mismatches 0; Indels 33; Gaps 3;
Qy 4 TLKAGDNLKIKQ----FTYSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKET 59
Db 109 TLKAGDNLKIKQNGTNTFTYSLKKDLTDLTSVGTEKLSFSANGKNVNITSDTKGLNFAKET 168
Qy 60 AGTNGDTTVHLNGIGSTLTD-----RAASVKDVLNAGWNITKV 97
Db 169 AGTNGDTTVHLNGIGSTLTDLTLLTGATTNVTNDVDEKKRAASVKDVLNAGWNITKV 228
Qy 98 K-----NVDFVRTVDTVEFLSADTKTTVNYESKDNKKTEVKIGAKTSVKEKDGKL 150
Db 229 KPFTTASDNVDFVRTVDTVEFLSADTKTTVNYESKDNKKTEVKIGAKTSVKEKDGKL 288
Qy 151 VTCKDKGSGSSDEGEGLVTAKEVIDAVNKGWRMKTTFANGTGQADKF 201
Db 289 VTCKDKGSGSSDEGEGLVTAKEVIDAVNKGWRMKTTFANGTGQADKF 339

RESULT 2
A81888
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain z
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81888
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: A81888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CA84461.1; PID:g737989
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1200

Query Match 88.8%; Score 903.5; DB 2; Length 592;
Best Local Similarity 79.3%; Pred. No. 4e-56; Indels 39; Gaps 3;
Matches 188; Conservative 3; Mismatches 7;
QY 4 TLKAGDNLKIRQ-----FYSYSLKKDLTSLVSGTEKLSFSAANGKNVITSDTKGL 53
DB 103 TLKAGDNLKIRQNTNENNTASSFYSLKKDLTGLINTEKLSFGANGKNVITSDTKGL 162
QY 54 NFAKETAGTNGDVTVHLNGIGSTLTD-----RAASVKDVLNAGWN 93
DB 163 NFAKETAGTNGDVTVHLNGIGSTLTDLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWN 222
QY 94 IKGVK-----NVDFVRYDYVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVIK 144
DB 223 IKGVKGTGTTQSENVDVRYDYVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVIK 282
QY 145 EKDGKLVTKDGKNGSGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGQADKF 201
DB 283 EKDGKLVTKGKNGSGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGQADKF 339
RESULT 3
I64138
adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C:Accession: I64138
R:Flaichmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gayney, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: I64138
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <TIGR>
A:Cross-references: GB:U32846; GB:U42023; NID:g1574588; PID:g1574589; TIGR:H11732

Query Match 36.7%; Score 374; DB 2; Length 298;
Best Local Similarity 44.4%; Pred. No. 3e-19;
Matches 92; Conservative 21; Mismatches 48; Indels 46; Gaps 6;
QY 4 TLKAGDNLKI-----KQFTYSLKKDLTSLVSGTEKLSFSAN-----GNKNVITSDT 50
DB 88 TLKAGNLKAKLDQGGKSVTFALAKDLVDKTAKVSDTLTIGGNTPAAGGATPKVSTSTA 147
QY 51 KGLNFAKETAGTNGDVTVHLNGIGSTLTD-----RAASVKDVLN 89
DB 148 DGLKAK---GTNGDVAHLNGLASTLPDVTNTGASTSVTFSPSDIEKTRAATIKDVLN 204
QY 90 AGWNKGVK-----NVDFVRYDYVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSV 142
DB 205 AGWNKAKVAGGNTENVDLVAGYDNVEFTGDKNTLDVLVLTAKENKTEVKTPKTSV 264
QY 143 IKEDKGLVTKD---KGNGSGSTDEGE 167
DB 265 IKDNGKLLTGKGLKADANTGTATNATE 291
RESULT 4

S33192
Phase-1 flagellin - Salmonella oranienburg (fragment)
C:Species: Salmonella oranienburg
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C:Accession: S33192
R:Master, B.J.; Joys, T.M.
submitted to the EMBL Data Library, September 1992
A:Description: Molecular analysis of the flagellar antigen complex of Salmonella.
A:Reference number: S33185
A:Accession: S33192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-507 <MAS>
A:Cross-references: EMBL:Z15070; NID:g297006; PIDN:CAA78779.1; PID:g297007
C:Superfamily: flagellin

Query Match 11.4%; Score 116.5; DB 2; Length 507;
Best Local Similarity 31.1%; Pred. No. 0.69; Indels 31; Gaps 11;
Matches 59; Conservative 27; Mismatches 73;
QY 4 TLKAGDNLKIQFTYSLKKDLTSLVSGTEKLSFSAANGKNVITSDTKGLNFAKET-AGT 62
DB 238 TADAQNNTAVDLFKSTKSAAGTD---DAKAIATSIKGGKVGDTFDYKGVSTFTIDTKAGD 293
QY 63 NGDITVH--LNG--IGSTLTDRASVKDVLNAGNKGKKNVDVFRVTDV---EFLSAD 115
DB 294 DNGTSTVTINGEKVTLTISDIGASATDVNSA--KIQSSKDV-----YTSVVSQGTTFAD 346
QY 116 TKTTVNVESKD---NGKKTEVKI---GAKTSVIKEDKGLVTKG---DKGENGSSTD 164
DB 347 -KTNESAKLSLEANNNAVKGESKITVNGAEYTAANAAGDKVTLAGKTMFIDKTAGSVSTL 405
QY 165 EGEGLVTAKE 174
DB 406 INEDAAAKK 415

RESULT 5
A53465
phase 1 flagellin - Salmonella banana
C:Species: Salmonella banana
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 26-Aug-1999
C:Accession: A53465
R:Li, J.; Nelson, K.; McWhorter, A.C.; Whittam, T.S.; Selander, R.K. Proc. Natl. Acad. Sci. U.S.A. 91, 2552-2556, 1994
A:Title: Recombinational basis of serovar diversity in Salmonella enterica.
A:Reference number: A53465; MUID:94195780; PMID:8146152
A:Accession: A53465
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-508 <RES>
A:Cross-references: EMBL:U06202; NID:g476243; PIDN:AAAL7861.1; PID:g476244
C:Genetics:
A:Gene: fliC
C:Superfamily: flagellin

Query Match 11.4%; Score 116.5; DB 2; Length 508;
Best Local Similarity 31.1%; Pred. No. 0.69; Indels 31; Gaps 11;
Matches 59; Conservative 27; Mismatches 73;
QY 4 TLKAGDNLKIQFTYSLKKDLTSLVSGTEKLSFSAANGKNVITSDTKGLNFAKET-AGT 62
DB 239 TADAQNNTAVDLFKSTKSAAGTD---DAKAIATSIKGGKVGDTFDYKGVSTFTIDTKAGD 294
QY 63 NGDITVH--LNG--IGSTLTDRASVKDVLNAGNKGKKNVDVFRVTDV---EFLSAD 115
DB 295 DNGTSTVTINGEKVTLTISDIGASATDVNSA--KIQSSKDV-----YTSVVSQGTTFAD 347
QY 116 TKTTVNVESKD---NGKKTEVKI---GAKTSVIKEDKGLVTKG---DKGENGSSTD 164
DB 348 -KTNESAKLSLEANNNAVKGESKITVNGAEYTAANAAGDKVTLAGKTMFIDKTAGSVSTL 406
QY 165 EGEGLVTAKE 174


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Db      | INEDAAAKK 416
|
RESULT 6
F90961
flagellin [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: F90961
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90961
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA036085.1; PID:g13362130; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs2662
C:Superfamily: flagellin

Query Match          11.1%   Score 113; DB 2; Length 585;
Best Local Similarity 27.1%; Pred. No. 1.4;
Matches 42; Conservative 27; Mismatches 62; Indels 24; Gaps 7;

QY    27 LTSVGTREKLFSANGKNVNITSDTGLNFAKETAGTNGDTTVHLNGIGSTLTDRASVKD 86
     | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db    138 LADGSMKIQVGANDGE-TTIDLLKKID--SDTLGLNG---FNVNGKG-TITNKAAATVSD 190
     | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY    87 VLNAGWNKIGKVNVDFVRTYDTVEFLSADTKTTVVNESKDNGKKTTEVKIGAKTSVIKEK 146
     | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db    191 LTSAGAKLNTTGILDKLTENTL-----LTDAAPDKLGNDK--VTGGVDYTNNAK 241
     | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY    147 DGKLVYTKDGKGENSGSTDEGEGLVTAKEVIDAVNK 181
     | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db    242 SGDFTTTRK-----STAGTGVDAQAQAADSASK 268
     | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 7
F85809
hypothetical protein flic [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: F85809
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85809
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-585 <STO>
A:Cross-references: GB:AE005174; MID:g12516024; PIDN:AAG56938.1; GSPDB:GN00145; UWGP:Z30
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: flic
C:Superfamily: flagellin

Query Match          11.1%   Score 113; DB 2; Length 585;
Best Local Similarity 27.1%; Pred. No. 1.4;
Matches 42; Conservative 27; Mismatches 62; Indels 24; Gaps 7;

QY    27 LTSVGTREKLFSANGKNVNITSDTGLNFAKETAGTNGDTTVHLNGIGSTLTDRASVKD 86
     | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db    138 LADGSMKIQVGANDGE-TTIDLLKKID--SDTLGLNG---FNVNGKG-TITNKAAATVSD 190
     | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY    87 VLNAGWNKIGKVNVDFVRTYDTVEFLSADTKTTVVNESKDNGKKTTEVKIGAKTSVIKEK 146
     | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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```
Df      191 LTSAGAKLNTTGLYDLKTNLT-----LTTDAADFCLKGNQDK--VTVGVDYTYNNAK   241

Dy      147 DGPLVTKGKGSGSSSTDEGEGLVTAKEVIDAVNK    181
          |         :         |         |         |         |         |         |         |
Dz      242 SGDFTTTTK-----STAGTGVDAAQAADSASK     268


RESULT 8
S61332
Iga-specific metalloendopeptidase (EC 3.4.24.13) homolog - Haemophilus influenzae (st
N Alternate names: Igal protease
C Species: Haemophilus influenzae
A Variety: HK635
C Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-Dec-2000
C Accession: S61332
R Lomholt, H.; Poulsen, K.; Mogensen, K.
Mol. Microbiol. 15, 495-506, 1995
A Title: Comparative characterization of the iga gene encoding Igal protease in Neisseria meningitidis strains NCTC 11469 and ATCC 49229
A Reference number: S61314; MUID: 95302961; PMID: 7783620
A Accession: S61332
A Status: preliminary; nucleic acid sequence not shown
A Molecule type: DNA
A Residues: 1-462 <LOM>
A Cross-references: EMBL:X82488; NID:g732714; PIDN:CAA57871.1; PID:g732715
A Experimental source: strain HK635
A Note: The authors did not translate the codon for residue 462
C Genetix:
A Gene: iga
C Superfamily: Iga-specific metalloendopeptidase
C Keywords: hydrolase; metalloproteinase

Query Match       11.1%; Score 112.5; DB 2; Length 462;
Best Local Similarity 25.5%; Pred. No. 1.2;
Matches           52; Conservative 24; Mismatches 59; Indels 69; Gaps 10;

Dy      10 NLKIQTYS-LKKDLTDLSVGTSEKLSPFSAANG-----KVNTSDPTKGLNFPAK   57
        ||| ||| ||| : ::::||| :||: ::: |||
Dz      259-NIIKSQFTKDVLKNKDSAGLLK-GNQTYNMWTFNSGMTSMISNGSELLEVNLFDPNFKHTN--R   315

Dy      58 ETAGTNGDTTVHLINGIGISTLTDRRAASVKOVNLNAG-----WNIKGV   97
        ||| ||| ||| ||| : ||| : ||| : |||
Dz      316 EKANYGSVFQNG---TLT-----LKINSIQAGGLFFEGNYTVVEGSSDNIVNWNCAGI   367

Dy      98 KNVDFVRTYDVTEFLSATDKTTVVNVESKONGKKTETEVKIGAKTSVIKEKDGKLVTGKDKG   157
        ||| ||| ||| : : : ||| : ||| ||| : |||
Dz      368 S-----VAEGRTVTWKVINPQSRL--AKICKGTILV-----BGKG   401

Dy      158 ENGSTDGEGCLVTAKEVIDAVNK    181
        ||| ||| ||| ||| ||| |||
Dz      402 ENKSLGSKVGDGTVILKOQADANNK   425


RESULT 9
A43855
high-molecular-weight surface-exposed protein HMW1 - Haemophilus influenzae
C Species: Haemophilus influenzae
C Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C Accession: A43855
R Barenkamp, S.J.; Leininger, E.
Infect. Immun. 60, 1302-1313, 1992
A Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Legionella pneumophila serogroup 4 proteins
A Reference number: A43855; MUID: 92192797; PMID: 1548058
A Accession: A43855
A Status: preliminary
A Molecule type: DNA
A Residues: 1-1536 <BAR>
A Cross-references: GB:I088876; GB:M84616; NID:g475770; PIDN:AAA20527.1; PID:g475771
A Note: sequence inconsistent with the nucleotide translation
A Note: sequence extracted from NCBI backbone (NCBIN:89235, NCPIP:89239)
```


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```
QY 63 NGDTTVH--LNG--IGSTLTDRAASVKDVLNAGWNKGVKNVDFVRYTDTV---EFLSAD 115
Db 294 DNGTGVSTINGEKVTLTISDIGASATVNSA--KIQSKDV-----YTSVVSQGTFFAD 346
QY 116 TKTTVVNESKD---NGKTEVKI---GAKTSVIKEDGKLVTKG---DKGENGSTD 164
Db 347 -KTKNESAKLSDEANNAVGESKITVNGAEYTAAGDKVTLAGKTFWIDKTAGSGVSTL 405
QY 165 EGEGLVTAKE 174
Db 406 INEDAAAAKK 415

RESULT 2
GIDA_RICPR
ID GIDA_RICPR STANDARD; PRT; 621 AA.
AC Q9ZFE90;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucose inhibited division protein A.
GN GIDA OR RP056.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: Belongs to the gida family.
CC
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CC
CC EMBL: AJ235270; CAAL4527.1; -.
DR PIR: H71713; H71713.
DR HAMAP: MF_00129; -.
DR InterPro: IPR001327; FAD_pyr_redox.
DR InterPro: IPR002218; GIDA.
DR InterPro: IPR004416; Gida.sub.
DR InterPro: IPR001100; Pyr_redox.
DR Pfam: PF01134; GIDA; 1.
DR PRINTS: PR00368; FADPNR.
DR PRINTS: PR00411; PNDPRTASEI.
DR ProDom: PD003738; GIDA; 1.
DR TIGRFAMs: TIGR00136; gida; 1.
DR PROSITE: PS01280; GIDA_1; 1.
DR PROSITE: PS01281; GIDA_2; 1.
KW Complete proteome.
SQ SEQUENCE 621 AA; 69195 MW; 7379A5B4E6ACADF CRC64;

Query Match
Best Local Similarity 10.3%; Score 105; DB 1; Length 621;
Matches 44; Conservative 26; Mismatches 67; Indels 24; Gaps 6;

QY 4 TLKAGDNLKIKQFTYSLKKDLTDSVGTESKLSFSAANGKNVNTSDTK---GLNFAKETA 60
Db 323 TIPGLENAQVLRPGYATEYDVDD-----PREINVTLETKKITGLYFAGQIN 368
QY 61 GTNGDTTVHLNGIGSTLTDRAASVKD-----VLNAGWNKGVKNVDFVRYTDTVEFLSADT 116
```

```
Db 369 GTTGYEEAAGGIITAGI--NAALSVKQDAPFILTRATSYIGVM-IDDLTFTGTVPEYRMT 426
QY 117 KTTTVNVESK--DNCKKTEVKIGAKTSVIKEDGKLVTKGDK 156
Db 427 SRSEYRLSLRADNADRLTLELGKIGKIGVITERKKKFFTKCK 467

RESULT 3
FLIC_SALSE
ID FLIC_SALSE STANDARD; PRT; 504 AA.
AC Q06983;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Flagellin (Phase-1-C flagellin).
GN FLIC.
OS Salmonella senftenberg.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=28150;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93374829; PubMed=7690024;
RA Masten B.J., Joys T.M.;
RT "Molecular analyses of the Salmonella g... flagellar antigen
RT complex."
RL J. Bacteriol. 175:5359-5365(1993).
CC -!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -!- MISCELLANEOUS: INDIVIDUAL SALMONELLA SEROTYPES USUALLY ALTERNATE
CC BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELLA, TERMED
CC PHASE-1 AND PHASE-2. EACH SPECIFIED BY SEPARATE STRUCTURAL GENES.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
CC
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CC
CC EMBL: Z15072; CAA78781.1; -.
DR PIR: S33194; S33194.
DR InterPro: IPR001029; Flagellin_C.
DR InterPro: IPR001492; Flagellin_N.
DR Pfam: PF00700; Flagellin_C; 1.
DR Pfam: PF00669; Flagellin_N; 1.
DR PRINTS: PR00207; FLAGELLIN.
DR KW Flagella.
FT INIT_MET
SQ SEQUENCE 504 AA; 52864 MW; BFD14C4F125C2BAC CRC64;

Query Match
Best Local Similarity 10.1%; Score 103; DB 1; Length 504;
Matches 53; Conservative 27; Mismatches 62; Indels 30; Gaps 11;

QY 25 TDLTSGVTEK---LSFSANGKNVNTSDTKGLNFAKET-AGTNGDTHVH--LNGIGSTLT 78
Db 249 TTKTAGTDEAKATSAIKGKEGDTFDYKGVSEFTIDTKAGDNGNGTVSTTINGEKVTLT 308
QY 79 --DRAASVKDVLNAGWNKGVKNVDFVRYTDTV---EFLSADTKTTTVNVESKD-----NG 129
Db 309 VADITAGANVND--TLOSSKNV-----YTSVVGQF-TFDDTKNESAKLSDEANNA 360
QY 130 KTEVKI---GAKTSVIKEDGKLVTKG---DKGENGSTDEGEGLVTAKE 174
Db 361 VKGESKITVNGAEYTAAGDKVTLAGKTFWIDKTAGSGVSTLINEADAAAANK 412

RESULT 4
FLIC_SALBU
```

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ID AC FLIC_SALBU STANDARD; PRT; 504 AA.
DT Q06969;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Flagellin (Phase-1-C flagellin).
GN FLIC.
OS Salmonella budapest.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=28143;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93374829; PubMed=7690024;
RA Masten B.J., Joys T.M.;
RT "Molecular analyses of the Salmonella g. . . flagellar antigen
complex.";
RL J. Bacteriol. 175:5359-5365(1993).
CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -1- MISCELLANEOUS: INDIVIDUAL SALMONELLA SEROTYPES USUALLY ALTERNATE
CC BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELLA, TERMED
CC PHASE-1 AND PHASE-2, EACH SPECIFIED BY SEPARATE STRUCTURAL GENES.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
CC
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CC
DR EMBL; Z15065; CAA78774.1;
DR PIR; S33186;
DR InterPro; IPR001029; Flagellin_C.
DR InterPro; IPR001492; Flagellin_N.
DR Pfam; PF00700; Flagellin_C; 1.
DR Pfam; PF00669; Flagellin_N; 1.
DR PRINTS; PR00207; FLAGELLIN.
KW Flagella.
FT INIT_MET 0 0 BY SIMILARITY.
SQ SEQUENCE 504 AA; 52790 MW; 1FD1498751B6475E CRC64;
Query Match 10.0%; Score 102; DB 1; Length 504;
Best Local Similarity 30.8%; Pred. No. 3.8;
Matches 53; Conservative 27; Mismatches 62; Indels 30; Gaps 11;
QY 25 TDLTSVGTCK---LSFSANGKNVITSDTKGLNFAKET-AGTNGDTTVH--LNGIGSTLT 78
Db TTRKSTAGTDEAKATAGAKGKEGDTFDYKGVSTFIDTKAGNDGNGTVSTTINGEKVTLT 308
QY 79 --DRAASVKDVLNAGNWKGVKNVDFVRYTDV---EELSADTKTTVNVESKD----NG 129
Db VADITAGANVNDK--TLQSSKNV-----YTSVVGQF--TFDDKTKNESAKLSLEANA 360
QY 130 KKEVTKI---GAKTSVIKERDGLVTGK----DKGSGNSSTDEGEGLVTAKE 174
Db VKGESKITVNGAEVYANAAGDKVTLACKTFWIDKTAGSVSTLINEADAAAKK 412
RESULT 5
FLIC_SHIFL
ID FLIC_SHIFL STANDARD; PRT; 550 AA.
AC Q08860;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Flagellin.
GN FLIC OR SF1966.
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
```

```
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IID642;
RX MEDLINE=94335647; PubMed=8057852;
RA Tomimaga A., Mahmoud M.A.-H., Mukahara T., Enomoto M.;
RT "Molecular characterization of intact, but cryptic, flagellin genes
in the genus Shigella.";
RL Mol. Microbiol. 12:277-285(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
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CC
DR EMBL; D16819; BAA04093.1;
DR EMBL; AE015215; AAM43516.1;
DR PIR; S44980; S44980.
DR InterPro; IPR001029; Flagellin_C.
DR InterPro; IPR001492; Flagellin_N.
DR Pfam; PF00700; Flagellin_C; 1.
DR Pfam; PF00669; Flagellin_N; 1.
DR PRINTS; PR00207; FLAGELLIN.
KW Flagella.
SQ SEQUENCE 550 AA; 56636 MW; CC921C9A8EF200B6 CRC64;
Query Match 9.9%; Score 100.5; DB 1; Length 550;
Best Local Similarity 25.8%; Pred. No. 5.4;
Matches 57; Conservative 29; Mismatches 96; Indels 39; Gaps 11;
QY 4 TLKAGDNLKIKQFTYSLKDLTDLTSVGTCKLSFANGKNVITSDTKGLNFAKETAGTN 63
Db TASNGDKLYI-DTTRGRTKNGSGASLSEASLSLTAANNKAT-TIDIGGTSISFTGNST 356
QY 64 GDT-TVHLNG--IGSTLTDRAASVK-----DVLNAGNWK-----VKNVDFVRYDIVEF 111
Db PDITITYSVTCAKVDQAAFDKAVSTSGNNVDFTTAGYSVNGTGTGAVTKGVDSV----YVDN 412
QY 112 LSADTKTTTVNVEKSKNGKKEVTKVIGAKTSVIKEDKGLVTGDKGSGNSSTDEGEGLVT 171
Db NEALTTSDDTVDFLYQDDGSVTN---GSKAVYKADCKLTT--DAETKAATT--ADPLKA 465
QY 172 AKEVIDAVNK-----AGWRMKTMTTANGQTGA 198
Db LDEAISSIDKFRSLGAVQNRLDSAVTNLNTNTNLSEAQ 506
RESULT 6
YMBJ_CABEL
ID YMBJ_CABEL STANDARD; PRT; 918 AA.
AC P34487;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein F59B2.12 in chromosome III.
```

```
GN F59B2.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser J., Jier M.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonnenhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -----
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CC -----
DR EMBL; Z11505; CAA77581.1; -.
DR PIR; G88545; G88545.
DR WormPep; F59B2.12; CE01024.
KW Hypothetical protein.
SQ SEQUENCE 918 AA; 96560 MW; E464FD86B14945DE CRC64;

Query Match          9.7%; Score 99; DB 1; Length 918;
Best Local Similarity 21.3%; Pred. No. 12;
Matches 54; Conservative 32; Mismatches 84; Indels 84; Gaps 9;

Qy 6 KAGDNLKIKQFTYSL-----KDLDTLTSVGTKEKLS-----FSANGKNVITS 48
Db 118 ENANTKIKSADGVIETGKSHNKSDDASSYGLEKSKTYADKNGTMLSSNTKINNQS 177
Qy 49 DTGKLN-----FAKETAG-----TNGDTTVHLNGIGSTLDR 80
Db 178 RSAALDEGNEFVNOONADGTFELRNTHGKNTDEHLNHLVLDENAOQMSIGADGTSHTNI 237
Qy 81 AASVKDVLNAGWNKIGVKNVDFVRYDTVEFLSADTKTTTVNVESKDKGKKTEYKIGAKT 140
Db 238 KGSVGDGSHNAASD-----AHSNFESLDAQG-----NKKSQNYSKKAASASGSA 281
Qy 141 SV-----IKEKDGKLVTKGDKGSGSTDEGGLVTAKEV-----IDAVNK 181
Db 282 DFESNLESKLNADGTSMSNGFNNTSYDK-----ATAEEYMSKKNVKNADGTSMEASHA 337
Qy 182 AGWRMKTTTANGQT 195
Db 338 GSNSSKINSASGQS 351

RESULT 7
Y456_CHLTR
ID Y456_CHLTR STANDARD; PRT; 1005 AA.
AC O84462;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein CT456 precursor.
GN CT456.
OS Chlamydia trachomatis.

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CC -----
DR EMBL; AE001319; AAC68056.1; -.
DR PIR; C71513; C71513.
DR PHC1-2DPAGE; O84462; -.
KW Signal; Complete proteome.
FT SIGNAL 1 40
FT CHAIN 41 1005
FT PROTEIN CT456.
SQ SEQUENCE 1005 AA; 102131 MW; EC47EC389851CD1E CRC64;

Query Match          9.7%; Score 99; DB 1; Length 1005;
Best Local Similarity 22.6%; Pred. No. 13;
Matches 48; Conservative 25; Mismatches 71; Indels 68; Gaps 11;

Qy 41 GNKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDRAASVKDVLNAGWNKIGVK-- 98
Db 490 GTQAGPSSEDDGISFSNETPGA-----GPAAPSPPTPSSI-PIINNVNNGGTVNV 539
Qy 99 ----NVDFVRYDTVEFLSADT-----KTTTVNVESKD-----NG--KKTE 133
Db 540 IGDTRVNTTPTTQSTDASTDSTDDIDTNNQDDINTYDKDSDGAGVNGDISETE 599
Qy 134 VKIGAKTSVI--KEKDGKLVTKGD-----KGEKSSSTPDEGEGLVTA 172
Db 600 SSSGDDSGSVSSSESDKNASVNGDGPAMKDLISAVRKHLVDVVPGEKGGST---EGPLPA 656
Qy 173 KEVI-----DAVNKAGWRMKTTTANGQTQAD 199
Db 657 NQTGLDVISDVENKGS--AODTKLSGNTGAGD 686

RESULT 8
YC00_MYCPN
ID YC00_MYCPN STANDARD; PRT; 798 AA.
AC Q50288;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical lipoprotein MPN200 precursor (GT9_orf798).
GN MPN200 OR MP631.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=96177562; PubMed=8604303;
RA Hilbert H., Himmelsreich R., Plagens H., Herrmann R.;
RT "Sequence analysis of 56 kb from the genome of the bacterium
RT Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a
RT cluster of ribosomal protein genes";
RL Nucleic Acids Res. 24:628-639(1996).
```

```
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/Cx;
RX MEDLINE=95000809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis";
RL Science 282:754-759(1998).
CC -!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0572/CT456/TC0741
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE001319; AAC68056.1; -.
DR PIR; C71513; C71513.
DR PHC1-2DPAGE; O84462; -.
KW Signal; Complete proteome.
FT SIGNAL 1 40
FT CHAIN 41 1005
FT PROTEIN CT456.
SQ SEQUENCE 1005 AA; 102131 MW; EC47EC389851CD1E CRC64;

Query Match          9.7%; Score 99; DB 1; Length 1005;
Best Local Similarity 22.6%; Pred. No. 13;
Matches 48; Conservative 25; Mismatches 71; Indels 68; Gaps 11;

Qy 41 GNKNVITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDRAASVKDVLNAGWNKIGVK-- 98
Db 490 GTQAGPSSEDDGISFSNETPGA-----GPAAPSPPTPSSI-PIINNVNNGGTVNV 539
Qy 99 ----NVDFVRYDTVEFLSADT-----KTTTVNVESKD-----NG--KKTE 133
Db 540 IGDTRVNTTPTTQSTDASTDSTDDIDTNNQDDINTYDKDSDGAGVNGDISETE 599
Qy 134 VKIGAKTSVI--KEKDGKLVTKGD-----KGEKSSSTPDEGEGLVTA 172
Db 600 SSSGDDSGSVSSSESDKNASVNGDGPAMKDLISAVRKHLVDVVPGEKGGST---EGPLPA 656
Qy 173 KEVI-----DAVNKAGWRMKTTTANGQTQAD 199
Db 657 NQTGLDVISDVENKGS--AODTKLSGNTGAGD 686

RESULT 8
YC00_MYCPN
ID YC00_MYCPN STANDARD; PRT; 798 AA.
AC Q50288;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical lipoprotein MPN200 precursor (GT9_orf798).
GN MPN200 OR MP631.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=96177562; PubMed=8604303;
RA Hilbert H., Himmelsreich R., Plagens H., Herrmann R.;
RT "Sequence analysis of 56 kb from the genome of the bacterium
RT Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a
RT cluster of ribosomal protein genes";
RL Nucleic Acids Res. 24:628-639(1996).
```



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[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=ATCC 29342 / M129;
RX  MEDLINE=97105885; PubMed=8948633;
RA  Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA  Herrmann R.;
RT  "Complete sequence analysis of the genome of the bacterium Mycoplasma
RL  pneumoniae.";
CC  Nucleic Acids Res. 24:4420-4449(1996).
CC  -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC  (Potential).
CC  -1- SIMILARITY: BELONGS TO THE MG185 / MG260 FAMILY.
CC  -----
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CC  entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: U34795; AAC43681.1; -.
DR  EMBL: AE000060; AAB96279.1; -.
DR  PIR: S62791.
DR  InterPro: IPR004890; Lipoprotein_10.
DR  InterPro: IPR004984; Lipoprotein_X.
DR  Pfam: PF03202; Lipoprotein_10; 1.
DR  Pfam: PF03305; Lipoprotein_X; 1.
DR  PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW  Hypothetical protein; Lipoprotein; Membrane; Signal;
KW  Complete proteome.
FT  SIGNAL 1 22 POTENTIAL.
FT  CHAIN 23 798 HYPOTHETICAL LIPOPROTEIN MPN200.
FT  LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ  SEQUENCE 798 AA; 87628 MW; 3E2471D7EFA03CA0 CRC64;

Query Match 9.7%; Score 98.5; DB 1; Length 798;
Best Local Similarity 21.1%; Pred. No. 11;
Matches 51; Conservative 33; Mismatches 95; Indels 63; Gaps 9;

QY 7 AGDNLKTKQFTYSLKDLTDLTSVGTETKLSFSGANGKVNKITSDTKGLNFAKETAGTNGDT 66
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
337 AAGNSDYNNFFYQVNGRADFSNFKNGSSYK---NLKNVFNFKNL-----IAQNG-- 385

QY 67 TVHLNGIGSLTD-----RAASVKDVLNAGNKGKVNDFVRYTYDVFSLSDTKTTT 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
386 -LYVKGSSVSSNFQKPHQLAYSLSSTSGFAYSFAGNSKRFET-DGTFVEYPSVYTE 443

QY 121 VNVEKDNQ-----KKEVYKIGAKTSVIEK--DGKLVYTKGD 155
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
444 VNAPESNNGNDGKQGGSDQGNLLGTPFVVVDKSTDIKVPKTAQESKSSDKQTANTG 503

QY 156 KGENSS-----TDEGEG-----LVTAKEVIDAVNKAGWRMKTITANGQTG 196
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
504 KGSNSKQOTPKTKTISLYTKTKIPQDKTENVDVDAFLVTDSELISKLEKAKNKKEETKASGSA 563

QY 197 QA 198
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
564 SA 565

RESULT 9
PMP7_CHLPP STANDARD; PRT; 936 AA.
ID PMP7_CHLPP
AC Q92898; Q9J542; Q9Z504;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable outer membrane protein pmp7 precursor (Polymorphic membrane
DE protein 7) (Outer membrane protein 12).
GN PMP7 OR OMP12 OR CPN0445 OR CP0308.
OS Chlamydia pneumoniae (Chlamydiales; Chlamydiales; Chlamydiales).
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiales; Chlamydiales.
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OX NCBI_TaxID=83558;
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=CWL029;
RX MEDLINE=99206606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP SEQUENCE OF 658-936 FROM N.A.
RX STRAIN=VR1310;
RX MEDLINE=20007584; PubMed=10539856;
RA Christiansen G., Boesen T., Hjerno K., Dagaard L., Mygind P.,
RA Madsen A.S., Knudsen K., Falk E., Birkelund S.;
RT "Molecular biology of Chlamydia pneumoniae surface proteins and their
RT role in immunopathogenicity.";
RL Am. Heart J. 138:S491-S495(1999).
CC -1- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: AE001627; AAD18589.1; -.
DR EMBL: AE002193; AAF38165.1; -.
DR EMBL: AP002546; BAA98653.1; -.
DR EMBL: AJ133034; CAB37067.1; -.
DR PIR: B81591; B81591.
DR PIR: C72078; C72078.
DR PIR: C86546; C86546.
DR PHCI-2DPAGE; Q92898; -.
DR TIGR: CP0308; -.
DR InterPro: IPR006315; Autotransport.
DR InterPro: IPR005546; Autotransporter.
DR InterPro: IPR003368; Chlamydia_PMP.
DR Pfam: PF03797; Autotransporter; 1.
DR Pfam: PF02415; DUF145; 2.
DR TIGRFAMS; TIGR01414; autotrans_bar1; 1.
DR TIGRFAMS; TIGR01376; POMP_repeat; 6.
KW Outer membrane; Signal; Multigene family; Complete proteome.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 936 PROBABLE OUTER MEMBRANE PROTEIN PMP7.
FT CONFLICT 658 666 PTRRGFRHI -> EDNIRYRHN (IN REF. 4).
FT CONFLICT 822 822 Y -> H (IN REF. 1 AND 4).
SQ SEQUENCE 936 AA; 100105 MW; 3981DB3C950AF95A CRC64;
```

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Query Match
Best Local Similarity 9.7%; Score 98.5; DB 1; Length 936;
Matches 59; Conservative 32; Mismatches 71; Indels 81; Gaps 13;

QY 27 LTSVCTEKLFSAN-----GNKYNITSYKGL---NFAKETAG----- 61
DB 274 VTLGNKLSFTNNALTLYGGAISGLKVSISAGGPTLFQSNISGSSAGGGGAINIASA 333
QY 62 -----TNGDTTVHLNGI---GSTLTDRASVKDVLNAGNIGKVNVDVFTYDTVBEFL 112
DB 334 GELALSATSGDITFNNQVTNGSTSTRAINIIDTAKV-TSIRATG-QSIYFYDPINP 391
QY 113 SADTKTTTVNVEDK-----NGKK-----TEVKIGAK-TSVIKE----- 145
DB 392 GTAASDTPLNLNLADANSEIEYGGAIVFSGEKLSPTEKAIAANVTSTIRQPAVLARGDLV 451
QY 146 -KDKGLVTGKDKGENSS--TDEGEGLVTAKEV-----IDAVNKAGWRMKT 189
DB 452 LRDGVTVTFKLTQSPGRILMDGGTTLISAKEANLSLNLGLAVNLSLDGTNKA--LKTE 509
QY 190 TAN 192
DB 510 AAD 512

RESULT 10
SLAP_LACAC STANDARD; PRT; 444 AA.
ID SLAP_LACAC
AC P35829;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE S-layer protein precursor (Surface layer protein) (SA-protein).
GN SLPA.
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1579;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 343-351 AND 440-444.
RX STRAIN=ATCC 4356;
RX MEDLINE=94012467; PubMed=8407780;
RA Boot H.J., Kolen C.P.A.M., van Noort J.M., Pouwels P.H.;
RT "S-layer protein of Lactobacillus acidophilus ATCC 4356:
RT purification, expression in Escherichia coli, and nucleotide sequence
RT of the corresponding gene.";
RL J. Bacteriol. 175:6089-6096(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4356;
RX MEDLINE=96099308; PubMed=8522531;
RA Boot H.J., Kolen C.P.A.M., Pouwels P.H.;
RT "Identification, cloning, and nucleotide sequence of a silent S-layer
RT protein gene of Lactobacillus acidophilus ATCC 4356 which has
RT extensive similarity with the S-layer protein gene of this species.";
RL J. Bacteriol. 177:7222-7230(1995).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- SIMILARITY: SOME, TO THE S-LAYER PROTEIN OF L.BREVIS.
CC
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CC
CC EMBL; X71412; CAA50535.1; -
CC EMBL; X89375; CAA61560.1; -
CC
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DR PIR: A36924; A36924.
DR InterPro; IPR004903; SLAP.
DR Pfam; PF03217; SLAP; 1.
KW Signal; Glycoprotein; Cell wall; S-layer.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 444 S-LAYER PROTEIN.
SQ SEQUENCE 444 AA; 46570 MW; 2090732F89099161 CRC64;

Query Match
Best Local Similarity 9.6%; Score 98; DB 1; Length 444;
Matches 57; Conservative 29; Mismatches 87; Indels 76; Gaps 12;

QY 7 AGDNLKIQFTSYLKKDLTDLTSGVTEKLSFSANG-----NKVNI-----TSDTKGLNF 55
DB 147 ANSNVK---FTGTNSDNOTE-TNVSTLKVLDQNGVASLTNVSIANVYAINITDINSVNF 202
QY 56 AKETAG---TNGDITVHLNGIGST-----LTDRAASVKDVLNA 90
DB 203 YDVTSGATVTNGAVSNADNOGVNVANVAINSKYFAAQYADKKLNTRTANTEDAIRA 262
QY 91 GWNIK--GVKNVDFVRYDTVEFLSADTKTTTVNVVESKDNKKTEVKIGAKTSVIKEDG 148
DB 263 ALKQKIDVNSVG-----FKAPHTFTVNVKATSNNGKSATLPVVVTVPNVAEPTV 314
QY 149 KLVTGK-----DKGENSGSTDEGEGLVTAKEVIDAVNKAGWRMKTGTTTANGQT----- 195
DB 315 ASVSKRIMHNAYYYDKDAKRVGTD-----VKRYNSVSVLPNTPTTNGKTYQV 364
QY 196 --GGA-DKF 201
DB 365 ENGRAVDKY 373

RESULT 11
FLIC_SALMC STANDARD; PRT; 504 AA.
ID FLIC_SALMC
AC Q06981;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Flagellin (Phase-1-D flagellin).
GN FLIC.
OS Salmonella mscow.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=28146;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC;
RX MEDLINE=93374829; PubMed=7690024;
RA Masten B.J., Joys T.M.;
RT "Molecular analyses of the Salmonella g... flagellar antigen
RT complex.";
RL J. Bacteriol. 175:5359-5365(1993).
CC -!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -!- MISCELLANEOUS: INDIVIDUAL SALMONELLA SEROTYPES USUALLY ALTERNATE
CC BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELLA, TERMED
CC PHASE-1 AND PHASE-2. EACH SPECIFIED BY SEPARATE STRUCTURAL GENES.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
CC
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CC
CC EMBL; Z15086; CAA78794.1; -
CC PIR: S33191; S33191.
DR InterPro; IPR001029; Flagellin_C.
DR InterPro; IPR001492; FlagellinN.
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DR Pfam: PF00700; Flagellin_C; 1.
DR Pfam: PF00669; Flagellin_N; 1.
DR PRINTS; PR00207; FLAGELLIN.
KW Flagella.
FT INIT_MET 0 0 BY SIMILARITY.
SQ SEQUENCE 504 AA; 52791 MW; FCAEA2180AF111A0 CRC64;

Query Match 9.5%; Score 97; DB 1; Length 504;
Best Local Similarity 27.6%; Pred. No. 8.5;
Matches 47; Conservative 22; Mismatches 75; Indels 26; Gaps 8;

QY 25 TDLTSVGT---EKLSPSANGKNVNTSDTKGLNFAKET---GTNGDTTVHLNGIGSTLT 78
DB 249 TTKSTAGTAEAIAAGAIKGGEGDFDYKGVTFITDTKTGOGNGKSVSTTINGEKVTLT 308
QY 79 DRAASVKVDNLNAGNNTKGVKNVDFVRYTDV---EFLSADTKTTTVNVESKD---NGKK 131
DB 309 -----VADTATGATNVAATLQSSKNVYTSVNGQF-TFDDTKNESAKLSDELEANNV 362
QY 132 TEVKI---GAKTSVKEKDGKLVTKG-----DKGENSGSTDEGGLVTAKE 174
DB 363 GESKITVNGAEVTANATGDKITLAGKTMFDKTAGSVSTLINEDAAAAAKK 412

RESULT 12
FLJB_SALTY STANDARD; PRT; 505 AA.
AC P52616; P97159;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phase-2 flagellin.
GN FLJB OR H2 OR STM2771.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL 375;
RX MEDLINE=95325331; PubMed=7541401;
RA Vanegas R.A., Joys T.M.;
RT "Molecular analyses of the phase-2 antigen complex 1,2... of
RL Salmonella spp.;"
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL LT2.;"
RN [3]
RP SEQUENCE OF 1-37 FROM N.A.
RX MEDLINE=82049491; PubMed=6271461;
RA Silverman M., Zieg J., Mandel G., Simon M.;
RT "Analysis of the functional components of the phase variation
RL system.;"
RN [4]
RP SEQUENCE OF 482-505 FROM N.A.
RC STRAIN=SJ2353;
RA Mingorance J., Tanaka S., Tominaga A., Enomoto M.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -1- MISCELLANEOUS: INDIVIDUAL SALMONELLA SEROTYPES USUALLY ALTERNATE
CC BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELLA, TERMED
```

RX MEDLINE=95219088; PubMed=7704263;
RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis
RL genome containing the hut and wpaA loci.";
RN Microbiology 141:337-343(1995).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSCIAL;
RX MEDLINE=97124196; PubMed=9969509;
RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
RA Miwa Y., Fujita Y.;
RT "Sequencing of a 65 kb region of the Bacillus subtilis genome
RT containing the lic and cel loci, and creation of a 177 kb contig
RT covering the gnt-sacXy region.";
RL Microbiology 142:3113-3123(1996).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Potwollik S., Prescott A.M.,
RA Prescann E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis";
RL Nature 390:249-256(1997).
CC -!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
CC MOTILITY, SECRETION OR DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
CC INTO THE MEDIUM.
CC -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS: THE N-TERMINUS, HAS THREE
CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE
CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
CC MOTIF REPEATED 31 TIMES.
CC -!- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
CC SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHS-A-D).
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CC -----
DR EMBL; L05634; AAA22883.1; -;
DR EMBL; D31856; BAA0656.1; -;
DR EMBL; D29985; BAA06260.1; -;
DR EMBL; D83026; BAA11683.1; -;

DR EMBL; Z99124; CAB15959.1; -;
DR PTR; S32920; S32920.
DR Subtilisin; BG10797; wpaA.
DR InterPro; IPR003305; CBM_CenC.
DR InterPro; IPR006530; YD.
DR Pfam; PF02018; CBM_4_9; 1.
DR TIGRfams; TIGR01643; YD_repeat_2x; 17.
KW Cell wall; Repeat; Signal; Complete proteome.
FT SIGNAL 1 28 OR 32 (POTENTIAL).
FT CHAIN 29 2334 WALL-ASSOCIATED PROTEIN.
FT DOMAIN 504 869 3 X 101 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 504 605 1-1.
FT REPEAT 636 736 1-2.
FT REPEAT 769 869 1-3.
FT DOMAIN 1021 2139 31 X 21 AA APPROXIMATE TANDEM REPEATS OF
FT X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
FT REPEAT 1021 1040 2-1.
FT REPEAT 1042 1061 2-2.
FT REPEAT 1063 1082 2-3.
FT REPEAT 1083 1102 2-4.
FT REPEAT 1109 1128 2-5.
FT REPEAT 1129 1148 2-6.
FT REPEAT 1150 1169 2-7.
FT REPEAT 1174 1193 2-8.
FT REPEAT 1199 1218 2-9.
FT REPEAT 1219 1238 2-10.
FT REPEAT 1246 1265 2-11.
FT REPEAT 1267 1286 2-12.
FT REPEAT 1290 1309 2-13.
FT REPEAT 1311 1330 2-14.
FT REPEAT 1332 1351 2-15.
FT REPEAT 1352 1371 2-16.
FT REPEAT 1372 1391 2-17.
FT REPEAT 1392 1411 2-18.
FT REPEAT 1412 1431 2-19.
FT REPEAT 1432 1451 2-20.
FT REPEAT 1452 1471 2-21.
FT REPEAT 1472 1491 2-22.
FT REPEAT 1492 1511 2-23.
FT REPEAT 1512 1531 2-24 (APPROXIMATE).
FT REPEAT 1532 1551 2-25.
FT REPEAT 1552 1571 2-26.
FT REPEAT 1572 1591 2-27.
FT REPEAT 1592 1611 2-28.
FT REPEAT 1612 1631 2-29.
FT REPEAT 1632 1651 2-30.
FT REPEAT 1652 1671 2-31.
SQ SEQUENCE 2334 AA; 258329 MW; B75138CCD278BAA3 CRC64;
Query Match 9.5%; Score 96.5; DB 1; Length 2334;
Best Local Similarity 25.1%; Pred. No. 52;
Matches 64; Conservative 24; Mismatches 76; Indels 91; Gaps 16;
Qy 16 FTSYSLKDLTDLTSVG-----TEKLSFSANGKNVNTSDTKG-----LN-FAKE 58
Db 1870 FSYD-ERNLVSSSLHIGDKNGDILTESYEYDANGNRRTINSASGKVOYEGKLNQLVKE 1928
Qy 59 TAGTNGDTTV---HLNGIGSTLTDRASVKD---VLNAGWNI-----K 95
Db 1929 ---THEGDTVIEYTDGFGNRKT--VTIKDSSKVTYNASFNIMNQLTKVNDESISYDKN 1983
Qy 96 GVKRWV--FVRYTDTVFELSADTKT-----TTVNESKD-----NGKTEVKI-GAK 139
Db 1984 GNRTSDGKFTYTWDAEDNLTAVTKKGEDKPFATYKYDEKGNRIQKTVNGKVTNFDGDS 2043
Qy 140 TSVYKEKDG-----KLVTKGDKGSGSSTDBGE-----GLVTAKEV 175
Db 2044 LNVLYETADANNVTKSYTGDGQLLSYTGNGKRYFYHNAHGDIIAISDSTGKTVAKYQ 2103
Qy 176 IDAVNKAGWRMKTPT 190
Db 2104 YDA-----WGNPTKT 2113

RESULT 14

```
FLIC_SALMO STANDARD; PRT; 504 AA.
AC Q06973;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Flagellin (Phase-1-C flagellin).
GN FLIC.
OS Salmonella montevideo.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=115981;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 8387; PubMed=7690024;
RX MEDLINE-93374829;
RA Masten B.J., Joys T.M.;
RT "Molecular analyses of the Salmonella g. . . flagellar antigen
complex."
RL J. Bacteriol. 175:5359-5365(1993).
CC -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
CC -1- MISCELLANEOUS: INDIVIDUAL SALMONELLA SEROTYPES USUALLY ALTERNATE
CC BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELLA, TERMED
CC PHASE-1 AND PHASE-2, EACH SPECIFIED BY SEPARATE STRUCTURAL GENES.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DE EMBL; Z15069; CAA78778.1; -
DR PIR; S33190.
DR InterPro; IPR001029; Flagellin_C.
DR InterPro; IPR001492; Flagellin_N.
DR Pfam; PF00700; Flagellin_C; 1.
DR Pfam; PF00669; Flagellin_N; 1.
DR PRINTS; PR00207; FLAGELLIN.
DR Flagella.
KW FLAGELLIN.
FT INIT.MET
SQ SEQUENCE 504 AA; 52862 MW; 5C090577F21ECA67 CRC64;
```

```
Query Match 9.4%; Score 96; DB 1; Length 504;
Best Local Similarity 30.2%; Pred. No. 10;
Matches 52; Conservative 23; Mismatches 67; Indels 30; Gaps 11;

Qy 25 TDLTSTVGTEK---LPSFANGKNVNIYSDTKGLNFAKETA---GTNGDITVHLNGICSTLT 78
Db 249 TTKSAAGTDEAKAIAAGKRGEDFDYKGVFTTIDTKGPDGNGKVSFTINGEKVTLT 308
Qy 79 --DRAASVDLVNAGNNIKGVKNVDFVRYTDV---EFLSADTKTTVNVEKSD---NG 129
Db 309 VADIATGATDV-NAA-TLOSSKNV-----YTSVVNGQF-TFDDKTKNESAKLSDLAENNA 360
Qy 130 KKEVKI---GAKTSVIKEKGLVTKGK-----DKGENGSTDRGELVTAKE 174
Db 361 VKGESKITVNGAEYTAAGDKVTLGAKTTFIDKTAGSVSTLINEDAAAKK 412
```

RESULT 15

```
RPOB_MYCGE STANDARD; PRT; 1390 AA.
AC P47583; Q49441;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
```

```
DE beta chain) (RNA polymerase beta subunit).
OS RPOB OR MG341.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 33530 / G-37;
RX MEDLINE-96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-P., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 533-644 AND 945-1067 FROM N.A.
RC STRAIN-ATCC 33530 / G-37;
RX MEDLINE-94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
sequencing."
RL J. Bacteriol. 175:7918-7930(1993).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DE EMBL; U39715; AAC71566.1; -
DR EMBL; U01737; AAD10547.1; -
DR EMBL; U01735; AAD10545.1; -
DR PIR; G64237; G64237.
DR HSSP; Q9KW07; IHQM.
DR TIGR; MG341; -
DR InterPro; IPR001572; RNA_pol_B.
DR Pfam; PF04563; RNA_pol_Rpb2_1; 1.
DR Pfam; PF04561; RNA_pol_Rpb2_2; 1.
DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
DR Pfam; PF00582; RNA_pol_Rpb2_6; 1.
DR Pfam; PF04560; RNA_pol_Rpb2_7; 1.
DR PROSITE; PS01166; RNA_POL_BETA; 1.
DR Transferrase; Transcription; DNA-directed RNA polymerase;
KW Complete proteome.
FT CONFLICT 1062 1062 H -> L (IN REF. 2).
SQ SEQUENCE 1390 AA; 156330 MW; 4D1888A07680912C CRC64;
```

```
Query Match 9.3%; Score 95; DB 1; Length 1390;
Best Local Similarity 25.0%; Pred. No. 37;
Matches 50; Conservative 39; Mismatches 65; Indels 46; Gaps 12;

Qy 5 LKAGDNLKIKQFTYSLYKLDLTDSVG-TEKLSFANGKNVNTSDTKGLNFAKETA-- 61
Db 413 LKDG-KLLKKGKLLKKEIDKIKQAANKNEISFV---NRMQLTDCGKAVDLAKESLFYE 468
Qy 62 -----TNGDITVHLNIG-----STLDRAASVDLVNAGNNIKGVKNVDFVRT 105
Db 469 TIDVYITNDNLNSVSPVIGIHNNENLKNAMTLSDFTIASISVINLPYGI-----GK 519
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 09:13:10 ; Search time 14.7627 Seconds
(without alignments)
3513.485 Million cell updates/sec

Title: US-09-771-382-39
Perfect score: 1018
Sequence: 1 SANTLKAGDNLKIKOFTYSL.....AGWRKMTTANGOTGQADRF 201

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_prodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	957.5	94.1	591	2 Q93QY3	Q93QY3 neisseria m
2	957.5	94.1	591	2 Q9JPS7	Q9JPS7 neisseria m
3	957.5	94.1	591	16 Q9JRI8	Q9JRI8 neisseria m
4	953.5	93.7	592	2 Q9AQF0	Q9AQF0 neisseria m
5	947.5	93.1	590	2 Q9JPS3	Q9JPS3 neisseria m
6	936.5	92.0	594	2 Q9JPI3	Q9JPI3 neisseria m
7	936.5	92.0	594	2 Q9JPS2	Q9JPS2 neisseria m
8	931.5	91.5	595	2 Q9JPH0	Q9JPH0 neisseria m
9	929.5	91.3	599	2 Q9JPS8	Q9JPS8 neisseria m
10	928.5	91.2	600	2 Q9JPS6	Q9JPS6 neisseria m
11	925.5	90.9	526	2 Q9JPS4	Q9JPS4 neisseria m
12	925.5	90.9	598	2 Q9JPT0	Q9JPT0 neisseria m
13	925.5	90.9	598	2 Q9JPT0	Q9JPT0 neisseria m
14	925.5	90.9	599	2 Q9JPS8	Q9JPS8 neisseria m
15	923.5	90.7	530	2 Q9JPS1	Q9JPS1 neisseria m
16	923.5	90.7	594	2 Q9JPH7	Q9JPH7 neisseria m

17	923.5	90.7	598	2 Q9JPR7	Q9JPR7 neisseria m
18	922.5	90.6	594	2 Q93QY4	Q93QY4 neisseria m
19	921.5	90.5	598	2 Q9JPR9	Q9JPR9 neisseria m
20	921.5	90.5	598	2 Q9JPS0	Q9JPS0 neisseria m
21	918.5	90.2	589	2 Q93QY1	Q93QY1 neisseria m
22	918.5	90.2	589	2 Q9JPI0	Q9JPI0 neisseria m
23	907.5	89.1	592	2 Q9JPS9	Q9JPS9 neisseria m
24	907.5	89.1	592	2 Q93QY2	Q93QY2 neisseria m
25	903.5	88.8	592	16 Q9JOW4	Q9JOW4 neisseria m
26	895.5	88.0	600	2 Q9JPS5	Q9JPS5 neisseria m
27	622.5	61.1	2353	2 P71401	P71401 haemophilus
28	618	60.7	1098	2 Q48152	Q48152 haemophilus
29	615.5	60.5	1096	2 Q8GM79	Q8GM79 haemophilus
30	595	58.4	1210	2 Q8GM75	Q8GM75 haemophilus
31	594	58.3	1210	2 Q8GM74	Q8GM74 haemophilus
32	570	56.0	1204	2 Q8GM76	Q8GM76 haemophilus
33	324	31.8	1002	2 Q8GM78	Q8GM78 haemophilus
34	322	31.6	1004	2 Q8GM77	Q8GM77 haemophilus
35	203.5	20.0	2314	2 Q8KOM8	Q8KOM8 moraxella c
36	199	19.5	1964	2 Q8KOM9	Q8KOM9 moraxella c
37	157.5	15.5	1264	2 Q8RO61	Q8RO61 actinobacil
38	123.5	12.1	1633	16 Q8CMP4	Q8CMP4 staphylococ
39	123.5	12.1	1733	2 Q9KI14	Q9KI14 staphylococ
40	122.5	12.0	588	2 Q9SOT6	Q9SOT6 escherichia
41	122	12.0	2712	16 Q9FX5	Q9FX5 pasteurella
42	118	11.6	507	2 Q53821	Q53821 salmonella
43	118	11.6	507	2 Q54415	Q54415 salmonella
44	116.5	11.4	1557	2 Q9RNI2	Q9RNI2 haemophilus
45	116	11.4	508	2 Q54515	Q54515 salmonella

ALIGNMENTS

RESULT 1

Q93QY3	PRELIMINARY;	PRT;	591 AA.
ID	Q93QY3		
AC	Q93QY3;		
DC	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)		
DE	NhaA outer membrane protein.		
GN	NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;		
OC	Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BG329;		
RA	Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RL	membrane protein of Neisseria meningitidis.";		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF157606; AAK68867.1; -		
DR	InterPro; IPR005594; Yada.		
DR	Pfam; PF03895; Yada; 1.		
SQ	SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;		
Query Match 94.1%; Score 957.5; DB 2; Length 591;			
Best Local Similarity 85.7%; Pred. No. 4.6e-48;			
Matches 198; Conservative 0; Mismatches 0; Indels 33; Gaps 3;			
QY	4 TLKAGNLKTKO----FTYSLKKDLTDLTSVGTEKLSFSGANGKVNITSDTKGLNPAKET 59		
DB	109 TLKAGNLKTKQNGTFTYSLKKDLTDLTSVGTEKLSFSGANGKVNITSDTKGLNPAKET 168		
QY	60 AGTNGDGTVHLNGIGSTLTD-----RAASVKDVLNAGWNKGV 97		
DB	169 AGTNGDGTVHLNGIGSTLTDLLTNGATTTVNDVTDDEKKRAASVKDVLNAGWNKGV 228		
QY	98 K-----NVDFVRYTDTVEFLSADTKTKTTTVNYESKDKGKTEVIGAKTSVTKEDGKL 150		


```

ID Q9AQF0 PRELIMINARY; PRT; 592 AA.
AC Q9AQF0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikantha Y., Dieckelmann M., Moxon E.R., Jennings M.P.;
RT "Identification and characterisation of a gene encoding a novel outer
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 93.7%; Score 953.5; DB 2; Length 592;
Best Local Similarity 85.3%; Pred. No. 7.9e-48;
Matches 197; Conservative 0; Mismatches 1; Indels 33; Gaps 3;

Qy 4 TLKAGDNLKIKQ-----FTYSLKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGLNFAKET 59
Dd 110 TLKAGDNLKIKQNGTNTYSLKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGLNFAKET 169
Qy 60 AGTNGDVTVHLNGIGSTLTD-----RAASKVDVLNAGWNKGV 97
Dd 170 AGTNGDVTVHLNGIGSTLTDLLNTGATNTVNDVDDKKRAASKVDVLNAGWNKGV 229
Qy 98 K-----NVDFTYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDGKL 150
Dd 230 KPGTTASDNVDVFTYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDGKL 289
Qy 151 VTGKDKGSGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKF 201
Dd 290 VTGKDKGSGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKF 340

RESULT 5
Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 62086 MW; 1B25E03B9D0D4B46 CRC64;

Query Match 92.0%; Score 936.5; DB 2; Length 594;
Best Local Similarity 82.3%; Pred. No. 7.7e-47;
Matches 195; Conservative 0; Mismatches 3; Indels 39; Gaps 3;

Qy 4 TLKAGDNLKIKQ-----FTYSLKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGL 53
Dd 105 TLKAGDNLKIKQNTDENTNASSFTYSLKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGL 164
Qy 54 NFAKETAGTNGDVTVHLNGIGSTLTD-----RAASKVDVLNAG 91
Dd 165 NFAKETAGTNGDVTVHLNGIGSTLTDLLNTGATNTVNDVDDKKRAASKVDVLNAG 224
Qy 92 WNKGKVK-----NVDFRTYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIR 144
Dd 225 WNKGKVKPTTASDNVDVFTYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIR 284
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DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 93.1%; Score 947.5; DB 2; Length 590;
Best Local Similarity 84.8%; Pred. No. 1.8e-47;
Matches 196; Conservative 1; Mismatches 1; Indels 33; Gaps 3;

Qy 4 TLKAGDNLKIKQ-----FTYSLKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGLNFAKET 59
Dd 107 TLKAGDNLKIKQNGTNTYSLKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGLNFAKET 166
Qy 60 AGTNGDVTVHLNGIGSTLTD-----RAASKVDVLNAGWNKGV 97
Dd 167 AGTNGDVTVHLNGIGSTLTDLLNTGATNTVNDVDDKKRAASKVDVLNAGWNKGV 226
Qy 98 K-----NVDFTYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDGKL 150
Dd 227 KPGTTASDNVDVFTYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIREKDGKL 286
Qy 151 VTGKDKGSGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKF 201
Dd 287 VTGKDKGSGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKF 337

RESULT 6
Q9JPI3 PRELIMINARY; PRT; 594 AA.
AC Q9JPI3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, and BZ232;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D0D4B46 CRC64;

Query Match 92.0%; Score 936.5; DB 2; Length 594;
Best Local Similarity 82.3%; Pred. No. 7.7e-47;
Matches 195; Conservative 0; Mismatches 3; Indels 39; Gaps 3;

Qy 4 TLKAGDNLKIKQ-----FTYSLKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGL 53
Dd 105 TLKAGDNLKIKQNTDENTNASSFTYSLKDLTDLTSVGTSEKLSFSGANGKVNITSDTKGL 164
Qy 54 NFAKETAGTNGDVTVHLNGIGSTLTD-----RAASKVDVLNAG 91
Dd 165 NFAKETAGTNGDVTVHLNGIGSTLTDLLNTGATNTVNDVDDKKRAASKVDVLNAG 224
Qy 92 WNKGKVK-----NVDFRTYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIR 144
Dd 225 WNKGKVKPTTASDNVDVFTYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIR 284
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QY 145 EKDGKLVTKGDKGKNGSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKF 201
Db 285 EKDGKLVTKGDKGKNGSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKF 341

RESULT 7
Q9JPS2
ID Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226360; AAF42509.1; -.
DR EMBL; AF226356; AAF42505.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 92.0%; Score 936.5; DB 2; Length 594;
Best Local Similarity 82.3%; Pred. No. 7.7e-47;
Matches 195; Conservative 0; Mismatches 3; Indels 39; Gaps 3;

QY 4 TLKAGDNLKIKQ-----FTYSLKKDLTSLVGTSEKLSFSAANGKVNITSDTKGL 53
Db 105 TLKAGDNLKIKQ-----FTYSLKKDLTSLVGTSEKLSFSAANGKVNITSDTKGL 164
QY 54 NFAKETAGTNGDITVHLNGIGSTLTD-----RAASVKDVLNAG 91
Db 165 NFAKETAGTNGDITVHLNGIGSTLTDLLNTGATTNVTNDVDEKKRAASVKDVLNAG 224
QY 92 WNIKGVK-----NVDFVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIK 144
Db 225 WNIKGVKPGTTASDNVDVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIK 284
QY 145 EKDGKLVTKGDKGKNGSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKF 201
Db 285 EKDGKLVTKGDKGKNGSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKF 341

RESULT 8
Q9JPH0
ID Q9JPH0 PRELIMINARY; PRT; 595 AA.
AC Q9JPH0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226379; AAF42528.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 92.3%; Score 936.5; DB 2; Length 594;
Best Local Similarity 82.3%; Pred. No. 7.7e-47;
Matches 195; Conservative 0; Mismatches 3; Indels 39; Gaps 3;

QY 4 TLKAGDNLKIKQ-----FTYSLKKDLTSLVGTSEKLSFSAANGKVNITSDTKGL 53
Db 105 TLKAGDNLKIKQ-----FTYSLKKDLTSLVGTSEKLSFSAANGKVNITSDTKGL 164
QY 54 NFAKETAGTNGDITVHLNGIGSTLTD-----RAASVKDVLNAG 91
Db 165 NFAKETAGTNGDITVHLNGIGSTLTDLLNTGATTNVTNDVDEKKRAASVKDVLNAG 224
QY 92 WNIKGVK-----NVDFVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIK 144
Db 225 WNIKGVKPGTTASDNVDVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIK 284
QY 145 EKDGKLVTKGDKGKNGSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKF 201
Db 285 EKDGKLVTKGDKGKNGSGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKF 341

RESULT 9
Q9JPS8
ID Q9JPS8 PRELIMINARY; PRT; 599 AA.
AC Q9JPS8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A22;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226364; AAF42513.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 91.3%; Score 929.5; DB 2; Length 599;
Best Local Similarity 80.1%; Pred. No. 2e-46;
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Matches 193; Conservative 2; Mismatches 3; Indels 43; Gaps 3;
Qy 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFANGKVNITSD 49
Db |||||
106 TLKAGDNLKIKQNTDENTNASSFTYSLKKDLTDLTSVETEKLSEFGANGKVNITSD 165
Qy 50 TKGLNFAKETAGTNGDTTVHLNGIGSLTLD-----RAASVKDVLN 89
Db |||||
166 TKGLNFAKETAGTNGDTTVHLNGIGSLTLDPLAGSSASHVDAGNQSTHYTRAASIKDVLN 225
Qy 90 AGWNIKGVK-----NVDFVRYDTVEFLSADTKTTTVNVEKSKNGKKEVKGAKT 140
Db |||||
226 AGWNIKGVKSTGQSENVDFVRYDTVEFLSADTKTTTVNVEKSKNGKRTVEKIGAKT 285
Qy 141 SVIKEKDKLVTKGDKGSGSSTDEGGLVTAKEVIDAVNKGAGWRMKTTTTANGOTGQADK 200
Db |||||
286 SVIKEKDKLVTKGDKGSGSSTDEGGLVTAKEVIDAVNKGAGWRMKTTTTANGOTGQADK 345
Qy 201 F 201
Db 346 F 346

RESULT 10
Q9JPS6 PRELIMINARY; PRT; 600 AA.
ID AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N65/88;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226371; AAF42520.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 600 AA; 62762 MW; 36255963E0598CD1 CRC64;

Query Match 91.2%; Score 928.5; DB 2; Length 600;
Best Local Similarity 81.4%; Pred. No. 2.3e-46;
Matches 193; Conservative 1; Mismatches 4; Indels 39; Gaps 3;
Qy 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFANGKVNITSDTKGL 53
Db |||||
112 TLKAGDNLKIKQNTDENTNASSFTYSLKKDLTDLTSVETEKLSEFGANGKVNITSDTKGL 171
Qy 54 NFAKETAGTNGDTTVHLNGIGSLTLD-----RAASVKDVLNAG 91
Db |||||
172 NFAKETAGTNGDTTVHLNGIGSLTLDLLNTGATNTVNDVDEKKRAASVKDVLNAG 231
Qy 92 WNIKGVK-----NVDFVRYDTVEFLSADTKTTTVNVEKSKNGKKEVKGAKTSVIK 144
Db |||||
232 WNIKGVKPGTASDNVDFVHTYDTVEFLSADTKTTTVNVEKSKNGKKEVKGAKTSVIK 291
Qy 145 EKDGKLVTKGDKGSGSSTDEGGLVTAKEVIDAVNKGAGWRMKTTTTANGOTGQADK 201
Db |||||
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Db 292 EKDGKLVTKGDKGSGSSTDEGGLVTAKEVIDAVNKGAGWRMKTTTTANGQGOADK 348

RESULT 11
Q9JPS4 PRELIMINARY; PRT; 526 AA.
ID AC Q9JPS4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Outer membrane protein GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N65/88;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226371; AAF42526.1; -.
DR InterPro; IPR005594; Yada.
DR Pfam; PF03895; Yada; 1.
SQ SEQUENCE 526 AA; 54732 MW; F543C4234AF807CA CRC64;

Query Match 90.9%; Score 925.5; DB 2; Length 526;
Best Local Similarity 80.1%; Pred. No. 2.9e-46;
Matches 193; Conservative 1; Mismatches 4; Indels 43; Gaps 3;
Qy 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFANGKVNITSD 49
Db |||||
34 TLKAGDNLKIKQNTNKNNTNNDSSFTYSLKKDLTDLTSVETEKLSEFGANGKVNITSD 93
Qy 50 TKGLNFAKETAGTNGDTTVHLNGIGSLTLD-----RAASVKDV 87
Db |||||
94 TKGLNFAKETAGTNGDTTVHLNGIGSLTLDLLNTGATNTVNDVDDKKRAASVKDV 153
Qy 88 LNAWNKIGVK-----NVDFVRYDTVEFLSADTKTTTVNVEKSKNGKKEVKGAKT 140
Db |||||
154 LNAWNKIGVKPGTASDNVDFVHTYDTVEFLSADTKTTTVNVEKSKNGKRTVEKIGAKT 213
Qy 141 SVIKEKDKLVTKGDKGSGSSTDEGGLVTAKEVIDAVNKGAGWRMKTTTTANGOTGQADK 200
Db |||||
214 SVIKEKDKLVTKGDKGSGSSTDEGGLVTAKEVIDAVNKGAGWRMKTTTTANGOTGQADK 273
Qy 201 F 201
Db 274 F 274

RESULT 12
Q93QY5 PRELIMINARY; PRT; 598 AA.
ID AC Q93QY5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NHA outer membrane protein.
GN NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
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RN RP SEQUENCE FROM N.A.
RC STRAIN=B210;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RL membrane protein of Neisseria meningitidis.";
DR Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157603; AAK68864.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 598 AA; 62687 MW; 18CEFF66410A15DF CRC64;

Query Match
Best Local Similarity 90.9%; Score 925.5; DB 2; Length 598;
Matches 194; Conservative 1; Mismatches 5; Indels 43; Gaps 3;

QY 2 ANTLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSGANGKVNIT 47
DB 103 AITLKAGDNLKIKQNTNENTNDSSFTYSLKKDLTDLTSVETSEKLSFGANGKVNIT 162
QY 48 SDTKGLNFAKETAGTNGDPTVHLNGIGSTLTD-----RAASVK 85
DB 163 SDTKGLNFAKETAGTNGDPTVHLNGIGSTLTD-----RAASVK 222
QY 86 DVLNAGWNKGVK-----NVDFVRYDTVEFLSADTKTTTVNVESKDKGKTEVKIGA 138
DB 223 DVLNAGWNKGVKPGTTASDNDVRYDTVEFLSADTKTTTVNVESKDKGKTEVKIGA 282
QY 139 KTSVKEKDKGLVTGCKGKENGSSDDEGGLVTAKEVIDAVNKAGWRMKTTFANGOTGOA 198
DB 283 KTSVKEKDKGLVTGCKGKENGSSDDEGGLVTAKEVIDAVNKAGWRMKTTFANGOTGOA 342
QY 199 DKF 201
DB 343 DKF 345

RESULT 14
Q9JPR8 PRELIMINARY; PRT; 599 AA.
ID Q9JPR8
AC Q9JPR8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Outer membrane protein GNA992 (NhaA outer membrane protein).
GN GNA992 OR NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -
DR EMBL: AF157608; AAK68869.1; -
DR InterPro: IPR005594; Yada.
DR Pfam: PF03895; Yada; 1.
SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match
Best Local Similarity 90.9%; Score 925.5; DB 2; Length 599;
Matches 193; Conservative 1; Mismatches 4; Indels 43; Gaps 3;

QY 4 TLKAGDNLKIKQ-----FTYSLKKDLTDLTSVGTSEKLSFSGANGKVNITSD 49
DB 106 TLKAGDNLKIKQNTNENTNDSSFTYSLKKDLTDLTSVETSEKLSFGANGKVNITSD 165
QY 50 TKGLNFAKETAGTNGDPTVHLNGIGSTLTD-----RAASVKDV 87
DB 166 TKGLNFAKETAGTNGDPTVHLNGIGSTLTD-----RAASVKDV 225
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